1000年の一年の

ļ

us-09-824-647-16.std.rag

```
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
```

OM nucleic - pr	OM nucleic - protein search, using frame_plus_n2p model
Run on:	July 7, 2003, 15:47:40 ; Search time 109 Seconds (without alignments) 5122.203 Million cell updates/sec
Title: Perfect score: Sequence:	US-09-824-647-16 694 .l cgcaggcagaccatgtggacataaagtttgtcactttctt 2095
Scoring table:	OLIGO Mgapop 60.0 , Mgapext 60.0 Fgapop 60.0 , Fgapext 60.0 Fgapop 6.0 , Fgapext 7.0 Delop 6.0 , Delext 7.0
Searched:	908470 seqs, 133250620 residues
Word size:	
Total number of	Total number of hits satisfying chosen parameters: 1687582

Post-processing: Listing first 45 summaries

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Command line parameters: -MODEL-frame+_n2p.model -DEV-x1p	-Q=/cgn2_1/USPTO_spool/US09824647/runat_07072003_154717_26015/app_query.fasta_1.2247	"DB="Cenesed_tolog" "Wrm!=rastan "SUrriA=sta.rag" "MinMATCH=U.1 "LOOPCL=U -LOOPEXT-0 "UNITS-bits "START-1 "END=-1 "MATRIX=Oligo "TRANS-human40.cd1	-LIST-45 -DOCALIGN-200 -THR_SCORE-quality -THR_MIN-1 -ALIGN-45 -MODE-LOCAL -OTTFWT-nto -NORM-ext -HEADSTZE-500 -MINIEW-0 -MAXIEW-200000000	-USER-US09824647_@CGN_1_1_149_@runat_07072003_154717_26015 -NCPU-6 -ICPU-3	-NO_MMAP -LARGEQUERY -NEG_SCORES-0 -WAIT -DSPBLOCK=100 -LONGLOG .	-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6	-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7	Database : A_Geneseq_101002:*	1: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*	2: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*	3: /SIDS2/gcgdata/geneseg/genesegp-embl/AA1982.DAT:*
--	--	---	---	--	---	---	--	-------------------------------	--	--	--

A_Geneseq_101002:* 1: /SIDS2/gcgdata/ger 2: /SIDS2/gcgdata/ger 4: /SIDS2/gcgdata/ger 5: /SIDS2/gcgdata/ger 6: /SIDS2/gcgdata/ger 7: /SIDS2/gcgdata/ger 8: /SIDS2/gcgdata/ger 8: /SIDS2/gcgdata/ger 9: /SIDS2/gcgdata/ger 11: /SIDS2/gcgdata/ger 12: /SIDS2/gcgdata/ger 13: /SIDS2/gcgdata/ger 14: /SIDS2/gcgdata/ger 15: /SIDS2/gcgdata/ger 16: /SIDS2/gcgdata/ger 17: /SIDS2/gcgdata/ger 18: /SIDS2/g		<pre>nneseq_101002:* /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:* /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*</pre>	/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:* /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*	/slubs/dyddata/geneseq/geneseq=embl/AA1985.DAT:* /SIDS2/grgdata/geneseq/geneseqp-embl/AA1985.DAT:* /SIDS2/grgdata/geneseq/geneseqp-embl/AA1985.DAT:*	/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:* /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1988.DAT:* /SIDS2/gcgdata/geneseq/aenseqp-embl/AA1988.DAT:*	/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:*	/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1992.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1993.DAT:*	/SIDS2/gcgdata/geneseg/genesegp-emb1/AA1994.DAT:* /SIDS2/gcgdata/geneseg/genesegp-emb1/AA1995.DAT:* /SIDS2/gcgdata/deneseg/aenesegp-emb1/AA1995.DAT:*	/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1997.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT:*	/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:* /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:* /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:* //SIDS2/gcgdata/geneseqf/geneseqp-embl/AA2001.DAT:*
--	---------	--	---	--	--	--	--	---	--	---

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Human GP88 autocri		Human granutin/epi	epithe		ain e	(24)	m ı	Granulin D. Homo	ain e	굡	c	receptor	Insulin receptor-r			Ω	epit		Mouse granuin/epi	ç	. 5	Rat granulin. Rat	in A-	Human granulin-A d		Human GP88 autocri	-	Basophil granule p	N-terminal amino a	Rat secreted facto	n beta 1	Human ORFX protein	Human musculoskele	onibact	human	novel proc	Human novel protei	
SUMMARIES	, ,	AAR48673	AAE20521	חת	AAB94550	AAM59508	AAR41886	AAR41880	AAR41882	AAM59509	AAR41885	AAR41887	ABB07323	ABB0/324	ABB07327	ABB07326	AAR14325	AAR14327	AAW85474	AAE20520	AAR4 18/3	AAW85480	AAR41883	AAU82636	AAU82638	AAR13420	AAW85481	AAR20737	AAR51665	AAR350/8	AAU70166	AAW03586	ABP04295	ABB03646	AAU42545	2:	450	ABB1/430 AAU14219	ALIGNMENTS
DB	202	3 14	~ -	-1 cm		7	7	ن ص	.n <														2	7	۲,	א ה	1 4	-	Н,	٦ ,		9	8	0	4	4		55 57 90	
Length	59	200												75	1											-		П	н,		. 4							א ס	
% Query Watch	85.4	. 77.5		n œ		ö	œ.	•	۲,			• .		۷. c		•	4.6	•	٠	٠					6.0	•		•	1.6		7.7			•	1.2	1.2	1.2	7.7	
7. 0.20	1	538	492	410	155	75	57	26	52	4 6	34	35	32	32	3 2	32	32	32	32	32	30	9 6	17	16	19	0 F	14	11	11	ס ס	0 00	ω	8	80	æ	æ (30 (20 00	
Result	-	7	m •	4 r.	9	7	80	6	10	c 12	-	14	15	14	18	19	20	21	22	23	7 C	26	27	28	29	30	1 C	33	34	יי ריי	37	· m	39	40	c 41	42	4.	4 4	

GP88; granulin; epithilin; human; growth factor; autocrine; tumour; cancer; viral infection; antagonist; therapy; diagnosis. Location/Qualifiers 340..364 /note= "E19V peptide used to raise antibody" 566..579 Homo sapiens. Key Peptide Peptide

CACTECAGTGCAGAGGGGGATCCTGCTTCCAAAGATCAGGTAACAA	101 ArgClyPheHisCysSerAlaAspClyArgSerCysPheGlnArgSerGlyAsnAsnSer 12	GTGGGTGCCATCCAGTGCCCTGATAGTCAGTTCGAATGCCCGGACTTC	Db 121 ValGlyAlaileGlnCySProAspSerGlnPheGluCySProAspPheSerThrCySCys 140	Oy 433 GTTATGGTCGATGGCTCCTGGGGGTGCTGCCCCAGGCTTCCTGCTGTGAAGAC 492	493 AGGGTGCACTGCTGTCCGCACGGTCCTTCTGCGACCTGGTTCACACCCGCTGCATCACA 55	Db 161 ArgvalHisCysCysProHisGlyAlaPheCysAspLeuvalHisThrArgCysIleThr 180	61	181 ProthrGlythrHisProLeuAlaLysLysLeuProAlaGlnArgThrAsnArgAlaVal 20	OY 613 GCCTTGTCCAGGTCGGTCATGTGTCCGGACGACGGTCCCGGTGCCCTGATGGTTCTACC 672	Oy 673 TGCTGTGAGCTGCCCAGTGGGAAGTATGGCTGCTGCTGCTGCTGC 732	Qy 733 TCCGATCACCTGCTGCCCCCAAGACACTGTGTGTGACCTGATCCAGAGTAAGTGC 792 [111111111111111111111111111111111111	Oy 793 CTCTCCAAGGAGAACGCTACCACGGACCTCCTCACTAAGCTGCGCACACAGGGGG 852	Qy 853 GATGTGAAATGTGACATGGAGGTGAGCTGCCCAGATGGCTATACCTGCTGCTGTCTACAG 912	Qy 913 TCGGGGCCTGGGGCTGCTGCTTTTACCCAGCTGTGGCTGTGAGGACCACATACAC 972	973 TGCTGTCCCGCGGGGTTTACGTGACACGCAGAAGGGTACCTGTGAACAGGGCCCCAC 10	Qy 1033 CAGGTGCCCTGGATGGAGAGCCCCAGCTCACCTCAGCCTGCCAGACCCACAGCCTTG 1092	ATGICCCTGTGATAATGICACAG 	Qy 1153 CTCACGTCTGGGGGTGGGGCTGCTGTCCAATCCCAGAGGCTGTCTGCTGCTGCTGCACAC 1212	Oy 1213 CAGCACTGCTGCCCCAGCGATACACGTGTAGCTGAGGGGCAGTGTCAGCGAGGAAGC 1272	Qy 1273 GAGATCGTGGGTGGACTGGAGAAGATGCCTGCCCGCGGGGTTCCTTATCCCACCCGAGA 1332	Qy 1333 GACATCGGCTGTGACAGCACAGCTGCCCGGTGGGCGGAACCTGCTGCCCGAGCCAG 1392
PP /notes "aldR nentide used to raise antibody"	WO9852607-A1.	XX PD 26-NOV-1998.	XX PF 22-MAY-1998; 98WO-US10555.	AA 16-DEC-1997; 97US-0991862. PR 23-MAY-1997; 97US-0863079. XX	(SERR/)		DK N-PSDB; AAV82825. XX		PT from altered GP88 expression XX PS Example 5; Fig 9A; 86pp; English.	This is the amino acid sequence of human GP88, an 88 kDa glycoprotein autocrine growth factor and epithilin/granulin precursor that is expressed in a tightly regulated manner in norm	cells, is overexpressed and unregulated in high derived from normal cells, and which acts as a growth stimulator for the tumorigenic cells. It expression or action in the tumorigenic cells ri			XX Sequence 593 AA;	0 Length: 593.00 Matches: 100.003 Conservative:	Dest Local Similarity: 100.00* Mishacines: 0 Query Match: 85.45% Indels: 0 DB: 20 Gaps: 0	US-09-824-647-16 (1-2095) x AANB5475 (1-593) QY 13 ATGIGGACCCTGGTGACGTGGCTGGTGGCTGGCTGGCTGGAACGCGGTGC 72	73 CCAGATGGTCAGTTCTGCCCTGTGCCTGCTGCCTGGACCCGGAGGAGCCAGCTACAGC 1	133 TGCTGCCGTCCCTTCTGGACAAATGCCCACAACACTGAGCAGCATCTGGGTGCCCC 1	193 TGCAGGTGATGCCCACTGCTGCCGCCACTGCATTACCGTCTAGGGACT 2	253 TCCAGTTGCTGCCCCTTCCCAGAGGCCGTGGCATGCGGGATGGCCATCACTGCTGCCCA 3

STATE AND THE

ignment Scor ed. No.: ore: rcent Simila st Local Sim ery Match: -09-824-647-	4 1 9 8	31. 100 37.	Oy 373 GTGGGTGCCATCCAGTGCCCTGATAGTCAGTTCGAATGCCCGGACTTCTCCACGTGCTGT 432 121 ValG1yAla11eGlnCysProAspSerGlnPheGluCysProAspPheSerThrCysCys 140 Qy 433 GTTATGGTCGATGGCTCCTGGGGGTGCTGCCCCATGCCCAGGCTTCTCTGTGAAGAC 495 141 ValMetValAspG1ySerTrpG1yCysCysProMetProGlnAlaSerCysCysG1uAsp 160		Qy 613 GCCTTGTCCAGCTCAGCTCAGGACGCACCGGTCCCGGTGCCCTGATGTTCTACC 67: D 111111111111111111111111111111111111	Qy 733 TCCGATCACCTGCACTGCTGCCCCCAAGACACTGTGTGTG	Qy 853 GATGTGAAATGTGACATGGAGGTGAGCTGCCCACATGCTATACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG
	Qy 1633 TGGGCCTGCTGCCCAGGGCGTCTGTTGTGCTGATCGGCGCCACTGCTGTCCT 1692 bb 111111111111111111111111111111111111	Db 581 AspAlaProLeuArgAspProAlaLeuArgGlnLeuLeu 593 RESULT 2 AAR48673 ID AAR48673 standard; Protein; 593 AA. XX AC AAR48673; XX	Granulin sequence. Granulin; keratinocy granulocytes; leucoc	KK Key Location/Qualifiers FT Misc-difference 452 FT Misc-difference 539 FT Mote- "Glycine encoded by ATG." XX XX XX XX XX XX XX	PD 05-AUG-1993. XX XX XX XX XX XX XX XX PR 03-FEB-1992; 92US-0829233. XX XX PA (SOLO/) SOLOMON S.	XX XX XX XX DR WPI; 1993-320328/40. DR WPI; 1993-320328/40. XX XX YF New cystine rich granulin peptide(s) from leucocyte(s) - are PT keratinocyte inhibitors useful topically for wound healing	XX PS Disclosure; Figure 4c; 53pp; English. XX CC The granulin inhibits keratinocytes and is useful in formulations CC for promoting the healing of wounds. XX XX SQ Sequence 593 AA;

```
SERRERO
                                                                                                                                                                                                                                       Percent Similarity:
23-MAY-1997;
08-DEC-1999;
                                                                                                                                                                                                                     Alignment Scores:
                               ΰ
                                                                                                                                                                                                                                                                                                                                                                                                               313
                                                                                                                                                                                                                                                                                   13
                                                                                                                                                                                                                                                                                                                                    133
                                                                                                                                                                                                                                                                                                                                                41
                                                                                                                                                                                                                                                                                                                                                             193
                                                                                                                                                                                                                                                                                                                                                                                     253
                                                                                                                                                                                                                                                                                                                                                                                                  81
                                                                                                                                                                                                                                                                                                                                                                                                                           101
                                                                                                                                                                                                                                                                                                                                                                                                                                        373
                                                                                                                                                                                                                                                                                                                                                                                                                                                    121
                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 433
                                                                                                                                                                                            protein.
                   (SERR/)
                                Serrero
                                                                                                                                                                                                                                  Score:
                                                                                                                                                                                                                            Pred.
ò
                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                            ð
                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                    å
                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                             ğ
                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ó
                                                        1152
                                                                                1212
     1092
                                                                                                                                                            GACATCGGCTGTGACCACACACCAGCTGCCCGGTGGGCGGAACCTGCTGCCCGAGCCAG 1392
                                                                                                                                                                                                                                      TCTGCCCAGCCTGCCACCTTCCTGGCCCGTAGCCCTCACGTGGGTGTGAAGGACGTGGAG 1572
                                                                                                          CAGCACTGCTGCCCCCAGCGATACACGTGTGTAGCTGAGGGGCCAGTGTCAGCGAGGAAGC 1272
                                                                                                                                   1332
                                                                                                                                                                                    GGTGGGAGCTGGCCTGCTGCCAGTTGCCCGTGTGTGCTGCTGCGAGGATCGCCAGCAC 1452
                                                                                                                                                                                                              380
                                                                                            400
                                                                                                                      420
                                                                                                                                                440
                                                                                                                                                                  500
                                                                                                                                                                                                                                                                                                                                                      precursor; GP88; cytostatic; tumourigenicity; tamoxifen; antioestrogen therapy; skin cancer.
                                                             CAGGTGCCCTGGATGGAGAGGCCCCCAGCTCACCTCCTGCCAGACCCACAAGCCTTG
                                                       CTCACGTCTGGGGGGTGGGGCTGTCCAATCCCAGAGGCTGTCTGCTGCTCGGACCAC
                                                                                                                GINHISCYSCYSPACGINATGTYTTATCYSVALALAGLUGLYGINCYSGLDATGGLYSSET
                                                                                                                                   GAGATCGTGGCTGGACTGGAGAAGATGCCTGCCCGCGGGTTCCTTATCCCACCCCAGA
                                                                                                                                                                                                                    = "Region used as antigen to develop anti-human neutralising antibody"
                                                                                                                                                                                                                                                               TGTGGGGAAGGACACTTCTGCCATGATAACCAGACCTGCTGCCGAGACAACCGA 1626
                                                                                                                                                                                                                                                                     Human granulin/epithelin precursor (GP88) protein
                                                                                                                                                                                                                                                                                                                                                                                            /note= "Encoded by AAG"
                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
273
                                                                                                                                                                                                                                                                                                     Ź
                                                                                                                                                                                                                                                                                                    AAE20521 standard; Protein; 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JUN-2001; 2001US-0880842
                                                                                                                                                                                                                                                                                                                              entry)
                                                                                                                                                                                                                                                                                                                                                                                                               /note-
                                                                                                                                                                                                                                                                                                                                                                                                                     GP88
                                                                                                                                                                                                                                                                                                                                                                                     Key
Misc-difference
                                                                                                                                                                                                                                                                                                                                                      Human; granulinantineoplastic;
                                                                                                                                                                                                                                                                                                                                                                                                                                US2002025543-A1
                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                             01-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                             28-FEB-2002
                              033
                                          341
                                                      660
                                                                   361
                                                                                1153
                                                                                            381
                                                                                                         1213
                                                                                                                                  1273
                                                                                                                                                           1333
                                                                                                                                                                                    1393
                                                                                                                                                                                                             1453
                                                                                                                                                                                                                                       1513
                                                                                                                                                                                                                                                               1573
      973
                  321
                                                                                                                                              421
                                                                                                                                                                                                 461
                                                                                                                                                                                                                         481
                                                                                                                                                                                                                                                  501
                                                                                                                     401
                                                                                                                                                                                                                                                                           521
                                                                                                                                                                                                                                                                                                                 AAE20521;
                                                                                                                                                                                                                                                                                                                                                                                                        Region
                                                                                                                                                                                                                                                                                               AAE20521
                                                                                                                                                                                                                                                                                        RESULT
                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                       a
                                                                                                                                                                                    ò
                                                                                                                                                                                                8
                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                 ద
                셤
                                         셤
                                                                  g
                                                                                           a
                                                                                                                     셤
                                                                                                                                  à
                                                                                                                                                          ò
                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                              ò
      ò
                             ò
                                                      õ
                                                                               ò
                                                                                                         ð
```

```
The invention relates to a method for diagnosing tumourigenicity in a human. The method comprises obtaining a biological sample containing cells from the patient, detecting GPB8 in the cells of the sample, and determining the number of GPB8 positive cells in the sample, and determining the invention also relates to a method for determining if a human patient his resistant to the antineoplastic effects of antioestrogen therapy. The method is useful for diagnosing tumourigenicity in a sample, such as blood, serum, plasma, urine, nipple appraise, cerebrospinal fluid, liver, Kidney, breast, bone, brain, lung, colon, or skin cancer. The method can be used to treat or prevent re-eccurrence of cancer in a patient, by administering tamoxifen if the sample contains less than 10 % GPB8, or less than 5 % GPB8 positive cells. The present sequence is human granulin/epithelin precursor (GPB8)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               372
                                                                                                                                                                                                                                                                                                                                                                                                                                                 cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTTATGGTCGATGGCTCCTGGGGGTGCTGCCCCATGCCCCAGGCTTCCTGCTGTGAAGAC 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80
                                                                                                                                                                                                                                              GP88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGCTGCCGTCCCCTTCTGGACAAATGGCCCACAACACTGAGCAGGCATCTGGGTGGCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CysCysArgProLeuLeuAspLysTrpProThrThrLeuSerArgHisLeuGlyGlyPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATGTGGACCCTGGTGAGCTGGGTGGCCTTAACAGCAGGGCTGGTGGTGGAACGCGGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGCCAGGTTGATGCCCACTGCTCTGCCGGCCACTCCTGCATCTTTACCGTCTCAGGGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCCAGTTGCTGCCCCTTCCCAGAGGCCGTGGCGTGCGGGGATGGCCATCACTGCTGCCCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CGGGGCTTCCACTGCAGTGCAGACGGGCGATCCTGCTTCCAAAGATCAGGTAACAACTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTGGGTGCCATCCAGTGCCCTGATAGTCAGTTCGAATGCCCGGACTTCTCCACGTGCTGT
                                                                                                                                                                                                                                              of
                                                                                                                                                                                                                            cell
                                                                                                                                                                                                                Diagnosing tumorigenicity in a human, comprising obtaining a cel sample, detecting GPB8 in the cells, and determining the number positive cells in the sample –
                                                                                                                                              Ale:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-824-647-16 (1-2095) x AAE20521 (1-593)
                                                                                                                                                                                                                                                                                                               Disclosure; Fig 9B; 50pp; English
970S-0863079.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       492.00
99.83%
99.83%
70.89%
                                                                                                                                                       WPI; 2002-267529/31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ä
                                                                    Ġ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity:
Query Match:
                                                                                                                                                                              N-PSDB; AAD32850
```

TO STATE OF THE PARTY OF THE PA

۵	Db 141		qa —	П
о п	Qy 493 Db 161	AGGGTGCACCTGCTCCGCACGGTGCCTTCTGCGACCTGGTTCACACCCGCTGCATCACA 552	QV Db	
δο Q	Qy 553 Db 181	CCCACGGGCACCCACCCCTGGCAAAGAAGTCCCTGCCCAGAGGACTAACAGGCCAGTG 612 	do oy	
φ. Δ	Oy 613 Db 201	GCCTTGTCCAGCTCGGTCATGTCCGGACGCACGGTCCCGGTGCCCTGATGGTTCTACC 672 	do do	-
· O A	Oy 673	TGCTGTG CysCysG	А	1753 GACGCCCTTTGAGGGACCCR
	Oy 733 Db 241	TCCGATCA SerAspHi	RESULT AAB4397 ID AA XX	NT 4 3971 AAB43971 standard; Protein; 63
9 6	Oy 793 Db 261	CTCTCCAAGGAGAACGCTACCACGGACCTCCTCACTAAGCTGCGCACCACAGTGGGC 852 	XDX	AAB439/1; 08-FEB-2001 (first entry)
	Qy 853 Db 281	GATGTGAAATGTGACATGGAGGTGAGCTGCCCAGATGGCTATACCTGCCGTCTACAG 912 	K K K E	<pre>Human cancer associated protes Human; cancer associated gene; diagnosis; cytostatic; prolife</pre>
0 0	Qy 913 Db 301	TCGGGGGCCTGGGGCCCCTTTTACCCAGGCTGTGTGCTGTGAGGACCACATACAC 972	KW KW	antidiabetic; antiastmmatic; antialidiamatory; antilihyroid dermatological; neuroprotectid vasotropic; antipsoriatic; anti
φ·Δ	Qy 973 Db 321	TGCTGTCCCGGGGGTTTACGTGTGACACGCAGAAGGGTACCTGTGAACAGGGGCCCCAC 1032 	K K K K K	immune disorder; haemalopoied: allergic reaction; graft versi haemostatic; thrombolytic; can neurological disease; drug sci
0 0	Qy 1033 Db 341	CAGGTGCCCTGGATGGAGAAGGCCCCAGCTCCAGCCTGCCAGACCCAGAAGCCTTG 1092 	XX O XX	Homo sapiens. WO200055350-Al.
	Qy . 1093 Db 361	3 AAGAGAGATGTCCCCTGTGATAATGTCAGCAGCTGTCCCTCCGATACCTGCTGCCAA 1152 	X & X &	21-SEP-2000. 08-MAR-2000; 2000WO-US05882.
O 11	Oy 1153 Db 381	3 CTCACGTCTGGGGGTGGGGCTGCTGTCCAATCCCAGAGGCTGTCTGCTGCTGCTCGACCAC 1212	P.X. P.X.	12-MAR-1999; 99US-0124270. (HUMA-) HUMAN GENOME SCI INC.
5 0	Oy 1213 Db 401	3 CAGCACTGCTGCCCCCAGCGATACACGTGTAGCTGAGGGCAGTGTCAGCGAGGAAGC 1272 	XX PI XX DR	Rosen CA, Ruben SM: WPI; 2000-587533/55.
5 1	Qy 1273 Db 421	273 GAGATCGTGGACTGGAGAAGATGCCTGCCGCGCGGGTTCCTTATCCCACCCCAGA 1332 	XX XX	N-PSDB; AAC/8180. Novel isolated nucleic acids ouseful for treating or diagnos
<u> </u>	Oy 1333 OD 441	GACATCGGCTGTGACCAGCACCACCTGCCCGGTGGGCGGAACCTGCTGCCGGAGCCAG 1392 	S X S	Claim 11; Page 2094-2096; 235:
0 11	Oy 1393 Db 461	GGTGGGGGCCTGCTGCTGCTGCTGTGCTGTGCTGCGGAGGATCGCCAGCAC 1452 	88888	in AAA43398 to AAA44239. The tissues and cells the genes an include: cytostatic, prolifer antidiabetic; antiasthmatic;
5 1	Oy 1453 Db 481	TGCTGCCCGGCTGGCTACACCTGCAAGGCTCGATCCTGCGAGAAGGAGGTGGTC 1512 	3888	dentifications of the control of the
U ,	Qy 1513	TCTGCCCAGCCTGCCACCTTCCTGGCCCGTAGCCCTCACGTGGGTGTGAAGGACGTGGAG 1572	888	amellorating medical condition Polynucleotides, polypeptides the present invention may be

```
of to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or inhibiting the proliferation, differentiation or mobilisation of immune cells, to treat disorders of haematopoietic cells, autoimmune disorders, allergic reactions, graft versus host disease and organ rejection, modulate haemostatic or thrombolytic activity, modulate inflammation, cancers, cardiovascular disorders, neurological disease and ascertain or vitral infections. The peptides, nucleotides, antibodies, agonists and antagonists may be also be used in drug screens. AAC7849 that AAC78457 and AAB44240 represent sequences used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                             240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     421 TCCACGTGCTGTGTTATGGTCGATGGCTCCTGGGGGTGCTGCCCCATGCCCCAGGCTTCC 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGCTGTGAAGACAGGGTGCACTGCTGTCCGCACGGTGCCTTCTGCGACCTGGTTCACACC 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GATGGTTCTACCTGCTGTGAGCTGCCCAGTGGGAAGTATGGCTGCTGCCCAATGCCCAAC 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCCAGCTACAGCTGCTGCCGTCCCCTTCTGGACAAATGGCCCACAACACTGAGCAGGCAT 180
                                                                                                                                                                                                                                                                                                                                                                                                                         GTCTCAGGGACTTCCAGTTGCTGCCCCTTCCCAGAGGCCGTGGCATGCGGGGATGCCCAT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AspGlySerThrCysCysGluLeuProSerGlyLysTyrGlyCysCysProMetProAsn 264
                                                                                                                                                                                                                                                                                                                 GGAACGCGGTGCCCAGAIGGTCAGTICTGCCCTGTGGCCTGCTGCTGCACCCCGGAGGA 120
                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                          44
                                                                                                                                                                                                                                                                                                                                                                                     84
                                                                                                                                                                                                                                                                                                                                       64
                                                                                                                                                                                                                                                                                CACTGCTGCCCACGGGGCTTCCACTGCAGTGCAGACGGGGGGATCCTGCTTCCAAAGATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTGGGTGGCCCCTGCCAGGTTGATGCCCACTGCTCTGCCGGCCACTCCTGCATCTTTACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGTAACAACTCCGTGGGTGCCATCCAGTGCCCTGATAGTCAGTTCGAATGCCCGGACTTC
                                                                                                                                                                                                                                                                  CGCAGGCAGACCATGTGGACCCTGGTGAGCTGGGTGGCCTTAACAGCAGGGCTGGTGGTGGCT
                                                                                                                                                                                                                                                                                                                              GlyThrArgCysProAspGlyGlnPheCysProValAlaCysCysLeuAspProGlyGly
                                                                                                                                                         621
410
0
0
                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                           (1-621)
                                                                                                                                                                                                                                           US-09-824-647-16 (1-2095) x AAB43971
                                                                                                                                                                   410.00
100.00%
100.00%
59.08%
                                                                                               the present invention
                                                                                                                                                                                        Best Local Similarity:
Query Match:
DB:
                                                                                                                        Ž
                                                                                                                                                                                Percent Similarity:
                                                                                                                                               Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       265
                                                                                                                                                                                                                                                                                                                                                                                     65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181
                                                                                                                                                                                                                                                                                         25
                                                                                                                                                                                                                                                                                                                 61
                                                                                                                                                                                                                                                                                                                                       45
                                                                                                                                                                                                                                                                                                                                                               121
                                                                                                                                                                                                                                                                                                                                                                                                             181
                                                                                                                                                                                                                                                                                                                                                                                                                                   82
                                                                                                                                                                                                                                                                                                                                                                                                                                                           241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               721
                                                                                                                       Sequence
                                                                                                                                                            ..
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
  88888888888888
                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                         8
                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                             ŏ
                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                             å
                                                                                                                                                                                                                                                                                                                                                                                                                                  a
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δŽ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δ
```

840	324	3 960 1 344	A 102	2 108 1 9 384	r 114	120 1 424	•												
CAGAGTAAGTGCCTCTCCAAGGAGAACGCTACCACGGACCTCCTCACTAAGCTGCCTGC	CACACAGTGGGGGATGTGAATGTGACATGGGGGTGAGCTGCCCAGATGGCTATACCTGC 	TGCCGTCTACAGTCGGGGCCTGGGGCTGCTGCCTTTTACCCAGGCTGTGTGTG	GACCACATACACTGCTGCTCCCGCGGGTTTACGTGTGACACGCAGAAGGGTACCTGTGAAAAAAAA	CAGGGGCCCCACCAGGTGCCTGGATGGAGAAGCCCCAGGTCACCTCAGCCTGCCAGAC	CCACAAGCTTGAAGAGAGATGTCCCCTGTGATAATGTCAGCAGCTGTCCCTCCTCCTGT 	ACCIGCTGCCAACTCACGTCTGGGGAGTGGGGCTGTGTCCAATCCCAGAGGTGTGTCTGC	TGCTCGGACCACCAGCACTGCTGCCCCCAG 1230 	rd; Protein; 593 AA.	(first entry)	epithelin precursor. Owth regulation; inhibition; stimulation.		Location/Qualifiers 1.593 /label- precursor /note= "claim 1, page 53"	2, page	EP-2 claim 3,	1, page 5	5, page	5, page 5	44249/ /lable_EP /note="claim 7, page 53" 519574	/label= EP /note= "claim 8, page 55"
CAGAGTA GlnSerL	CACACAG HisThrV	TGCCGTC' 	GACCÁCA aspHisi	CAGGGGC GlnGlyp	CCACAAG	ACCTGCT ThrCysC	TGCTCGG CysSerA	standard;	192 (fi	thelin h requl									
781	305	901	961	1021	1081	1141	1201	LT 5 4326 AAR14326 AAR14326;	17-JAN-1992	Human epith	0	Key Protein	Protein	Protein	Peptide	Peptide	Peptide	Peptide Peptide	
OY Dp	07 Dp	Qy Db	oy Oy	Oy Db	Oy Db	Oy.	QY Dp	RESULT AAR143: ID A: XX AC A:	XEX	X X E	X S X	ELLL	FT FT	EEE	EEE	FT	EEE		FT
															,		•		٠
								·····											

```
GATGTGAAATGTGACATGGAGGTGAGCTGCCCAGATGGCTATACCTGCTGCTGCTATACAG
                                                                                                                                                                                                                                                                                    TGCTGTCCCGCGCGCGTTTACGTGTGACACGCAGAAGGGTACCTGTGAACAGGGCCCCAC
                                                                                                                                                                                                                                                                                                                                    CTCACGTCTGGGGGGGGGGCTGCTGTCCCAGAGGCTGTCTGCTGCTCGGACCAC
                                                                                TCCGATCACCTGCACTGCCCCCCAAGACACTGTGTGTGACCTGATCCAGAGTAAGTGC
     AGGGTGCACTGCTGCGCACGGTGCCTTCTGCGACCTGGTTCACACCCGCTGCATCACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             detection; diagnosis; antisense therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NO:15310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ŕ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAGCACTGCTGCCCCCAG 1230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB94550 standard; Protein; 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GludisCysCysProGln 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-JUL-2000; 2000EP-0116126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-FEB-2001
                                                                 181
                                                                                                                                                                                                                                                                                                                                                                                                                                               1153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         401
                                                                                                      201
                                                                                                                                                                 733
                                                                                                                                                                                     241
                                                                                                                                                                                                       793
                                                                                                                                                                                                                          261
                                                                                                                                                                                                                                               853
                                                                                                                                                                                                                                                                                                         301
                                                                                                                                                                                                                                                                                                                            973
                                                                                                                                                                                                                                                                                                                                               321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB94550;
                                                                                   613
                                              553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB94550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                    g
                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                               ŏ
                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                          å
                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                         9
                                                                 셤
                                                                                                      a
                                                                                                                                             윱
                                                                                                                                                                 ö
                                                                                                                                                                                                        å
                                              ŏ
                                                                                    ö
                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCCAGTTGCTGCCCCTTCCCAGAGGCCGTGGCATGCGGGGATGGCCATCACTGCTGCTGCCCA 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ArgGlyPheHisCysSerAlaAspGlyArgSerCysPheGlnArgSerGlyAsnAsnSer 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGGGGCTTCCACTGCAGTGCAGACGGCCGATCCTGCTTCCAAAGATCAGGTAACAACTCC 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              192
                                                                                                                                                                                                                                                                                                                                                                                                                                    20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTTATGGTCGATGCTCCTGGGGGTGCTGCCCCATGCCCCAGGCTTCCTGCTGTAAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                  TGCCAGGTTGATGCCCACTGCTCTGCCGGCCACTCCTGCATCTTTACCGTCTCAGGGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTGGGTGCCATCCAGTGCCCTGATAGTCAGTTCGAATGCCCGGACTTCTCCACGTGCTGT
                                                                                                                                                                                                               ET-1 is a bifunctional growth regulator, capable of stimulating the growth of some cell types while inhibiting the growth of others. ET-2 is functionally similar to ET-1 w.r.t. growth inhibitory bloactivity. In contrast, however, ET-2 is apparently not capable of eliciting the growth stimulatory activity characteristic of ET-1 and, in fact, antagonises this ET-1 activity. See also AAQ14338-40, AAQ14952-53, AAR14328-9 and AAR15315-20.
                                                                                                                                                         - useful
                                                                                                                                                      New cysteine-rich growth modulating proteins, epithelins - us as inhibitors of neoplastic cell growth and to promote wound healing and treat psoriasis
                                                                                                                                                                                                                                                                                                                            593
406
0
0
                                                                                                                                                                                                                                                                                                                            Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                              Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                (1-593)
                                                                                                                                                                                              Disclosure; Fig 22; 97pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                 US-09-824-647-16 (1-2095) x AAR14326
                                                                                                                                                                                                                                                                                                                                      406.00
100.00%
100.00%
58.50%
                                      91WO-US02321
                                                       910S-0083796
900S-0504508
                                                                                     (BRIM ) BRISTOL-MYERS SQUIB
                                                                                                        Plowman GD;
                                                                                                                            WPI; 1991-325168/44.
                                                                                                                                                                                                                                                                                                   Ä
                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
                                                                                                                                     N-PSDB; AAQ14339.
                                                                                                                                                                                                                                                                                                593
                                                                                                                                                                                                                                                                                                                    Alignment Scores:
                                                       13-MAR-1991;
03-APR-1990;
                                      03-APR-1991;
W09115510-A
                  17-0CT-1991
                                                                                                        Shoyab M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          101
                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                           73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     433
                                                                                                                                                                                                                                                                                                                                                                      Query Match
```

셤 ò a

ö

8 ð a

셤 . &

ò

. <u>අ</u>

ç

ò

1092

1032

340

972 320

852

280 912

240 792 260

672 220 732

200

1152

```
ò
                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes primer sets for synthesising 5602 (ull-length cDNAs defined in the specification. Where a primer set comprises: (a) an oilgo-dr primer and an oilgouncleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oilgonucleotide comprises at least 15 nucleotides; or (b) a combination of an oilgonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oilgonucleotide comprising a sequence complementary to a polynucleotide which comprises at least 15 nucleotides and the combination of the 5'-end sequence. 3'-end sequence; where the oilgonucleotide which comprises at least 15 nucleotides and the combination of the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the full-length cDNAs. The primers are also useful for the full-length cDNAs. The primers are also useful for the full-length cDNAs asily without any specialised methods. AAH13628 and AAH13623 represent human amino acid sequences; and AAH13629 to AAH13632 represent human amino acid sequences; and AAH13629 to AAH13632 represent human amino acid sequences; and AAH13629 to AAH13632 represent human anino acid sequences; and AAH13629 to AAH13632 represent human anino acid sequences; and AAH13629 to AAH13632 represent human anino acid sequences; and AAH13629 to AAH13632 represent human anino acid sequences; and AAH13629 to AAH13632 represent human anino acid sequences; and AAH13632 to AAH13632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1006 AAGGTACCTGTGAACAGGGCCCCACCAGGTGCCCTGGATGCAGAAGGCCCCAGCTCAC 1065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 946 GCTGTGTGCTGTGAGGACCACATACACTGCTGTCCCGCGGGGTTTACGTGTGACACGCAG 1005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92 ThrLysLeuProAlaHisThrValGlyAspValLysCysAspMetGluValSerCysPro 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTGTGTGACCTGATCCAGAGTAAGTGCCTCTCCAAGGAGAACGCTACCACGGACCTCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            826 ACTAAGCTGCCTGCGCACACAGTGGGCGATGTGAAATGTGACATGGAGGTGAGCTGCCCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GATGGCTATACCTGCTGCCGTCTACAGTCGGGGGCCTGGGGGCTGCTGCCCTTTTACCCAG
                                                                                                                                                                                                                                                           Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNas defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNas -
                                                                                                                                                                         Yamamoto J;
                                                                                                                                                                       Saito K, Yr
, Otsuki T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         413
1155
0
0
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                              Claim 8; SEQ ID 15310; 2537pp + CD ROM; English.
                                                                                                                                                                       Hayashi K, S
A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-824-647-16 (1-2095) x AAB94550 (1-413)
                                                                                                                                                                                            Wakamatsu
                                                                                                                                                                  , Isogai T, Nishikawa T,
S, Sugiyama T, Wakamatsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.25e-139
155.00
100.00%
100.00%
22.33%
                       99JP-0300253.
2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
    99JP-0248036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of the present invention.
                                                                                                                                (HELI-) HELIX RES INST.
                                                                                                                                                                                                                                 WPI; 2001-318749/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          413 AA;
29-JUL-1999;
27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              988
                                                                                                                                                                                            Ishii
                                                                                                                                                                         ota
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred.
```

g ð

ò 셤 ð 셤 ŏ 셤 ò

```
The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of the probes of the invention.
                                     .066 CTCAGCCTGCCAGACCCACAAGCCTTGAAGAGATGTCCCCTGTGATAATGTCAGCAGC 112:
152 LysGlyThrCysGluGlnGlyProHisGlnValProTrpMetGluLysAlaProAlaHis 171
                                                                                                                                                                                                                                                                                                                                                                                                                                          Human brain expressed single exon probe encoded protein SEQ ID NO: 31613.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Single exon nucleic acid probes for analyzing gene expression in human brains -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; brain expressed exon; gene expression analysis; probe; microarray; Alzhelmer's disease; multiple sclerosis; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 4; SEQ ID NO: 31613; 650pp + Sequence Listing; English.
                                                                                                                                                                                                1186 CCAGAGGCTGTCTGCTCGGACCACCAGCACTGCTGCCCCCAG 1230
                                                                                                                                                                                                                     77
75
0
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                  Hanzel DK, Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                      AAM59508 standard; Protein; 77 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-0632366.
2000US-0234687.
2000US-0236359.
2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.73e-62
75.00
100.00%
100.00%
10.81%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-0180312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-0207456
2000US-0608408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-JAN-2001; 2001WO-US00667
                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-483446/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          epilepsy; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200157275-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-AUG-2000;
21-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                    05-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                         1066
                                                                                                                                                                                                                                       212
                                                                                                                                                                                                                                                                                                                                                             AAM59508;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match:
                                                                                                                                                                                                                                                                                                   AAM59508
                                                                                                                                                                                                                                                                                   RESULT 7
```

WPI; 2002-083093/11

The present invention relates to a phage display library of variable heavy domain (VHH or VH) fragments (sdab fragments) derived from liama antibodies. The library is useful for in vitro selection against any antigen of interest as a target. Single domain anti-idiotypic antibody fragments are isolated from the library using phage display technology and an antibody serving as an antigen. Such anti-idiotypic antibody fragments have great potential in evoking the immune system response to pathological antigens and in vaccine development. The large size of the library considerably increases the probability of isolating from it predetermined target (antigen of interest). The library eliminates the development of anti-idiotypic antibodies by immunisation and allows isolation of anti-idiotypic antibodies Anu82636-AAM82640 represent peptides used in panning experiments in the present invention. New phage display library of variable heavy domain antigen-binding fragments derived from llama antibodies, useful for in vitro selection against any antigen of interest as a target Disclosure; Page 20; 46pp; English. 30 AA; Sequence

0000 Length: Matches: Conservative: Mismatches: Indels: Gaps: 4.49e-06 16.00 100.00% 100.00% 2.31% 23 Best Local Similarity: Percent Similarity: Alignment Scores: Query Match: Score:

(1-30)US-09-824-647-16 (1-2095) x AAU82636 853 GATGTGAAATGTGACATGGAGGTGAGCTGCCCAGATGGCTATACCTGC 900 RESULT 29

AAU82638 standard; peptide; 30 AA. AAU82638

23-APR-2002 (first entry)

AAU82638;

Human granulin-A derived peptide substituted version p1781.

Human; phage display library; variable heavy domain fragment; VHH; VH; sdab fragment; single domain anti-idiotypic antibody fragment; phage display technology; immune system response; CDRI/HH; CDR2; CDR3; complementarity determining region; granulin-A; p1781.

Homo sapiens.

Synthetic.

WO200190190-A2. 39-NOV-2001. 25-MAY-2001; 2001WO-CA00763.

26-MAY-2000; 2000US-207234P.

(CANA) NAT RES COUNCIL CANADA.

Panha J, Dubuc G, Narang S;

WPI; 2002-083093/11.

New phage display library of variable heavy domain antigen-binding fragments derived from llama antibodies, useful for in vitro selection

The present invention relates to a phage display library of variable havy domain (VHH or VH) fragments (sdAb fragments) derived from llama antibodies: The library is useful for in vitro selection against any antigen of interest as a target. Single domain anti-idiotypie antibody fragments are isolated from the library using phage display technology and an antibody serving as an antigen. Such anti-idiotypic antibody fragments havy great potential in evoking the immune system response to pathological antigens and in vaccine development. The large size of the library considerably increases the probability of isolating from it antigen-binding fragments having high affinity to almost any predetermined target (antigen of interest). The library eliminates the development of anti-idiotypic antibodies by immunisation and allows isolation of anti-idiotypic antibodies. AAU82636-AAU82640 represent propertiments in the present invention. 853 GATGTGAAATGTGACATGGAGGTGAGCTGCCCAGATGGCTATACCTGC 0000 Conservative: Mismatches: Indels: ET; growth regulation; inhibition; stimulation. against any antigen of interest as a target Matches: Length: US-09-824-647-16 (1-2095) x AAU82638 (1-30) Bovine epithelin precursor (partial). AAR15426 standard; Protein; 179 AA. Disclosure; Page 20; 46pp; English 74.49e-06 16.00 100.00% 100.00% 2.31% 17-JAN-1992 (first entry) Best Local Similarity: Percent Similarity: Alignment Scores: AAR15426; Sequence Query Match: RESULT 30

The epithelins appear to comprise several distinct members sharing significant structural homology. Two members of the epithelin family, epithelins - uséful New cysteine-rich growth modulating proteins, epithelins - us as inhibitors of neoplastic cell growth and to promote wound healing and treat psoriasis Disclosure; Fig 24; 97pp; English. 910S-0083796. 900S-0504508. 91WO-US02321 (BRIM) BRISTOL-MYERS SQUIB. Shoyab M, Plowman GD; WPI; 1991-325168/44. N-PSDB; AAQ14952. 03-APR-1991; 13-MAR-1991; 03-APR-1990; WO9115510-A. 17-0CT-1991 Bos taurus.

```
Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score:
                                                                                            ŏ
                                                                                                                                                                        EP-1 and EP-2, have been purified from natural sources, and cDNAs encoding these and several other members of the epithelin family have been isolated from rat (AAQ14338), human (AAQ14339), bovine, murine (AAQ14340) and chicken (AAQ14953).

ET-1 is a bifunctional growth requiator, capable of stimulating the growth of some cell types while inhibiting the growth of others.

ET-2 is functionally similar to ET-1 w.r.t. growth inhibitory bioactivity. In contrast, however, ET-2 is apparently not capable of eliciting the growth stimulatory activity characteristic of ET-1 and, in fact, antagonises this ET-1 activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid sequence of purified bowine TGFe indicated no homology to other known growth factors. However the N-terminal sequence exhibits considerable amino acid sequence identity to the deduced N-terminal amino acid sequence of human granulin A and the N-terminus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transforming growth factor E produced in commercial quantities -
used for wound healing and burns treatment, comprises monomeric
protein which acts as mitogen for fibroblasts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGFe is a glycoprotein with an Mr of about 25,000. The partial
                                                                                                                                                                                                                                                                       892 TATACCTGCTGCCGTCTACAGTCGGGGGCCTGGGGCTGCTGCTTTT 939
                                                                                                                                                                                                                                                                                             81
                                                                                                                                                                                                                                                                                  Transforming frowth factor e; cell proliferation; mitogen.
                                                                                                                                                                                                                                                                                                                                                                                                         N-terminal amino acid sequence of human granulin A.
                                                                                                                                                                    Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                           Gaps:
                                                                                                                                                                                                                                               US-09-824-647-16 (1-2095) x AAR15426 (1-179)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UYGE-) UNIV GEORGIA RES FOUND INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ğ
                                                                                                                                                                                                                                                                                                                                        . AAR35077 standard; protein; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example; Page 49; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Parnell
                                                                                                                                                                     3.45e-06
16.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92WO-US08417.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91US-0770585
                                                                                                                                                                                                                                                                                                                                                                                  09-AUG-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Halper J, Mcgraw RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1993-134386/16.
                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                    Sequence 179 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of epithelin 1.
                                                                                                                                                         Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-OCT-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-OCT-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9307173-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-APR-1993
                                                                                                                                                                                                                                                                                                                                                               AAR35077;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                   RESULT 31
                                                                                                                                                                                                                                                                                                                               AAR3507
   888888888888888888
                                                                                                                                                                                                                                                                                            윤
                                                                                                                                                                                                                                                                                                                                                   ð
```

4.48e-05

```
This is the amino acid sequence of peptide A14R, comprising amino acid residues A566-R579 of human GPBB (see AAMB5475). GPBB is an 8B ABD STYCOPTORING TOWARD ACTOR THAT is expressed in a Lightly regulated manner in normal cells, is overexpressed and unregulated in highly tumorigenic cells derived from normal cells, and which acts as a stringently required growth stimulator for the tumorigenic cells. A14R was used in an attempt to raise neutralising antibodies to GPBB (see also AAWB5480). Antagonists to GPBB, such as anti-GPBB antibodies, are used to treat diseases associated with increased expression of GPBB, particularly cancer but also viral infections. Anti-GPBB antibodies can also be used as diagnostic reagents and to deliver toxins or other compounds to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Composition containing antagonist of growth factor GP88 - useful for treating cancer and viral diseases and also for diagnosing disease from altered GP88 expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GP88; granulin; epithilin; human; growth factor; autocrine; tumour; cancer; viral infection; antagonist; therapy; diagnosis; antigen;
                                                                                                                                                                                 853 GANGIGAAAIGIGACAIGGAGGIGAGCIGCCCAGAIGGCIAIACC 897
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human GP88 autocrine growth factor antigenic peptide A14R.
                                                                                                                                                                                                        ASPWallySCysAspMetGluValSerCysProAspGlyTyrThr
    0000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                440000
                         Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
    Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps:
                                                                                                                                    US-09-824-647-16 (1-2095) x AAR35077 (1-15)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 8; Page 45; 86pp; English.
                                                                                                                                                                                                                                                                                                                   AAW85481 standard; Peptide; 14 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97US-0991862.
97US-0863079.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98WO-US10555,
15.00
100.00%
100.00%
2.16%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.000408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14.00
100.00%
100.00%
2.02%
                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3P88-expressing cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-045276/04.
                                            Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SERR/) SERRERO G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14 AA;
                         Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     409852607-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-DEC-1997;
23-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                          15-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ΰ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antibody.
                                                                                                                                                                                                                                                                                                                                                                AAW85481;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Serrero
```

Hi.

AAR20737;

AAR2073 RESULT

ð

```
AAR51665 shows an N-terminal sequence of a basophil granule protein. The BGP can be extracted from human basophil granules by treatment at pH 9.0 or greater. This can be used to generate its corresponding nucleic acid an antibodies. Anti-BGPs are useful for the diagnosis of prepathologic conditions as well as chronic and acute diseases, such as parasitic infection and leukaemia, where there is a change in the amount or distribution of BGPs.
                                                                                                                                                                                                                                                                                                                                                                                                                    New human basophil granule proteins - and related nucleic acid, expression systems, antibodies, etc., for diagnosis and treatment of e.g. inflammation, parasitic infection, leukaemia etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transforming frowth factor e; cell proliferation; mitogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative:
Mismatches:
                                                  sequence;
Leukaemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GACATGGAGGTGGCCCAGATGGCTATACC 897
             Basophil granule protein N-terminal sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-terminal amino acid sequence of epithelin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-824-647-16 (1-2095) x AAR51665 (1-15)
                                              Basophil granule protein; N-terminal BGP specific antibodies; Antibodies;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR35078 standard; protein; 14 AA.
                                                                                                                                                                                                                                                                                                                                                  Scott RW, Wilde CG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 2; Page 34; 55pp; English.
                                                                                                                                                                                                                  93WO-US08511.
                                                                                                                                                                                                                                                       92US-0943813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92WO-US08417.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     910S-0770585.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.296
11.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-AUG-1993 (first entry)
                                                                                                                                                                                                                                                                                          (INCY-) INCYTE PHARM INC
                                                                                                                                                                                                                                                                                                             (MAYO-) MAYO FOUNDATION.
                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1994-118398/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15
                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-OCT-1992;
                                                                                                                                         WO9406829-A.
                                                                                                                                                                                                                  10-SEP-1993;
                                                                                                                                                                                                                                                     11-SEP-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-OCT-1991;
                                                                                                                                                                              11-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W09307173-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-APR-1993
                                                                                                                                                                                                                                                                                                                                              Gleich GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR35078;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               red. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR35078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  score:
             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Treatments of cytophoresis from which basophils were recovered.
These were used to search for novel basophil granule proteins (BGP).
The proteins were fractioned. Ca. 25 peaks were identified.
Several fractions were pure enough to allow for the determination of a single amino acid sequence. The N-terminal sequences of eight such fractions are represented in AAR20736-42 and AAR22455.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A patient with a form of chronic myelogenous leukemia underwent two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New basophil granule proteins obtd. from cytoplasmic granules for diagnosis and treatment of pathologies involving inflammatory and IgE-mediated responses, infection, hypersensitivity and leukaemia(s)
                                      1708 GCACGCAGGGTACCAAGTGTTTGCGCAGGGAGGCCCCGGGC 1749
                                                          Basophil granule protein; chronic myelogenous leukemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    865 GACATGGAGGTGAGCTGCCCAGATGGCTATACC 897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AspWetGluValSerCysProAspGlyTyrThr 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels:
US-09-824-647-16 (1-2095) x AAW85481 (1-14)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-824-647-16 (1-2095) x AAR20737 (1-15)
                                                                                                                                                   AAR20737 standard; Protein; 15 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR51665 standard; protein; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 2; Page 22; 28pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wilde GG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       91WO-US04869.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90US-0551263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.296
11.00
100.00%
100.00%
1.59%
                                                                                                                                                                                                                                                               BGP N-terminal fraction 11
                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (INCY-) INCYTE PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gleich GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1992-056828/07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ë
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15
                                                                                                                                                                                                                                                                                                                                          Homo saptens
                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-JUL-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-JUL-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alignment Scores:
                                                                                                                                                                                                                              19-MAY-1992
                                                                                                                                                                                                                                                                                                                                                                               WO9201000-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-0CT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                    23-JAN-1992
```

Scott RW,

NAME OF STREET O

Sequence

:. 9

Score: Pred

S

ò

RESULT 34 **AAR51665**

Query Match: DB:

AAR51665;

ocoporalista de como o referencia de como de c

```
The present invention describes a method for isolating a polynucleotide of interest that is present or is expressed in a genome of a first mycobacterium strain and that is absent or altered in a genome of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mycobacterium tuberculosis; Mycobacterium bovis; mycobacterium; detection; BAC vector; bacterial artificial chromosome; tuberculosis.
                                                                                                                                            Tighe is a glycoprotein with an Mr of about 25,000. The partial amino acid sequence of purified boyine Tighe indicated no homology to other known growth factors. However the N-terminal sequence exhibits considerable amino acid sequence identity to the deduced N-terminal amino acid sequence of human granulin A and the N-terminus
                                                                             Transforming growth factor E produced in commercial quantities used for wound healing and burns treatment, comprises monomeric protein which acts as mitogen for fibroblasts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolation of polynucleotides from mycobacterial genomes, detection of Mycobacteria and for combating tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gordon S, Billault A;
                                                                                                                                                                                                                                                                400000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mycobacterium tuberculosis PGRS peptide sequence.
                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                               Indels:
                                                                                                                                                                                                                                                                                                                                                                 Gaps:
                                                                                                                                                                                                                                                                                                                                            US-09-824-647-16 (1-2095) x AAR35078 (1-14)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 14; 161pp; English.
                (UYGE-) UNIV GEORGIA RES FOUND INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB81227 standard; Peptide; 29 AA
                                       Parnell PG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Buchrieser-Brosch R,
                                                                                                                            Example; Page 49; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98US-0060756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-IB00740
                                                                                                                                                                                                                                                                 24.3
9.00
100.00%
100.00%
1.30%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (INSP ) INST PASTEUR.
                                        Mcgraw RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-013262/01.
                                                              WPI; 1993-134386/16.
                                                                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                  Sequence 14 AA;
                                                                                                                                                                                                            of epithelin 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W09954487-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-OCT-1999.
                                                                                                                                                                                                                                                          Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABB81227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cole S,
                                           Halper J,
                                                                                                                                                                                                                                                                                                                  Query Match:
                                                                                                                                                                                                                                                                      Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
                                                                                                                                                                                                                                                                                   Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                       ð
```

```
second mycobacterium strain, which is different from the first strain using a bacterial artificial chromosome (BAC) vector. Recombinant BAC using a bacterial artificial chromosome (BAC) vector. Recombinant BAC vectors, which are preferably immobilised, can be used to detect mycobacterial nucleic acids (genomic DNA, cDNA or mRNA) in biological mycobacterial nucleic acids (genomic DNA, cDNA or mRNA) in biological samples. The polynucleotides identified are useful as probes or primers for detecting a given mycobacterium of interest. By aligning the polynucleotides contained in the recombinant BAC vectors it is possible to polysically map a polynucleotide of mycobacterial origin ig a ten useful in providing information for combating tuberculosis. It is are useful in providing information for combating tuberculosis. It is possible to compare genomes between different strains or species and their non-pathogenic strains or species counterparts. ABG62492 to their non-pathogenic trains or species counterparts. ABG62492 to ABG63228 and ABB81227 to ABB81230 represent sequences used in the campilification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rat; secreted factor polypeptide; cardiac disease; renal disease; kidney; inflammatory disease; congestive heart failure; myocarditis; asthma; dilated congestive cardiomyopathy; angine pectoris; cardiac arrhythmia; myocardial infarction; pulmonary hypertension; arterioscies; stroke; renal infarction; hereditary nephritis; polycystic kidney disease; chronic renal infarction; hereditary nephritis; polycystic kidney disease; chemmatodia arthritis; osteoarthritis; polycystic kidney; rheumatodia arthritis; osteoarthritis; psoriasis; restenosis; graft versus host reaction; Crohn's disease; ulcerative colitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel secreted factor polypeptide useful for treating cardiac diseases such as arteriosclerosis, myocardial infarction, inflammatory diseases such as asthma, stroke, and rheumatoid arthritis and renal diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rat secreted factor protein encoded by DNA clone P0239_C11.
                                                                                                                                                                                                                                                                                                                                                                                                0000873
                                                                                                                                                                                                                                                                                                                                                                                                                       Matches:
Conservative:
Mismatches: Indels:
                                                                                                                                                                                                                                                                                                                                                                                              Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1231 GCTGGGGGCAGCAGTGCTGGTGGT 1208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-824-647-16 (1-2095) x ABB81227 (1-29)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alzheimer's disease; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU70166 standard; Protein; 46 AA.
                                                                                                                                                                                                                                                                                                                                                                                                              6.00
100.008
1.100.008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-MAR-2000; 2000US-193548P.
14-MAR-2001; 2001US-0809545.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-MAR-2001; 2001WO-US09555.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-010779/01.
N-PSDB; AAS94714.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stanton LW, White
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SCIO-) SCIOS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                           Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200174901-A2.
                                                                                                                                                                                                                                                                                                                                           53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-OCT-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                        Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU70166;
                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU70166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                      Score:
```

```
RESULT 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   THE STATE OF THE S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ğ
                                                           The invention relates to rat secreted factor polypeptides and the polynucleotides encoding them. The sequences are useful for treating cardiac, renal or inflammatory diseases. These include cardiac diseases such as congestive heart failure, myocarditis, dilated congestive cardiomyopathy, angina pectoris, myocardial infarction, cardiac ardiac tumours, renal diseases such as glomerulonephritis, nephrotic syndrome, renal infarction, hereditary nephritis, polycystic kidney disease, chronic renal failure, renal vein thrombosis and medullary sponge kidney and inflammatory diseases such as asthma, rheumatorid arthitis, osteoarthritis, stroke, psorlasis, restenosis, graft versus chost reaction, cohn's disease, ulcerative colitis and Alzheimer's disease. Sequences AAU70178 represent the secreted factor polypeptides of the invention.
                                                                                                                                                                            and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proteins AAW02657-W02720 represent a range of G-protein coupled receptor (GPR) proteins selected from CAMP, adenosine, muscarinic acetylcholine,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 G-protein coupled receptor; ligand binding assay; transmembrane domain; schizophrenia; dopamine; cAMP; adenosine; thrombin; adrenergic; opsin; muscarinic acetylcholine; endothelin; bombesin; endocrine; rhodopsin; odorant; cytomegalovirus; serotonergic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New dopamine receptor peptide - useful as antipsychotic agent, e.g. for treating schizophrenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4
8
0
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human betà 1 adrenergic #1 GPR N-terminal sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 8B(1); 184pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-824-647-16 (1-2095) x AAU70166 (1-46)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       494 CTGTCTTCACAGCAGGAAGCCTGG 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW03586 standard; peptide; 56 AA
                         Claim 18; Fig 22; 189pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93US-0118270.
92US-0943236.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UYNY ) UNIV NEW YORK STATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92US-0943236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.00%
100.00%
1.16%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schuster DI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1996-208785/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                     46 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-SEP-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-SEP-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JS5508384-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Murphy RB,
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW03586;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..
20
.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW03586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
```

```
The present invention describes substantially purified human proteins (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1
               odorant, cytomegaloviral and other GPR proteins. The peptides AAW03578-W03651 represent the N-terminal fragments of the above proteins. The receptor proteins were used to design polypeptides, pref. based on the transmembrane domains, for use in G-protein coupled receptor ligand binding assays. The polypeptide fragments retain biological activity such as binding a GPR ligand or modulating GPR ligand binding to a GPR (see AAW0277-W02999 for examples of polypeptide fragments). The polypeptide fragments can be used in compositions for treating subjects suffering from a pathology related to a GPR abnormality e.g. a psychotic disorder such as schizophrenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis; hyperproliferative disorder; psoriasis; benign tumour; haemorrhage; degenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; hypertension; hypothyroidism: cholesterol ester storage disease; immune deficiency; immune disorder; infectious disease; autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
endothelin, bombesin, endocrine, rhodopsin, opsin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hyperproliferative disorders and autoimmune disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                        980000
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human ORFX protein sequence SEQ ID NO:8572.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID 8572; 1037pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1209 CCACCAGCACTGCTGCCCCCAGCG 1232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-824-647-16 (1-2095) x AAW03586 (1-56)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38 ProProAlaLeuLeuProProAla 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABP04295 standard; Protein; 58 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-MAY-2000; 2000US-206132P.
29-AUG-2000; 2000US-228716P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-MAY-2001; 2001WO-US10836.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        179
8.00
100.00%
100.00%
1.15%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-JUN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Leach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-106308/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       myasthenia gravis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; ABN20047.
                                                                                                                                                                                                                                                                                                                                                                      56 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200192523-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shimkets RA,
                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-DEC-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABP04295;
                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No.:
```

```
14-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-SEP-2000;
29-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                       14-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-SEP-200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-SEP-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5-SEP-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32-0CF
in the specification). ABM15762 to ABM27252 encode the human ORFX proteins given in ABP00010 to ABP11500. ORFX proteins are useful for treating or preventing a pathology associated with an ORFX-associated disorder in humans, and in the manufacture of a medicament for treating syndrome associated with ORFX-associated disorder. ORFX polynucleotide sequences can be used in the treatment of cancer, hyperproliferative disorders, cirrhosis of liver, psoriasis, benign tumours, keloid, degenerative disorders, increased to spear transplantation, cardiovascular disorders, disorders related to organ transplantation, cardiovascular diseases, disorders infectious storage diseases, various immune deficiencies and disorders; infectious arthritis, autoimmune disorders such as multiple sclerosis, rheumatoid arthritis, autoimmune inflammatory eye disease. ORFX proteins are also necessis to the property of the protein of the protein or and the property of the protein are also necessis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antidecterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein;
                                                                                                                                                                                                                                                                                                                                                                                             N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                              useful for treating burns, incisions, ulcers, for treating osteoporosis, bone degenerative disorders, or periodontal disease, and for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues and conditions resulting from systemic cytokine damage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human musculoskeletal system related polypeptide SEQ ID NO 1593.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-824-647-16 (1-2095) x ABP04295 (1-58)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABB03646 standard; Protein; 60 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.00%
100.00%
1.15%
23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-JAN-2001; 2001WO-US01338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000US-0179065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000US-0180628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :0000US-0184664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000US-0189874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-0190076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000US-0198123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000US-0205515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-JAN-2002 (first.entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 musculoskeletal system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200155367-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24 - FEB - 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABB03646;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABB03646
      ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
```

Tue Jul

us-09-824-647-16.std.rag

```
20-OCT-2000;
20-OCT-2000;
01-NOV-2000;
                                                                              05-JAN-2001;
                                                                     08-DEC-2000;
                                                                        08-DEC-2000
         NOV-2
                                       NOV-
           NOV-
                                 -NON-
                                                          NOV-
    20-0CT-
                 Š
                                                                          08-DEC
                                                                            11-DEC
```

(HUMA-) HUMAN GENOME SCI INC

Isolated polypeptide for treating, preventing and/ or prognosing disorders related to the musculoskeletal system including musculoskeletal cancers and also for testing and detection e.g. Barash SC, Ruben SM; WPI; 2001-451937/48. N-PSDB; AAL35228. Rosen CA,

Claim 11; SEQ ID NO 1593; 781pp + Sequence Listing; English.

diagnosis

The invention relates to novel genes (AAL34669-AAL37666) and proteins (ABB03087-ABB04109) associated with the musculoskeletal system useful for preventing, treating or ameliorating medical conditions e.g. by

Example 1; SEQ ID No 3740; 1069pp; English.

```
SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
                                                                                                                                                                                                               and (f) infectious diseases sucn as virgit, parasitic infections.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp. Wipo.int/pub/published_pct_sequences.
                                                                                                                                                                       (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for treating acne vulgaris -
protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (antibagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital, (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anneanta, autoimmune thyroiditis, diabetes mellitus, Crohn's glasease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mitcham JL, Wang SS, Bhatla A; Jen S, Carter D;
                                                                                                                                                                                                                                                                                                                                                                                        တ္တိတ္တဝဝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Propionibacterium acnes immunogenic protein #3441.
                                                                                                                                                                                                                                                                                                                                                                                                          Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              dermatological; osteopathic; neuroprotectant.
                                                                                                                                                                                                                                                                                                                                                                                        Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-824-647-16 (1-2095) x ABB03646 (1-60)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          L'maisonneuve J, Zhang Y, Jen S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU42545 standard; Protein; 64 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-APR-2000; 2000US-199047P.
02-JUN-2000; 2000US-208841P.
07-JUL-2000; 2000US-216747P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-APR-2001; 2001WO-US12865.
                                                                                                                                                                                                                                                                                                                                                                                                      8.00
100.00%
100.00%
1.15%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Skeiky YAW, Persing DH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Propionibacterium acnes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI: 2001-616774/71
                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                60 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAS59517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200181581-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                      Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU42545;
                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                          Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU42545
                                                                                                                                                                                                                                                                                                                                                                                                                Score:
```

the treatment, prevention and unerly associated by sequences are used in the treatment, prevention and quantum associated by access. The disorders include SAPHO syndrome (synovitis, acce, pustulosis, hypertosis and offecenyellitis).

P. access is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acner vulgaris. A method for detecting the presence or absence of P. acces in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acces proteins. These antibodies can be used to chemisted a contacting a series of the invention and activity of P. acces polypeptides and crivity of P. acces polypeptides and determining P. acces proteins. The antibodies may also be used as diagnostic agents for determining P. acces presence, for example, by when the new polyperides are accessive the sample of the protein assay (ELISA). Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic their associated DNA sequences are used in Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO **0**0000 Length:
Matches:
Conservative:
Mismatches:
Indels: at ftp.wipo.int/pub/published_pct_sequences Gaps: 176 8.00 100.00\$ 100.00\$ 1.16\$ Percent Similarity: Best Local Similarity: Query Match: 64 AA; Alignment Scores: Seguence .. Q

US-09-824-647-16 (1-2095) x AAU42545 (1-64) 1317 GGAACCGCGGCGGCAGCCATCTT 1294 43 GlyThrAlaAlaGlyArgHisLeu 50 ò q

ABG03704 standard; Protein; 84 AA. RESULT 42

(first entry) 13-FEB-2002 ABG03704;

Novel human diagnostic protein #3695.

Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.

WO200175067-A2. Homo sapiens.

11-OCT-2001.

30-MAR-2001; 2001WO-US08631

31-MAR-2000; 2000US-0540217; 23-AUG-2000; 2000US-0649167.

(HYSE-) HYSEQ INC

Drmanac RT, Liu C,

Tang YT;

WPI; 2001-639362/73. N-PSDB; AAS67891.

New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess biodiversity

useful in f mutations

The invention relates to isolated polynucleotide (I) and probes, polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The cand gene mapping, and in recombinant production of (II). The cand gene mapping are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving to generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful in reating disorders involving aberrant protein expression or biological activity. The polypeptide and polynuclectide sequences have applications in casponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and canno acid sequences of data and products dependent on DNA and diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO **8**80000 Conservative: Mismatches: Indels: at ftp.wipo.int/pub/published_pct_sequences Length: Matches: SEQ ID No 34063; 103pp; English. Gaps: US-09-824-647-16 (1-2095) x ABG03704 (1-84) 288 CGGGGATGGCCATCACTGCTGCCC 311 20 ArgGlyTrpProSerLeuLeuPro 100.00% 100.00% 1.15% Percent Similarity: Best Local Similarity: Query Match: 84 AA; Alignment Scores: Claim 20; Score: ð

AAU14455 standard; Protein; 89 AA 24-OCT-2001 (first entry) AAU14455;

Human novel protein #326.

antibacterial; antiallergic; dermatological; haemostatic; antiasthmatic; thrombolytic; immunogen; antibody; gene therapy; neurological disorder; Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis; tissue regeneration; immune disorder. immunomodulatory; cytostatic; neuroprotective; vulnerary; nootropic; anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiviral; Human; novel protein; Antianaemic; osteopathic; antiinflammatory;

Homo sapiens

WO200155437-A2

32-AUG-2001.

25-JAN-2001; 2001WO-US02623.

25-JAN-2000; 2000US-0491404

(HYSE-) HYSEQ INC

rang YT, Liu C, Drmanac RT;

```
17-JAN-2001; 2001WO-US01334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -SEP-2000;
                                                                                                                                                                                                                                                                17-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              )8-SEP-200(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .4-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1-JUL-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -AUG-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1-AUG-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1-AUG-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1-SEP-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-SEP-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-SEP-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein levels, as tissue markers, and to isolate receptors or ligands. Polypeptides of the invention may also be useful in treating platelet disorders, stem cell disorders, regenerating bone, cartilage, tendon, ligament and/or nerve tissue, wound healing, treating burns, promoting the proliferation, differentiation and survival of stem cells, as a contraceptive, treating osteoporosis and osteoarthritis, aneamla, Alzheimer's, Parkinson's and Huntington's diseases, amylotrophic lateral sclerosis, stroke, immune deficiencies resulting from bacterial, viral or
                                                                                                                                                                                                                                                   The invention relates to polynucleotides encoding novel human proteins or their active domains. The polypeptides, polynucleotides and antibodies raised against the polypeptides are used in a method of treatment of a mammal and prevention of disorders caused by the aberrant protein expression or activity. The polypeptides can be used as molecular weight markers, food supplements, and in antibody production. The polypeptides are used to identify compounds which bind to the polypeptides. Polynucleotides of the invention are used as probes and primers, for sequencing, for chromosome or gene mapping, in the production of recombinant proteins, and in generating anti-sense DNA or target drugs to a tumour, in assays to determine biological activity, to target drugs to a tumour, in assays to determine biological activity, to refine a manule response, to determine quantitative protein and a manule response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer; antithamatic; hepatotropic; cerebroprotective; antiinflammatory; antiallergic; antidiabetic; antiulos anticonvulsant; antifungal; antiparasitic; cardiant; immune disorder; cardiovascular disorder; neurological disease; infection; nephrotropic; gene therapy; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;
                                                                                                 Isolated polypeptides useful for treating anti-inflammatory diseases, nervous system disorders, and for regenerating bone and cartilage -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fungal infection or from autoimmunity, cancer, allergy, asthma, graft-versus.host disease, eczema, haemophilia, thrombosis, anti-inflammatory diseases, nervous system discorders, and infection. The present sequence represents a protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human nervous system related polypeptide SEQ ID NO 6087.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    880000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [ndels:
                                                                                                                                                                                                Example 4; Page 821-822; 894pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1511 TCTCTGCCCAGCCTGCCACCTTCC 1534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-824-647-16 (1-2095) x AAU14455 (1-89)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50. SerLeuProSerLeuProProSer 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABB17430 standard; Protein; 95 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.00%
100.00%
1.15%
22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8.00
WPI; 2001-451939/48.
N-PSDB; AAS22760.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200159063-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABB17430;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score:
```

ö

```
Ruben SM
                                                                                                                                                                                                                                                                                       (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                Rosen CA, Barash SC,
                                                                                                                                                                                                                                                                                                        WPI; 2001-541565/60.
N-PSDB; ABA13756.
12-OCT-2000
                                                           NOV-2000
                                                                NOV-2000
                                                                     NOV-2000
                  -OCT-200
                                                  NOV-200
                                                                                                                                                                                                             NOV-200
                                                                                  NOV-200
                                                                                                                                                                NOV-200
                                                                                                                                                                                                                       DEC-2
                                                                                                                   NOV-
                                                       NOV-
                                                                         NOV-
                                                                                       NOV-
                                                                                           NOV-
                                                                                                NOV-
                                                                                                          NOV-
```

ð

AAU14219 standard; Protein; 96 AA

RESULT 45 AAU14219 (first entry)

24-OCT-2001

AAU14219;

Human novel protein #90.

Human; novel protein; Antianaemic; osteopathic; antiinflammatory; immunomodulatory; cytostatic; neuroprotective; vulnerary; nootropic; anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiviral; antiboacterial; antiallergic; dermatological; haemostatic; antiasthmatic; thrombolytic; immunogen; antibody; gene therapy; neurological disorder; Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis; tissue regeneration; immune disorder.

Drmanac RT;

(HYSE-) HYSEQ INC

25-JAN-2001; 2001WO-US02623 25-JAN-2000; 2000US-0491404

40200155437-A2.

02-AUG-2001.

Homo sapiens

```
(ABB1678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis) diabetes mellitus, Crohn's
                                                                                                                                                                                                                                                                                                                                                                                             (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and apilepsy; and (f) infectious diseases such as viral, bacterial, fungal
                 Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system cancers and metastases
                                                                                                                                     The invention relates to novel genes (ABAl1004-ABA21534) and proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                    disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias;
                                                                                                   Claim 11; SEQ ID NO 6087; 1701pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-824-647-16 (1-2095) x ABB17430 (1-95)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        166
8.00
100.00%
100.00%
1.15%
                                                                                                                                                                                                                                                                                                                                                                                                                     epilepsy; and (f) infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..
Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred.
```

WPI; 2001-451939/48. N-PSDB; AAS22524 Isolated polypeptides useful for treating anti-inflammatory diseases nervous system disorders, and for regenerating bone and cartilage -

Example 4; Page 572; 894pp; English.

The invention relates to polynucleotides encoding novel human proteins or their active domains. The polypeptides, polynucleotides and antibodies raised against the polypeptides are used in a method of treatment of a mammal and prevention of disorders caused by the aberrant protein expression or activity. The polypeptides can be used as molecular weight markers, food supplements, and in antibody production. The polypeptides are used to identify compounds which bind to the polypeptides. Polynucleotides of the invention are used as probes and primers, for sequencing, for chromosome or gene mapping, in the production of recombinant proteins, and in generating anti-sense DNA or RNA and in gene therapy. Polypeptides of the invention can be used to target drugs to a tumour, in assays to determine biological activity, to raise antibodies/elicit an immune response, to determine quantitative protein levels, as tissue markers, and to isolate receptors or ligands. Polypeptides of the invention may also be useful in treating platelet disorders, stem cell disorders, regenerating bone, cartilage, tendon, ilgeneration, differentiation and survival of stem cells, as a contraceptive, treating osteopoxosis and osteoarthritis, anaemia, and contraceptive, treating osteopoxosis and osteoarthritis, anaemia, and the proliferation of Hutington's diseases, and the proposition is a supplement and contraceptive, treating osteopoxosis and osteoarthritis, anaemia, and the proliferation of Hutington's diseases, and the proposition is a supplement and contraceptive is an entity of the manual and an entity of the manual and an entity of stem cells. stroke, immune deficiencies resulting from bacterial, viral or graft-versus-host disease, eczema, haemophilia, thrombosis, anti-inflammatory diseases, nervous system disorders, and infection. The present sequence represents a protein of the invention. ungal infection or from autoimmunity, cancer, allergy, asthma, clerosis.

Conservative: Mismatches: Indels: Length: Matches: Gaps: 100.00% 100.00% 1.15% Percent Similarity: Best Local Similarity: Query Match: Alignment Scores: Pred. No.: Score:

US-09-824-647-16 (1-2095) x AAU14219 (1-96)

1511 TCTCTGCCCAGCCTGCCACCTTCC 1534 57 SerLeuProSerLeuProProSer 64 ŏ

7, 2003, 15:55:14 Search completed: July Job time : 140 secs

Title: Perfect score:

Run on:

Sequence:

Scoring table:

Word size:

Searched:

```
Sequence 1416, Apple Sequence 4353, A Sequence 4354, A Sequence 5, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 6, Appli Sequence 7, Appli Sequence 1593, Appli Sequence 11, Appli Sequence 11, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 18, Appl
Sequence 12579, A
Sequence 48, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 17, Application US/09824647

Publication No. US2020183270A1

GENERAL INFORMATION:

APPLICANT: Serrero, Ginette

TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS

FILE REFERENCE: 29996.489.7001-A

CURRENT APPLICATION NUMBER: BANGA 4.647

CURRENT FILING DATE: 2001-04-04

FRIOR FILING DATE: BARLIER FILING DAPE: 1998-08-17

FRIOR FILING DATE: EARLIER FILING DATE: 1997-05-23

FRIOR FILING DATE: EARLIER FILING DATE: 1997-05-23

NUMBER: PATENTION OF 17.00

SOFTWARE: PATENTIN OF 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             593
0
0
0
                                                                                                                                                                                                                                            9 US-00-824-647-6
9 US-10-218-509-6
9 US-10-218-160-6
10 US-09-813-156-6
10 US-09-824-807-6
9 US-09-874-056-5
9 US-09-874-056-6
9 US-09-874-056-6
9 US-09-874-056-7
10 US-09-824-647-7
10 US-09-824-807-7
                 US-09-925-301-1416
US-09-864-761-43653
US-09-864-761-43654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-237-271-18
US-10-156-761-12579
US-10-245-103-48
US-10-245-107-48
US-10-245-143-48
US-10-245-143-48
US-10-245-851-48
US-10-245-883-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-925-301-1558
US-09-934-465-11
                                                                                                                                                                                                         US-09-813-156~2
US-09-824-807-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              593.00
100.00%
100.00%
85.45%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Human GP88 cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-824-647-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Aliqument Scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 17
US-09-824-647-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Command line parameters:
-WODEL-frame+.n2p.mcdal-DEV-xlp
-WODEL-frame+.n2p.mcdal-DEV-xlp
-De-/cgn2_1/USPTO_spool/USO9824647/runat_07072003_154720_26102/app_query.fasta_1.2247
-DB-Published_Applications_AA -0FWT-fastan -SUFFIX-std.rapb -MINMATCH-0.1
-LOOPEXT-0 -INNITS-bits -START-1 -RND-1 -MATRIX-ollgo
-TRAMS-human40.cdi -LIST-45 -DOCALIGN-200 -TRAMS-CRE-quality -THR.MIN-1
-ALIGN-45 -NODE-LOCAL -OUTFMT-pto -NORM-cxt -HEAPSIXE-500 -MINLEN-0
-MAXLEN-2000000000 -USER-GOS9824647 @CGN 1.1.24 @tunat_07072003_154720_26102
-NCFU-6 -ICPU-3 -NO_MMAP -LARGEQUERY -NEG_SCORES-0 -WAIT -DSPBLOCK-100
-NCFU-6 -ICPU-3 -NO_MMAP -LARGEQUERY -NG_SCORES-1 -XGAPOP-60 -XGAPEXT-60
-KGAPEXT-7 -YGAPOP-60 -YGAPEXT-60 -DELOP-6 -DELOF-6 -DELEXT-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 17, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 17, Appl
                                                                                                                                                             (without alignments)
6257.407 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                    1 cgcaggcagaccatgtggac.....ataaagtttgtcactttctt 2095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /ggn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
                                                                                                                                       July 7, 2003, 15:49:17; Search time 77 Seconds
                 GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                              OM nucleic - protein search, using frame_plus_n2p model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-813-156-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-218-509-17
US-10-218-509-17
US-10-281-160-17
                                                                                                                                                                                                                                                                                                                                                                                                                                      440863 seqs, 114992915 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Published_Applications_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                             Xgapop 60.0 , Xgapext 60.0 Ygapop 60.0 , Ygapext 60.0 Fgapop 6.0 , Fgapext 7.0 Delop 6.0 , Delext 7.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                    US-09-824-647-16
694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              593
593
593
                                                                                                                                                                                                                                                                                                           OFIGO
```

Jatabase

Score

Result Š

AND THE PROPERTY OF A STATE OF THE PROPERTY OF

m

à q ò a ö 셤 ογ ·B ò g ò

셤

Qγ g ŏ qq à g ö g ö 셤 ð

g

g

ά 셤 ò 셤 à 셤

δ

```
1212
                                                                                                                                                                                                                                   1272
                                                                                                                                                                                                                                                                                                 1332
                                                                                                                                                                                                                                                                                                                                                              1392
                                                                                                                                                                                                                                                                                                                                                                                                                            1452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1692
                                                                                                          1152
                                             1092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               540
              340
                                                                           360
                                                                                                                                       380
                                                                                                                                                                                                      400
                                                                                                                                                                                                                                                                  420
                                                                                                                                                                                                                                                                                                                                440
                                                                                                                                                                                                                                                                                                                                                                                             460
                                                                                                                                                                                                                                                                                                                                                                                                                                                        480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCTGGCTTCCGCTGCGCACGCACGCGTACCAAGTGTTTGCGCAGGGAGGCCCCGGCGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGTGGGGAAGGACACTTCTGCCATGATAACCAGACCTGCTGCCGAGACAACCGACAGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAGATGGTGGCTGGACTGGAGAAGATGCCTGCCCGCCGCGGTTCCTTATCCCACCCCAGA
                                                                                                                                                                                                                                                                                                                                                                              CysCysProAlaGlyTyrThrCysAsnValLysAlaArgSerCysGluLysGluValVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCTGCCCAGCCTGCCACCTTCCTGGCCCGTAGCCCTCACGTGGGTGTGAAGGACGTGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGGGCCTGCTGTCCCTACGCCCAGGGCGTCTGTTGTGCTGATCGGCGCCACTGCTGTCCT
GINHISTORYSCYSProGInArgTyrThrCysValalaGluGlyGlnCysGlnArgGlySer
                                                                                                                                                                                                                                                                                                                                                                GACATCGGCTGTGACCAGCACACCAGCTGCCCGGTGGGCGGAACCTGCTGCCCGAGCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                            GGTGGGAGCTGGGCCTGCTGCCAGTTGCCCCATGCTGTGTGCTGCGAGGATCGCCAGCAC
                                                                                                            AAGAGAGATGTCCCCTGTGATAATGTCAGCAGCTGTCCCTCCTCCGATACCTGCTGCCAA
                                                                                                                                                                        CTĈACGTCTGGGGAGTGGGGCTGCTGTCCAATCCCAGAGGCTGTCTGCTGCTCGGACCAC
                                                                                                                                                                                                                                      CAGCACTGCTGCCCCCAGCGATACACGTGTGTAGCTGAGGGGCAGTGTCAGCGAGGAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AND ANTAGONISTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GACGCCCCTTTGAGGGACCCAGCCTTGAGACAGCTGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GROWTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVERTION, GINETTE
TITLE OF INVERTION, 88 KDA TUMORIGENIC GROWTI
FILLE REFERENCE: 29996.488/P001-A
CURRENT APPLICATION NUMBER: US/10/281,160
CURRENT FILING DATE: 100-10-28
PRIOR FILING DATE: 1998-08-17
PRIOR FILING DATE: 1997-05-23
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PATENTIN VET. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 17, Application US/10281160 Publication No. US20030108950A1 GENERAL INFORMATION:
```

```
RESULT 4
US-09-813-156-17
                                                                                                                                                                                                                 1513
                                                                                                                                                                                                                                    1573
                                                                                                                                                                                                                                                        1633
                                                                                                                                                                                                                                                                           1693
                                                                                                                                                                                                                                                                                               1753
                                                                                                                                                                          1393
                                                                                                                                                                                    461
                                                                                                                                                                                              1453
                                                                                                                                                                                                       481
                                                                                                                                                                                                                          501
                                                                                                                                                                                                                                              521
                                                                                                                                                                                                                                                                 541
                                                                                                                                                                                                                                                                                     561
                                                                                                                                                                                                                                                                                                         581
                                                                        1093
                                                                                           1153
                                                                                                     381
                                                                                                               1213
                                                                                                                         401
                                                                                                                                   1273
                                                                                                                                             421
                                                                                                                                                       1333
                                                                                                                                                                 441
                                                    1033
                                                                                 361
              913
                                973
                                                              341
                                          321
    281
                       301
                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                               δ
                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                     g
                                                                                                                                                                                                                ŏ
                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                        ğ
                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                           ò
                                                                                                                                  Q
D
                                                                                                                                                               셤
                                                                                                                                                                                  g
                                                                                                                                                                                             Š
                                                                                                            Q
Dp
                                                                                                                                                       ŏ
                                                                                                                                                                        ð
                                          g
                                                    ğ
                                                            g
                                                                     ò
                                                                                8 6 G
             ò
                               ð
                                                                                                                                                                                                                                                                                                                                                      280
                                                                                                                                                                                                                                                                                                                                  260
                                                                                                                                                                                                                                                                                                                                                                912
                                                                                                                                                                                                  612
                                                                                                                                                                                                                                                                                GCCTTGTCCAGCTCGGTCATGTCCGGACGCACGGTCCCGGTGCCTGATCTACC 672
                                                                                                                                                                                                                                                                                                     732
                                                                                                                                                                                                                                                                                                                         792
                                                                                                                                                                                                                                                                                                                                            852
                                                                                                                                                                                                                                          552
                                                                                                                                                                                                                                                    180
                                                                                                                                                                                                                                                                       200
                                                                                                                     192
                                                                                                                                        252
                                                                                                                                                            312
                                                                                                                                                                 372
                                                                                                                                                                                         120
                                                                                                 132
                                                                                                          40
                                                                                                                              9
                                                                                                                                                  80
                                                                                      20
                                                                              75
                                                                                                                                                                                                                                                                                                     TCCGATCACCTGCACTGCCCCCCAAGACACTGTGTGTGACCTGATCCAGAGTAAGTGC
                                                                                                                                                                                                                                                                                                                                                                GATGTGAAATGTGACATGGAGGTGAGCTGCCCAGATGGCTATACCTGCTGCCGTCTACAG
                                                                                                                                                                                                                                                                                      AGGGTGCACTGCTCCCCACGGTGCCTTCTGCGACCTGGTTCACACCCGCTGCATCACA
                                                                                                                                                                                                                                               TGCCAGGTTGATGCCCACTGCTCTGCCGCCACTCCTGCATTACCGTCTCAGGGACT
                                                                                                                                                             TCCAGTTGCTGCCCCTTCCCAGAGGCCGTGGCATGCGGGGATGGCCATCACTGCTGCCCCA
                                                                                                                                                                                 CGGGGCTTCCACTGCAGTGCAGACGGGCGATCCTGCTTCCAAAGATCAGGTAACAACTCC
                                                                                                                                                                                     CCCACGGGCACCCACCCCTGGCAAGAAGCTCCCTGCCCAGAGGACTAACAGGGCAGTG
                                                                             CCAGATGGTCAGTTCTGCCCTGTGGCCTGCTGCCTGGACCCCGGAGGAGCCAGCTACAGC
                                  593
0
0
0
0
                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                     (1-593)
                                                                     (1-2095) \times US-10-281-160-17
                                                           Gaps:
                                   0
593.00
100.00%
100.00%
85.45%
               CDNA
               GP88
                                             Percent Similarity:
Best Local Similarity:
; SEQ ID NO 17
; LENGTH: 593
; TYPE: PRT
; ORGANISM: Human G1
US-10-281-160-17
                                                                      US-09-824-647-16
                              Alignment Scores
                                                                                                                                                                                                                                                                                            201
                                                                                                                                                                                                                                                                                                       673
                                                                                                                                                                                                                                                                                                                221
                                                                                                                                                                                                                                                                                                                          733
                                                                                                                                                                                                                                                                                                                                     241
                                                                                                                                                                                                                                                                                                                                               793
                                                                                                                                                                                                                                                                                                                                                                  853
                                                                                                                       133
                                                                                                                                                              253
                                                                                                                                                                       81
                                                                                                                                                                                  313
                                                                                                                                                                                           101
                                                                                                                                                                                                     373
                                                                                                                                                                                                             121
                                                                                                                                                                                                                       433
                                                                                                                                                                                                                                 141
                                                                                                                                                                                                                                            493
                                                                                                                                                                                                                                                     161
                                                                                                                                                                                                                                                               553
                                                                                                                                                                                                                                                                        181
                                                                                                                                                                                                                                                                                  613
                                                                                                                                                                                                                                                                                                                                                        261
                                                                                                                                           193
                                                                                                                                                    61
                                                                                                           21
                                                                                                                                41
                                                                                                   73
                                                  Best Local Si
Query Match:
DB:
                                    Pred. No.:
                                         Score
                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                       οχ
                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                       පු
                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                  a
                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                            õ
                                                                                                                                                                                        ద
                                                                                                                                                                                                           셤
                                                                                                                                                                                                                    à
                                                                                                          g
                                                                                                                               d y
                                                                                                                                                 a
                                                                                                                                                           ò
                                                                                                                                                                     g
                                                                                                                                                                              δ
                                                                                                                                                                                                   õ
                                                                              ò
                                                                                       g
                                                                                                  οy
                                                                                                                   δ
```

1692 1752 1632 1512 1572 1392 1452 1032 1092 1152 1212 1272 1332 480 520 540 560 580 500 420 440 340 360 380 400 972 320 300 TCTGCCCAGCCTGCCACCTTCCTGGCCCCTAGCCCTCACGTGGGTGTGAAGGACGTGGAG TGTGGGGAAGGACACTTCTGCCATGATAACCAGACCTGCTGCCGAGACAACCGACACGGGC TGGGCCTGCTGTCCCTACGCCCCAGGGCGTCTGTTGTGCTGATCGGCGCCCACTGCTGTCCT CAGĠTGCCCTGGATGGAGGAAGGCCCCAGCTCACCTCAGCCTGCCAGACCCACAAGCCTTG **AAGAGAGATGTCCCCTGTGATAATGTCAGCAGCTGTCCCTCCTCCGATACCTGCTGCCAA** CTCACGTCTGGGGGGGTGGGGGCTGTCCAGAGGCTGTCTGCTGCTCGGACCAC CAGCACTGCTCCCCAGCGATACACGTGTGTAGCTGAGGGGCAGTGTCAGCGAGGAAGC GINHISCYSCYSProGINALGTYThTCYSValalaGluGlyGlnCysCysDaAgGlySer ANTAGONISTS APPLICANT: SETTETO, GINETTE
TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND
FILE REPERENCE: 29996.488/7P001-A
CURRENT APPLICATION UNBER: US/09/813,156
CURRENT FILING DATE: 2001-03-21 Sequence 17, Application US/09813156 Patent No. US20020061859Al GENERAL INFORMATION:

S

Tue

```
RESULT 5
US-09-824-807-17
                  261
                                                                                                                 341
                                                                                                                                        361
                                                                                                                                                                381
                                                                                                                                                                                       401
                                                                                                                                                                                                   1273
                                                                                                                                                                                                               421
                                                                                                                                                                                                                           1333
                                                                                                                                                                                                                                      441
                                                                                                                                                                                                                                                  1393
                                                                                                                                                                                                                                                                          1453
                                                                                                                                                                                                                                                                                                 1513
                                                                                                                                                                                                                                                                                                                         1573
                                                                                                                                                                                                                                                                                                                                                 1633
                                                                                                                                                                                                                                                                                                                                                                         1693
                                                                                                                                                                                                                                                                                                                                                                                                1753
                                                                                                                             1093
                                                                                                                                                    1153
                                                                                                                                                                            1213
                                                                                                                                                                                                                                                              461
                                                                                                                                                                                                                                                                                     481
                                                                                                                                                                                                                                                                                                             501
                                                                                                                                                                                                                                                                                                                                     521
                                                                                                                                                                                                                                                                                                                                                             541
                                                                                                                                                                                                                                                                                                                                                                                                           581
                                                                                                     1033
                                                                              973
                              853
                                          281
                                                      913
                                                                  301
                                                                                          321
                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                              a
                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                         ŏ
                                                                                                                                                                                                                                                                                                                                                                                    요
                                                                                                                                                                                                                                                                                                                                                                                                           음
                                                                                                                ద
                                                                                                                                      a
                                                                                                                                                    å
                                                                                                                                                                셤
                                                                                                                                                                                      g
                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                 ç
                                                                                                                                                                                                                                                                                                                                                                                                à
                g
                              ò
                                          셤
                                                      ò
                                                                g
                                                                              à
                                                                                          윱
                                                                                                     ò
                                                                                                                            ò
                                                                                                                                                                            ð
                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                432
                                                                                                                                                                                                                                                                                            140
                                                                                                                                                                                                                                                                                                        492
                                                                                                                                                                                                                                                                                                                                552
                                                                                                                                                                                                                                                                                                                                           180
                                                                                                                                                                                                                                                                                                                                                       612
                                                                                                                                                                                                                                                                                                                                                                               672
                                                                                                                                                                                                                                                                                                                                                                                                                  240
                                                                                                                                                                                                                                 312
                                                                                                                                                                                                                                            100
                                                                                                                                                                                                                                                        372
                                                                                                                                                                                                                                                                    120
                                                                                                                                                                                                                                                                                                                  160
                                                                                                                                                                                                                                                                                                                                                                  200
                                                                                                                                                                                                                                                                                                                                                                                          220
                                                                                                                                                                                                                                                                                                                                                                                                      732
                                                                                                                                                                                                                                                                                                                                                                                                                              792
                                                                                                                                                          132
                                                                                                                                                                                  192
                                                                                                                                                                                                          252
                                                                                                                                              20
                                                                                                                                                                      40
                                                                                                                                                                                             9
                                                                                                                                                                                                                     80
                                                                                                                                   72
                                                                                                                                                                                                                                                                                                      TGCTGCCGTCCCCTTCTGGACAAATGGCCCACAACACTGAGCAGGCATCTGGGTGGCCCC
                                                                                                                                                                                                          TGCCAGGTTGATGCCCACTGCTCTGCCGCCCACTCTTTACCGTCTCAGGGACT
                                                                                                                                                                                                                                 TCCAGTTGCTGCCCCTTCCCAGAGGCCGTGGCATGCGGGGATGGCCATCACTGCTGCCCA
                                                                                                                                                                                                                                                         CGGGGCTTCCACTGCAGTGCAGACGGGCGATCCTGCTTCCAAAGATCAGGTAACAACTCC
                                                                                                                                                                                                                                                                                                                                                      CCCACGGGCACCCACCCCTGGCAAAGAAGTCCCTGCCCAGAGGACTAACAGGGCAGTG
                                                                                                                                                                                                                                                                                                                                                                               GCCTTGTCCAGCTCGGTCATGTGTCCGGACGCACGGTCCCCGGTGCCCTGATGGTTCTACC
                                                                                                                                                                                                                                                                                                                                                                                                      TGCTGTGAGCTGCCCAGTGGGAAGTATGGCTGCTGCCCAATGCCCAACGCCACCTGCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                              CCAGATGGTCAGTTCTGCCCTGTGGCCTGCTGCCTGGACCCCGGAGGAGCCAGCTACAGC
                                                                              Conservative:
Mismatches:
Indels:
                                                                                                                       US-09-824-647-16 (1-2095) x US-09-813-156-17 (1-593)
                                                                              Length:
Matches:
 08/991,862
PRIOR APPLICATION NUMBER: 08/991,86:
PRIOR FILING DATE: 1997-12-16
PRIOR APPLICATION NUMBER: 08/863,86:
PRIOR FILING DATE: 1997-05-23
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 17
                                                                                   593.00
100.00%
100.00%
85.45%
                                                      CDNA
                                                      ; ORGANISM: Human GP88
US-09-813-156-17
                                                                                         Similarity:
                                                                        Scores
                                          593
                                                                                                                                   13
                                                                                                                                                          73
                                                                                                                                                                     21
                                                                                                                                                                                 133
                                                                                                                                                                                             41
                                                                                                                                                                                                         193
                                                                                                                                                                                                                                253
                                                                                                                                                                                                                                            81
                                                                                                                                                                                                                                                        313
                                                                                                                                                                                                                                                                    101
                                                                                                                                                                                                                                                                                373
                                                                                                                                                                                                                                                                                          121
                                                                                                                                                                                                                                                                                                        133
                                                                                                                                                                                                                                                                                                                  141
                                                                                                                                                                                                                                                                                                                               493
                                                                                                                                                                                                                                                                                                                                           191
                                                                                                                                                                                                                                                                                                                                                      553
                                                                                                                                                                                                                                                                                                                                                                  181
                                                                                                                                                                                                                                                                                                                                                                               613
                                                                                                                                                                                                                                                                                                                                                                                          201
                                                                                                                                                                                                                                                                                                                                                                                                      673
                                                                                                                                                                                                                                                                                                                                                                                                                  221
                                                                                                                                                                                                                                                                                                                                                                                                                             733
                                                                                                                                                                                                                     61
                                                                                              Best Local Si
Query Match:
DB:
                                          LENGTH:
                                                                              :.
9
                                                                       Alignment
Pred. No.:
                                                 TYPE:
                                                                                          Percent
                                                                                     Score:
                                                                                                                                                                                                                                                                                                                  <u>a</u>
                                                                                                                                                                                                                                                                                                                                                      ŏ
                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                              g
                                                                                                                                                                                            g
                                                                                                                                                                                                                     a
                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                õ
                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                               ď
                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                      ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                  8
                                                                                                                                   8
                                                                                                                                                          å
                                                                                                                                                                     셤
                                                                                                                                                                                  å
                                                                                                                                                                                                         ð
                                                                                                                                                                                                                                Q
                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                             ò
```

```
1632
                                                                                                                                                                                                                                                                                                                                                                                                1392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1752
                                                                                                                                                                                                                                                                                                                                                     1332
                                                                                                                                                                                                                                                                                                                                                                                                                                           1452
                                                                                                                               1032
                                                                                                                                                                          1092
                                                                                                                                                                                                                      1152
                                                                                                                                                                                                                                                               1212
                                                                                                                                                                                                                                                                                                          1272
                                                                                                                                                                                                                                                                                                                                                                          440
                                                                                                                                                     340
                                                                                                                                                                                                360
                                                                                                                                                                                                                                          380
                                                                                                                                                                                                                                                                                    400
                                                                                                                                                                                                                                                                                                                                420
                                                                                                                                                                                                                                                                                                                                                                                                                    460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            560
                                                                                   972
                                                                                                         320
                                                             300
                    280
                                         912
852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GluIleValAlaGlyLeuGluLySMetProAlaArgArgGlySerLeuSerHisProArg
                                                                                                                                                                                                                                                                                                                                                                                                 GACATCGGCTGTGACCAGCACCAGCTGCCCGGTGGGCGGAACCTGCTGCCCGAGCCAG
                                                                                                                                                                                                                                                                                                                                                                                                              GGTGGGAGCTGGCTGCTGCTGCTGCTGCTGTGTGCTGCTGCGAGGATCGCCAGCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                      GlyGlySerTrpAlaCySCysGlnLeuProHisAlaValCySCysGluAspArgGlnHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGCTGTCCCGCGGGGTTTACGTGTGACACGCAGAAGGGTACCTGTGAACAGGGGCCCCAC
                                                                                                                                          CysCysProAlaGlyPheThrCysAsPThrGlnLysGlyThrCysGluGlnGlyProH1s
CysCysProAlaGlyPheThrCysAsPThrGlnLysGlyThrCysGluGlnGlyProH1s
                                                                                                                                                                                    TCTGCCCAGCCTGCCTTCCTGGCCCGTAGCCCTCACGTGGGTGTGAAGGACGTGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCTGGCTTCCGCTGCGCACGCAGGGTACCAAGTGTTTGCGCAGGGAGGCCCCCCCGCGCTGG
          GATGTGAAATGTGACATGGAGGTGAGCTGCCCAGATGGCTATACCTGCTGCCGTCTACAG
                                                 AspvallysCysAspWetGluValSerCysProAspGlyTyrThrCysCygargLeuGln
                                                                                    CAGGTGCCCTGGATGGAGAAGGCCCCAGCTCACCTCAGCCTGCCAGACCCACAAGCCTTG
                                                                                                                                                                                                                                                                                                                                                       GAGATCGTGGCTGGACTGGAGAGATGCCTGCCCGCCGCGGGTTCCTTATCCCACCCCAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GACGCCCCTTTGAGGGACCCAGCCTTGAGACAGCTGCTG 1791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 17, Application US/09824807
Patent No. US20020094966A1
```

Jul

Tue

```
1513
                                                                                                                                                                                                                                                                                                                                                                                                                                              1573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1753
                                                                                                                                                                                                                                                                                                                                                                                 1453
                                                                                                                                                                    1033
                                                                                                                                                                                                 1093
                                                                                                                                                                                                                               1153
                                                                                                                                                                                                                                             381
                                                                                                                                                                                                                                                           1213
                                                                                                                                                                                                                                                                          401
                                                                                                                                                                                                                                                                                         1273
                                                                                                                                                                                                                                                                                                       421
                                                                                                                                                                                                                                                                                                                      1333
                                                                                                                                                                                                                                                                                                                                     441
                                                                                                                                                                                                                                                                                                                                                    1393
                                                                                                                                                                                                                                                                                                                                                                  461
                                                                                                                                                                                                                                                                                                                                                                                                481
                                                                                                                                                                                                                                                                                                                                                                                                                              501
                                                           261
                                                                                         281
                                                                                                        913
                                                                                                                                                    321
                                                                                                                                                                                  341
                                                                                                                                                                                                                 361
                                            793
                                                                         853
                                                                                                                                     973
               733
                                                                                                                      301
221
                              241
                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                      δ
                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                               a
                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                              윤
                                                                                                                                                                                                                                                                                                                                                                                                               Q
                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                          g
                                                                                     . <u>a</u>
                                                                                                        ò
                                                                                                                      셤
                                                                                                                                      ð
                                                                                                                                                   g
                                                                                                                                                                   ò
                                                                                                                                                                                 g
                                                                                                                                                                                                 ò
                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                          g &
                           셤
                                                                         ö
               ò
                                          à
                                                                                                                                                                                                                                       132
                                                                                                                                                                                                                                                                  TGCTGCCGTCCCCTTCTGGACAAATGGCCCACAACAGTGAGCAGGCATCTGGGTGGCCCC 192
                                                                                                                                                                                                                                                                                                                              312
                                                                                                                                                                                                                                                                                                                                                                                        552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               732
                                                                                                                                                                                                                                                                                                252
                                                                                                                                                                                                                                                                                                                                     CGGGGCTTCCACTGCAGTGCAGACGGGCGATCCTGCTTCCAAAGATCAGGTAACAACTCC 372
                                                                                                                                                                                                                                                                                                                                                                    GTTATGGTCGATGCCTCCTGGGGGTGCTGCCCCATGCCCCAGGCTTCCTGCTGTGAAGAC 492
                                                                                                                                                                                                                                                    40
                                                                                                                                                                                                                                                                                                              80
                                                                                                                                                                                                                        20
                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGGGTGCACTGCTGCCGCACGGTGCCTTCTGCGACCTGGTTCACACCCGGTGCATCACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCCACGGGCACCCACCCCTGGCAAAGAAGCTCCCTGCCCAGAGGACTAACAGGGCAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGCTGTGAGCTGCCCAGTGGGAAGTATGGCTGCTGCTGCTAATGCCCAACGCCACCTGCTGC
                                                                                                                                                                                                                                               21 ProAspGlyGlnPheCysProValAlaCysCysLeuAspProGlyGlyAlaSerTyrSer
                                                                                                                                                                                                                                                                                                       CysGlnValAspAlaHisCysSerAlaGlyHisSerCysIlePheThrValSerGlyThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCAGATGGTCAGTTCTGCCCTGTGGCCTGCTGGACCCCGGAGGAGCCAGCTACAGC
                                                                                                                                                                                                                                                                                                 TGCCAGGTTGATGCCCACTGCTCTGCCGCCACTCCTGCATCTTTACCGTCTCAGGGACT
                                                                                                                                                                                                                                                                                                                               TCCAGTTGCTGCCCCTTCCCAGAGGCCGTGGCATGCGGGGATGCCCATCACTGCTGCCCA
                                                                                                                                                                                                          ATGTGGACCCTGGTGAGCTGGGTGGCTTAACAGCAGGGCTGGTGGCTGGAACGCGGTGC
         FACTOR AND ANTAGONISTS
                                                                                                                                      593
0 0
0 0
                                                                                                                                       Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                          US-09-824-647-16 (1-2095) x US-09-824-807-17 (1-593)
         GROWTH
TITLE OF INFERIOR, Ginette
TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWT
FILE REFERENCE: 2999.488/P001-A
CURRENT APPLICATION NUMBER: US/09/824,807
CURRENT FILING DATE: 2001-04-04
PRIOR FILING DATE: 1997-12-16
PRIOR FILING DATE: 1997-12-16
PRIOR FILING DATE: 1997-05-23
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver: 2.0
SOFTWARE: 933
                                                                                                                                                                      Indels:
                                                                                                                                             593.00
100.00%
100.00%
85.45%
                                                                                                          CDNA
                                                                                                                                           .ercent Similarity:
Best Local Similarity: 1
Query Match:
DB:
                                                                                                        ; ORGANISM: Human GP88
US-09-824-807-17
                                                                                                                               Alignment Scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                673
                                                                                                                                                                                                                                                                                                                                                                                                                                       141
                                                                                                                                                                                                                                                                                                                                                                                                                                                      493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                201
                                                                                                                                                                                                                                                                                                                                                                           101
                                                                                                                                                                                                                                                                                                                                                                                           373
                                                                                                                                                                                                                                                                                                                                                                                                         121
                                                                                                                                                                                                                                                                                                                                                                                                                        433
                                                                                                                                                                                                                                       73
                                                                                                                                                                                                                                                                   133
                                                                                                                                                                                                                                                                                   41
                                                                                                                                                                                                                                                                                                  193
                                                                                                                                                                                                                                                                                                               19
                                                                                                                                                                                                                                                                                                                              253
                                                                                                                                                                                                                                                                                                                                             81
                                                                                                                                                                                                                                                                                                                                                            313
                                                                                                   TYPE: PRT
                                                                                                                                        Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                      a
                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                      90
90
90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a
                                                                                                                                                                                                                      a
                                                                                                                                                                                                                                       8 P
                                                                                                                                                                                                                                                                               a
                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                            a
                                                                                                                                                                                                                                                                                                                              9
9
                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                          δ
                                                                                                                                                                                                                                                                                                                                                                                                                        õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                          ð
```

1212 1272 1332 1392 1452 1512 1572 1632 1692 1752 1032 1152 1092 420 440 460 480 500 520 540 560 580 280 320 340 360 400 300 972 380 260 852 912 240 792 GAGATCGTGGCTGGACTGGAGAAGATGCCTGCCCGCCGCGGTTCCTTATCCCACCCCAGA GlulleValalaGlyLeuGluLySMetProAlaArgArgGlySerLeuSerH1SProArg GACATCGGCTGTGACCAGCACACCAGCTGCCCGGTGGGCGGAACCTGCTGCCCGAGCCAG TCTGCCCAGCCTGCCACCTTCCTGGCCCGTAGCCCTCACGTGGGTGTGAAGGACGTGGAG GGTGGGAGCTGGGCTGCCAGTTGCCCCATGTGTGTGTGCTGCGAGGATCGCCAGCAC GCTGGCTTCCGCTGCGCACGCAGGGGTACCAAGTGTTTGCGCAGGGAGGCCCCGCGCTGG GATGTGAAATGTGACATGGAGGTGAGCTGCCCAGATGGCTATACCTGCTGCCGTCTACAG TGCTGTCCCGCGGGGTTTACGTGTGACACGCAGAAGGGTACCTGTGAACAGGGGCCCCAC CAGGTGCCCTGGATGGAGGAGGCCCCAGCTCACCTCAGCCTGCCAGACCCACAAGCCTTG GINVALPROTYPMETGIULYSALAPROALAHISLEUSErLeuProAspFroGlaAlaLeu AAGAGAGATGTCCCCTGTGATAATGTCAGCAGCTGTCCCTCCTCCGATACCTGCTGCCAA GACGCCCCTTTGAGGGACCCAGCCTTGAGACAGCTGCTG 1791

720 264

us-09-824-647-16.std.rapb

```
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-X-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCTGCTGCCAACTCACGTCTGGGGGTGGGGCTGCTCCAATCCCAGAGGCTGTCTGC 1200
                                                                                                                   385 ProGlnAlaLeuLysArgAspValProCysAspAsnValSerSerCysProSerSerAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45 AspGlySerThrCysCysGluLeuProSerGlyLysTyrGlyCysCysPromethronsn
                                                                                                                                                                         CACACAGTGGGCGATGTGAAATGTGACATGGAGGTGAGCTGCCCAGATGGCTATACCTGC
                                                                                                                                                                                                                                                                                   CCACAAGCCTTGAAGAGAGATGTCCCCTGTGATAATGTCAGCAGCTGTCCCTCCTCCGAT
                                                                 GATGGTTCTACCTGCTGTGAGCTGCCCAGTGGGAAGTATGGCTGCTGCCCAATGCCCAAC
           AACAGGGCAGTGGCCTTGTCCAGCTCGGTCATGTGTCCGGACGCACGGTCCCGGTGCCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1201 TGCTCGGACCACCAGCACTGCTGCCCCCAG 1230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-05-04
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
PRIOR FLING DATE: 2000-09-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: PCT/US01/00666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PCT/US01/00667
FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 43653, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-864-761-43653
                                                                                                                                                265
                                                                                                                                                                                                                                                          305
                                                                                                                                                                                                                                                                                                              325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1141
                                                                                                                                                                                                     285
                                                                                                                                                                                                                                                                                     901
                                                                                                                                                                                                                                                                                                                                                                                                1021
                                                                                                                                                                                                                                                                                                                                                                                                                                                    1081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       425
                                                                                                                                                                           781
                                                                                                                                                                                                                                841
                                                                  661
                                                                                                                      721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR
PRIOR
PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a
                                   g
                                                                                          ద
                                                                                                                                              셤
                                                                                                                                                                            ð
                                                                                                                                                                                                     윱
                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                      ð
                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                  ð
                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                  ð
                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCCAGCTACAGCTGCTGCCGTCCCCTTCTGGACAAATGGCCCACAACACTGAGCAGGCAT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGAACGCGGTGCCCAGATGGTCAGTTCTGCCCTGTGGCCTGCTGCCTGGACCCCGGAGGA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTGGGTGGCCCCTGCCAGGTTGATGCCCACTGCTGCGGCCACTCCTGCATCTTTACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCCACGTGCTGTGTTATGGTCGATGGCTCCTGGGGGTGCTGCCCCATGCCCCAGGCTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGCTGTGAAGACAGGGTGCACTGCTGTCCGCACGGTGCCTTCTGCGACCTGGTTCACACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGCTGCATCACACCACGGGCACCCCCCCTGGCAAAGAAGCTCCCTGCCCAGAGGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CACTGCTGCCACGGGGCTTCCACTGCAGTGCAGACGGGCGATCCTGCTTCCAAAGATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGTAACAACTCCGTGGGTGCCATCCAGTGCCCTGATAGTCAGTTCGAATGCCCGGACTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CGCAGGCAGACCATGTGGACCCTGGTGAGCTGGGTGGCCTTAACAGCAGGGCTGGTGGCT
                                                                                                          and Antibodies
                                                                                                                                                                                                                                                                                                                                          621
410
0
0
0
AspAlaProLeuArgAspProAlaLeuArgGlnLeuLeu 593
                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-824-647-16 (1-2095) x US-09-925-301-1416 (1-621)
                                                                                                                                                                                                                                                                                                                                                                     Conservative:
Mismatches:
Indels:
                                                                                         APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and
FILE REFERENCE: PA106
CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05882
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1694
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 1416
                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                              Gaps:
                                                     US/09925301
                                                                                                                                                                                                                                                                                                                                                      410.00
100.00%
100.00%
59.08%
                                                  Sequence 1416, Application
Patent No. US20020052308A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
                                                                                                                                                                                                                                                                                                   US-09-925-301-1416
                                      09-925-301-1416
                                                                                                                                                                                                                                                                                                                              Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      205
                                                                                                                                                                                                                                                                                                                                                                                                Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                             ..
02
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <u>B</u>.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            윱
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
```

셤

à 셤 ð ద

à

ð 셤 ö à

ò

ö

1020

364

960

344

840

304

284

900

324

1080

384

1140

404

```
1650 GTAGGGACAGCCCAGCCCTGTCGGTTGTCTCGGCAGCAGGTCTGGTTATCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EXPRESSED IN BRAIN, SIGNAL - 0.65
EST_HUMAN HIT: BE742164.1, EVALUE 6.00e-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-824-647-16 (1-2095) x US-09-864-761-43654 (1-48)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
                            PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR PILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-06-08
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-09-27
PRIOR PILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: PCT/USO1/00670
FILING DATE: 2001-01-30
APPLICATION NUMBER: US 60/234,687
                                                                                                                                                                                                                                                              APPLICATION NUMBER: PCT/USO1/00666
PILING DAPE: 2001-01-30
FILING DAPE: 2001-01-30
FILING DAPE: 2001-01-30
APPLICATION NUMBER: PCT/USO1/00667
APPLICATION NUMBER: PCT/USO1/00664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: PCT/US01/00665
FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: PCT/US01/00662
FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: PCT/USO1/00669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: PCT/US01/00661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 09/774,203
FILLING DATE: 2001-01-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MAP TO AC003043.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1530 GGTGGCAGGCTGGGCAGA 1513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GlyGlyArgLeuGlyArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.00%
100.00%
6.69%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.5e-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION:
US-09-864-761-43654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Annom SEQ ID NO 43654 LENGTH: 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
CURRENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCTGTGTGCTGCGAGGATCGCCAGCACTGCTGCCCGGCTGCTACACCTGCAAGCTGAAG 1485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1486 GCTCGATCCTGCGAGAAGGAAGTGGTCTCTGCCCAGCCTGCCACCTTCCTGGCCCGTAGC 1545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1546 CCTCACGTGGGTGTGAAGGACGTGGAGTGTGGGGAAGGACACTTCTGCCATGATAACCAG 1605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AlaValCysCysGluAspArgGlnHisCysCysProAlaGlyTyrThrCysAsnValLys 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 AlaArgSerCysGluLysGluValValSerAlaGlnProAlaThrPheLeuAlaArgSer 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1606 ACCTGCTGCCGAGACAACCGACAGGGCTGGGCCTGCTGTCCCTAC 1650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EXPRESSED IN BRAIN, SIGNAL = 0.65
EST_HUMAN HIT: BF344549.1, EVALUE 8.00
SWISSPROT HIT: P28799, EVALUE 8.00e-47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Annomax Sequence Listing Engine vers. 1.1 SEQ ID NO 43653 LENGTH: 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-824-647-16 (1-2095) x US-09-864-761-43653 (1-77)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps:
                                                                                                                   FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00668
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00663
                                                                                                                                                                                                                    FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00662
                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: PCT/USO1/00661
FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
                                                 PCT/US01/00669
                                                                                                PPLICATION NUMBER: PCT/US01/00665
APPLICATION NUMBER: PCT/US01/00664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 43654, Application US/09864761
Patent No. US20020048763A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: MAP TO AC003043.1 OTHER INFORMATION: EXPRESSED IN BRAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8.26e-60
75.00
100.00%
100.00%
                    ING DATE: 2001-01-30
                                                                                                                                                                                                                                                                           FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Hanzel, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Penn, Sharron G. APPLICANT: Rank, David R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: Aeomica-X-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-864-761-43654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-864-761-43653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   名
```

```
Sequence 7, Application US/09874056

Folication No. US20020192704A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: OXANO, Akira
APPLICANT: ETO, Yuzuru
APPLICANT: IZUMI, Tetsuro
APPLICANT: IZUMI, Tetsuro
APPLICANT: IZUMI, Tetsuro
APPLICANT: Same
FILE REFERENCE: 2094270S0
CURRENT FPLIKG DATE: 2001-06-06
PRIOR APPLICATION NUMBER: US 2000-170912
PRIOR FILING DATE: 2000-06-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1396 GGGAGCTGGGCCTGCTGCCCAGTTGCCCCATGTGTGCTGCGAGGATCGCCAGCACTGC 1455
21 GlySerTrpAlaCysCysGlnLeuProHisAlaValCysCysGluAspArgGlnHisCys 40
                     22 GlySerTrpalaCysCysGlnLeuProHisAlaValCysCysGluAspArgGlnHisCys 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/09824647

Sequence 2, Application US/09824647

Publication No. US20020183270A1

GENERAL INFORMATION:

APPLICANT: Seriero, Ginette

TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS

FILE REFERENCE: 29996.488/P001-A

CURRENT FILING DATE: 2001-04-04

PRIOR APPLICATION NUMBER: US/09/824,647

PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-17

PRIOR FILING DATE: EARLIER FILING DATE: 1997-05-23

NUMBER OF SEQ ID NOS: 17

SOFTWARE: PATENTIN VET. 2.0
                                                                                                                                   .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        000328
                                                                                1456 TGCCCGGCTGGCTACACCTGCAACGTGAAGGCTCGA 1491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1456 TGCCCGGCTGGCTACACCTGCAACGTGAAGGCTCGA 1491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41 CysProAlaGlyTyrThrCysAsnValLysAlaArg 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative:
Mismatches:
                                                                                                 42 CysProAlaGlyTyrThrCysAsnValLysAlaArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-824-647-16 (1-2095) x US-09-874-056-7 (1-58)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Mouse epithelin/granulin US-09-824-647-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.36e-20
32.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Mus musculus
US-09-874-056-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 2
LENGTH: 589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-824-647-2
                                                                                                                                                                  RESULT 11
US-09-874-056-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                ò
                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: OKANO, Akira
APPLICANT: ETO, Yuzuru
APPLICANT: ETO, Yuzuru
APPLICANT: ETO, Yuzuru
APPLICANT: IZUMI, Tetsuru
APPLICANTION: Same
FILE OF INVENTION: Same
FILE REFERENCE: 2004-27050
CURRENT APPLICATION NUMBER: US/09/874,056
CURRENT FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: JP 2000-170912
PRIOR APPLICATION NUMBER: JP 2000-06-07
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin version 3:1
SEQ ID NO 5
                   Sequence 4, Application US/09874056
Publication No. US20020192704a1
GENERAL INFORMATION:
APPLICANT: OKANO, AKITA
APPLICANT: ETO, YUZUTU
APPLICANT: IZUMI, Tetsuro
TITLE OF INVENTION: Insulin Receptor-Related Receptor Binding Protein and Utilization
TITLE OF INVENTION: Same
FILE REFERENCE: 209427USO
CURRENT APPLICATION NUMBER: US/09/874,056
CURRENT FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: 1P 2000-170912
PRIOR FILING DATE: 2000-06-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1336 GGGAGCTGGGCCTGCTGCCAGTTGCCCCATGCTGTGTGCGAGGATCGCCAGCACTGC 1455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21 GlySerTrpAlaCySCySGlnLeuProHisAlaValCySCySGluAspArgGlnHisCys 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57
0
0
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-824-647-16 (1-2095) x US-09-874-056-4 (1-57)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-824-647-16 (1-2095) x US-09-874-056-5 (1-58)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5, Application US/09874056 Publication No. US20020192704A1
                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.37e-20
32.00
100.00%
100.00%
4.61%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.36e-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.008
100.008
4.618
                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Mus musculus
US-09-874-056-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Mus musculus US-09-874-056-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 10
US-09-874-056-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
```

```
Alignment Scores:
Pred. No.:
                                                                           Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-824-807-2
                                                                                                                                                                                                                                                                                                                                                           RESULT 15
US-09-813-156-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 589
LENGTH: 589
                                           US-10-281-160-2
                TYPE: PRT
                                                                                          Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 16
                                                                                                           Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    윱
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1396 GGGAGCTGGGCCTGCTGCCCAGTTGCCCCATGCTGTGCGGAGGATCGCCAGCACTGC 1455
                                                                                                                           1396 GGGAGCTGGGCCTGCTGCCAGTTGCCCCATGCTGTGTGCTGCGAGGATCGCCAGCACTGC 1455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/10281160
; Sequence 2, Application US/2030108950a1
; GENERAL INFORMATION:
    APPLICANT: Serrero, Ginette
; TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
; FILE REFERENCE: 29996.488/P001-A
; CURRENT APPLICATION NUMBER: US/10/281,160
; CURRENT FILING DATE: 1090-10-28
; PRIOR APPLICATION NUMBER: US/08/991,862
; PRIOR PLILING DATE: 1999-04-17
; PRIOR FILING DATE: 1997-05-23
                                                                                                                                                                                                                                                                           Sequence 2, Application US/10218509
Publication No. US20030092661A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REFERENCE: 29996.488/P001-A
CURRENT APPLICATION NUMBER: US/10/218,509
CURRENT FILING DATE: 1998-08-15
PRIOR APPLICATION NUMBER: 08/991,862
PRIOR APPLICATION NUMBER: 08/991,862
PRIOR PLILING DATE: 1999-08-17
PRIOR FILING DATE: 1999-08-17
PRIOR FILING DATE: 1997-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           589
32
0
0
0
 0000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative:
Mismatches:
Indels:
                Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-824-647-16 (1-2095) x US-10-218-509-2 (1-589)
                                                                                           US-09-824-647-16 (1-2095) x US-09-824-647-2 (1-589)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Mouse epithelin/granulin US-10-218-509-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.73e-20
32.00
100.00$
100.00$
4.61$
32.00
100.00%
100.00%
4.61%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
                                Best Local Similarity:
Query Match:
DB:
                 Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
US-10-281-160-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 2
LENGTH: 589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..
Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                      셤
                                                                                                                                                        g
                                                                                                                             ð
                                                                                                                                                                                       ò
```

```
1396 GGGAGCTGGGCCTGCTGCCCAGTTGCCCCATGTGTGCTGCGAGGATCGCCAGCACTGC 1455
                                                                                                                                                                                                  479
                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/09813156

Sequence 2, Application US/09813156

Patent No. US20020061859A1

GENERAL INFORMATION:

APPLICANT: Serrero, Ginette

TITLE REFERENCE: 29996.488PP001-A

CURRENT APPLICATION NUMBER: 08/991,862

PRIOR PLILING DATE: 1997-12-16

PRIOR PLILING DATE: 1997-12-16

PRIOR PLILING DATE: 1997-12-16

PRIOR PLILING DATE: 1997-05-23

NUMBER OF SEQ ID NOS: 17

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  460 GlySerTrpAlaCySCysGlnLeuProHisAlaValCySCySGluAspArgGlnHisCyS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/09824807

Patent No. US2002004966A1

GENERAL INFORMATION:
APPLICANT: Serrero, Ginette
TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REFERENCE: 29996.488/PF001-A
CURRENT APPLICATION NUMBER: US/09/824,807
CURRENT FILING DATE: 2001-04-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           589
32
0
0
                                                          589
32
0
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1456 TGCCCGGCTGCTACACCTGCAACGTGAAGGCTCGA 1491
                                                                                                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                          Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-824-647-16 (1-2095) x US-09-813-156-2 (1-589)
                                                                                                                                                                   US-09-824-647-16 (1-2095) x US-10-281-160-2 (1-589)
                                                                                                                                            Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Mouse epithelin/granulin
US-09-813-156-2
ORGANISM: "Mouse epithelin/granulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.73e-20
32.00
100.008
100.008
4.618
                                                         1.73e-20
32.00
100.008
100.008
4.618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                        Percent Similarity:
Best Local Similarity:
Query Match:
```

Pred. No.:

ð

```
Sequence 6, Application US/10218509

Publication No. US20030092661A1

GENERAL INFORMATION:

APPLICANT: Serrero, Ginete

TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS

FILE REFERENCE: 29996.488/P001-A

CURRENT PAPLICATION NUMBER: US/10/218,509

CURRENT FILING DATE: 1999-08-15

PRIOR FILING DATE: 1999-08-17

PRIOR FILING DATE: 1997-05-23

NUMBER OF SEQ ID NOS: 17

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 6

LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6, Application US/10281160

Publication No. US20030108950A1

GENERAL INFORMATION:

APPLICANT: Serreco, Ginette

TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS

FILE REPREBENCE: 29996.4886/P001-A

CURRENT APPLICATION NUMBER: US/08/291,862

PRIOR FILING DATE: 1999-08-17

PRIOR FILING DATE: 1999-08-17

PRIOR FILING DATE: 1997-05-23

NUMBER OF SEQ ID NOS: 17

SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1048 GAGAAGGCCCCAGCTCACCTCAGCCTGCCAGACCCACAAGCCTTGAAGAGAGATGTC 1104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KET: PEPTIDE

LOCATION: (1)...(19)

O'THER INFORMATION: Internal peptide of human GP88 used to develop

CTHER INFORMATION: neutralizing anti-human GP88 monoclonal antibody.
US-10-218-509-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KET: PEPTIDE
LOCATION: (1)..(19)
OTHER INFORMATION: Internal peptide of human GP88 used to develop other information: neutralizing anti-human GP88 monoclonal antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-824-647-16 (1-2095) x US-10-218-509-6 (1-19)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.00%
100.00%
2.74%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.3e-08
19.00
100.00$
100.00$
2.74$
                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Human granulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Human granulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-281-160-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1396 GGGAGCTGGGCCTGCTGCCCAGTTGCCCCATGCTGTGTGCTGCGAGGATCGCCAGCACTGC 1455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              460 GlySerTrpAlaCysCysGlnLeuProHisAlaValCysCysGluAspArgGlnHisCys 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1048 GAGAAGGCCCCAGCTCACCTCAGCCTGCCAGACCCACAAGCCTTGAAGAGAGATGTC 1104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Serrero, Ginette
TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REFERENCE: 29996.488/P001-A
CURRENT APPLICATION NUMBER: US/99/824,647
CURRENT FILING DATE: 2001-04-04
PRIOR APPLICATION NUMBER: BARLIER APPLICATION NUMBER: 08/991,862
PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-17
PRIOR FILING DATE: EARLIER FILING DATE: 1997-05-23
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 6
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IOCATION: (1)..(19)
OTHER INFORMATION: Internal peptide of human GP88 used to develop
OTHER INFORMATION: neutralizing anti-human GP88 monoclonal antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1456 TGCCCGGCTGCTACACCTGCAACGTGAAGGCTCGA 1491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              480 CysProAlaGlyTyrThrCysAsnValLysAlaArg 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-824-647-16 (1-2095) x US-09-824-807-2 (1-589)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-824-647-16 (1-2095) x US-09-824-647-6 (1-19)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                      Indels:
                                                                                                                                                                                                                                                                                                                                                                                          Gaps:
    PRIOR APPLICATION NUMBER: 08/991,862
PRIOR FILING DATE: 1997-12-16
PRIOR PRICATION NUMBER: 08/863,862
PRIOR FILING DATE: 1997-05-23
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PATENTIN Ver: 2.0
SEQ ID NO 2
LENGTH: 589
                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Mouse epithelin/granulin
US-09-824-807-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6, Application US/09824647 Publication No. US20020183270A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                       1.73e-20
32.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2.3e-08
19.00
100.00%
100.00%
2.74%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Human granulin
                                                                                                                                                                                                                                                                                                                                            Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
                                                                                                                                                                                                                                                                                                                         Percent Similarity:
                                                                                                                                                                                                                                                              Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-824-647-6
```

0000

00000

Query Match:

RESULT 18 US-10-218-509-6

```
1.36e-06
17.00
100.00%
100.00%
2.45%
                                                                                                      100.00%
100.00%
2.74%
                                                               2.3e-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Mus musculus
US-09-874-056-3
                                                                                                        Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alignment Scores:
                                           Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                         US-09-874-056-3
JS-09-824-807-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGIH: 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match:
                                                                                                                                                   Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
0
                                                                 Pred No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 23
                                                                                          Score:
                                                                                                                                                                                                                                                                ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-824-807-6

Sequence 6, Application US/09824807

Partent No. US20004966A1

GENERAL INFORMATION:
APPLICANT: Serrero, Ginette

TITLE OF INVENTION: 88 RDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REFERENCE: 2996-488/F001-A

CURRENT APPLICATION NUMBER: US/09/824,807

CURRENT FILING DATE: 1997-12-16

PRIOR PAPLICATION NUMBER: 08/991,862

PRIOR PELING DATE: 1997-12-16

PRIOR PELING DATE: 1997-12-16

PRIOR PELING DATE: 1997-12-16

NUMBER OF SEQ ID NOS: 17

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1048 GAGAAGGCCCCAGCTCACCTCAGCCTGCCAGACCCACAAGCCTTGAAGAGAGATGTC 1104
                                                                    1048 GAGAAGGCCCCAGCTCACCTCAGCCTGCCAGACCCACAAGCCTTGAAGAGAGATGTC 1104
                                                                                                                                                                        GENERAL INFORMATION:

Sequence 6, Application US/09813156

FECTOR NO. USZOUZOZOG1859A1

GENERAL INFORMATION:

APPLICANT: Serrero, Ginette

FITLE OF INVENTION: 8 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS

FILE REFERENCE: 2996.488/P001-A

CURRENT APPLICATION NUMBER: US/09/813,156

CURRENT FILING DATE: 1997-12-16

FRIOR PELICATION NUMBER: 08/991,862

FRIOR PELICATION NUMBER: 08/991,862

FRIOR PELICATION NUMBER: 08/991,862

FRIOR PELICATION NUMBER: 08/991,862

FRIOR PELICATION NUMBER: 08/863,862

FRIOR APPLICATION NUMBER: 08/863,862

FRIOR APPLICATION NUMBER: 08/863,862

FRIOR PELICATION NUMBER: 08/863,862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (1)...(19)
OTHER INFORMATION: Internal peptide of human GP88 used to develop
OTHER INFORMATION: neutralizing anti-human GP88 monoclonal antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)..(19)
OTHER INFORMATION: Internal peptide of human GP88 used to develop
OTHER INFORMATION: neutralizing anti-human GP88 monoclonal antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-824-647-16 (1-2095) x US-09-813-156-6 (1-19)
                        US-09-824-647-16 (1-2095) x US-10-281-160-6 (1-19)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.3e-08
19.00
100.00%
100.00%
2.74%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Human granulin FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Human granulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 19
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-813-156-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a
                                                                          ð
```

```
Sequence 3, Application US/09874056
; Sequence 3, Application US/09874056
; Publication No. US20020192704A1
; GENERAL INFORMATION:
    APPLICANT: OKANO, AKira
    APPLICANT: ETO, Yukuru
; APPLICANT: IZUMI, Tetsuro
; TITLE OF INVENTION: Insulin Receptor-Related Receptor Binding Protein and Utilizat
; TITLE OF INVENTION: Same
; FILE REFERENCE: 2094270S0
; CURRENT APPLICATION NUMBER: US/09/874,056
; CURRENT PILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: JP 2000-170912
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin Version 3.1
; SEQ ID NO 3
; SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-874-056-6

Sequence 6, Application US/09874056

Sequence 6, Application US/09874056

Publication No. US20020192704A1

SEQUENCE A. WILL OF INFORMATION:

APPLICANT: CRANO, ARITA

APPLICANT: IZUMI, Tetsuro

TITLE OF INVENTION: Insulin Receptor-Related Receptor Binding Protein and Utiliza

TITLE OF INVENTION: Same

FILE REFERENCE: 209427USO

CURRENT APPLICATION NUMBER: US/09/874,056

CURRENT APPLICATION NUMBER: JP 2000-170912

PRIOR FILING DATE: 2000-06-07
                                                                                                                                                                                             1396 GGGAGCTGGGCCTGCTGCCAGTTGCCCCATGCTGTGTGCTGCGAGGATCGC 1446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22 GlySerTrpAlaCysCysGlnLeuProHisAlaValCysCysGluAspArg 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57
0
0
0
0
60000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative:
                                           Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-824-647-16 (1-2095) x US-09-874-056-3 (1-57)
                                                                                                                                                    US-09-824-647-16 (j-2095) x US-09-824-807-6 (1-19)
                    Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches:
  Length:
                                                                                          Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn version 3.1
```

Pred. No.:

Score:

ð

us-09-824-647-16.std.rapb

```
Sequence 7, Application US/10281160
Publication No. US20030108950A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REFERENCE: 20996.488/P001.A
CURRENT FILING DATE: 2002-10-28
PRIOR APPLICATION NUMBER: US/10/281,160
CURRENT FILING DATE: 1998-08-17
PRIOR FILING DATE: 1998-08-17
PRIOR FILING DATE: 1999-05-23
                                                                                                            NAME/KET: PEPTIDE

COCATION: (1)...(14)

O'THER INFORMATION: Internal peptide of human GP88 used to develop

CTHER INFORMATION: neutralizing anti-human GP88 monoclonal antibody
US-10-218-509-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (1)..(14)
OTHER INFORMATION: Internal peptide of human GP88 used to develop
OTHER INFORMATION: neutralizing anti-human GP88 monoclonal antibody
                                                                                                                                                                                                                                                                                                                                                                                                                          1708 GCACGCAGGGGTACCAAGTGTTTGCGCAGGGAGGCCCCGCGC 1749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                          Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-824-647-16 (1-2095) x US-10-281-160-7 (1-14)
                                                                                                                                                                                                                                                                                                                                                                                        US-09-824-647-16 (1-2095) x US-10-218-509-7 (1-14)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
                                                                                                                                                                                                                                                    Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels:
                                                                                                                                                                                                                                                                                                                                Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7, Application US/09813156
Patent No. US20020061859A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.000925
14.00
100.008
100.008
2.028
                                                                                                                                                                                                                                                    0.000925
                                                                                                                                                                                                                                                                    14.00
100.00%
100.00%
2.02%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Serrero, Ginette
PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Human granulin
                                                        TYPE: PRT
ORGANISM: Human granulin
                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alignment Scores:
                                                                                                                                                                                                                                  Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-813-156-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-281-160-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-281-160-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 14
                    SEQ ID NO 7
LENGTH: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 7
  SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match:
                                                                                                FEATURE:
                                                                                                                                                                                                                                                  Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 7, Application US/10218509
Eublication No. US20030092661A1
GENERAL INFORMATION:
APPLICANT: Serrero, Ginette
TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REFERENCE: 2996.488/P001-A
CURRENT APPLICATION UNDERS: US/10/218,509
CURRENT FILING DATE: 2002-08-15
                                                                                                                                                                                                                                                                                                                                                              Sequence 7, Application US/09824647
Publication No. US20020183270a1
CENERAL INFORMATION:
APPLICANT: Serrero, Ginette
TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REFERENCE: 29996.488,P001-A
CURRENT APPLICATION NUMBER: US/09/824,647
CURRENT FILING DATE: 2001-04-04
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/991,862
PRIOR PPLING DATE: EARLIER REPLICATION NUMBER: 08/863,862
PRIOR PLING DATE: EARLIER FILING DATE: 1997-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: PEPTIDE
COCATION: (1)...(14)
OTHER INFORMATION: neutralizing anti-human GP88 used to develop
OTHER INFORMATION: neutralizing anti-human GP88 monoclonal antibody
                                                                                                                                                                                                                                                  770000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                              US-09-824-647-16 (1-2095) x US-09-874-056-6 (1-59)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-824-647-16 (1-2095) x US-09-824-647-7 (1-14)
                                                                            Length:
Matches:
                                                                                                                                                                          Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 08/991,862
PRIOR FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: 08/863,862
PRIOR FILING DATE: 1997-05-23
                                                                    1.12e-05
16.00
100.00$
100.00$
2.31$
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.000925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14.00
100.008
100.008
2.028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Human granulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 17
  ; ORGANISM: Mus musculus
US-09-874-056-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                              Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
                                                          Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 25
US-10-218-509-7
                                                                                                                                                                                                                                                                                                                          RESULT 24
US-09-824-647-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-824-647-7
                                                                                                                                                  Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
```

Pred. No.:

Score:

å

```
APPLICANT: Stanton, Lawrence W.
APPLICANT: White, R. Tyler
TITLE OF INVENTION: SECRETED FACTORS
FILE REFERENCE: SCIOS.017A
CURRENT APPLICATION NUMBER: US/09/809,545A
CURRENT FILING:DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 43
LENGTH: 46
                                                                                                US-09-809-545A-43;
Sequence 43, Application US/09809545A;
Sequence 43, Application US/09809545A;
Patent No. US20020110804A1;
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: SITE LOCATION: (19)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT. 30
ns-09-764-877-1593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-764-877-1593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-809-545A-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No.:
TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS FILE REFERENCE: 2996.488/P001-A CURRENT APPLICATION NUMBER: US/09/813,156 CURRENT APPLICATION NUMBER: US/09/813,156 CURRENT PILING DATE: 2001-0.3-21 PRIOR APPLICATION NUMBER: 08/991,862 PRIOR PILING DATE: 1997-12-16 PRIOR PILING DATE: 1997-0.5-23 NUMBER OF SEQ ID NOS: 17 SOFTWARE: PATENT NET: 1997-05-23 NUMBER PATENT NET: 1997-05-23 SOFTWARE: PATENT NET: 1.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: 68 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS FILE OF INVENTION: 68 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS FILE REFERENCE: 29996.488/P001-A CURRENT APPLICATION NUMBER: US/09/824,807 CURRENT FILING DATE: 2001-04-04 PRIOR APPLICATION NUMBER: 08/991,862 PRIOR FILING DATE: 1997-12-16 PRIOR FILING DATE: 1997-05-23 NUMBER OF SEQ ID NOS: 17 SOFTWARE: Patentin Ver: 2.0 SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : LOCATION: (1)..(14)
; CTHER INFORMATION: Internal peptide of human GP88 used to develop
; CTHER INFORMATION: neutralizing anti-human GP88 monoclonal antibody
US-09-824-807-7
                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (1)..(14)
OTHER INFORMATION: Internal peptide of human GP88 used to develop
OTHER INFORMATION: neutralizing anti-human GP88 monoclonal antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-824-647-16 (1-2095) x US-09-824-807-7 (1-14)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-824-647-16 (1-2095) x US-09-813-156-7 (1-14)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 7, Application US/09824807
Patent No. US20020094966Al
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.000925
14.00
100.008
100.008
2.028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.000925
14.00
100.008
100.008
2.028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Human granulin
                                                                                                                                                                                                                                                                                                              ORGANISM: Human granulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Aliqnment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-824-807-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-813-156-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            õ
```

```
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 4031
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1593
                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PC005
CURRENT APPLICATION NUMBER: US/09/764,877
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-824-647-16 (1-2095) x US-09-764-877-1593 (1-60)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative:
Mismatches:
                                                                                                                 Conservative:
                                                                                                                                                                                                            US-09-824-647-16 (1-2095) x US-09-809-545A-43 (1-46)
                                                                                                                                   Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
                                                                          Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels:
                                                                                                                                                   ndels:
                                                                                                                                                                                                                                                  494 CIGICITCACAGCAGGAAGCCTGG 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 ArgGlyProThrArgCysProGly 10
                                                                                                                                                                                                                                                                      25 LeuSerSerGlnGlnGluAlaTrp 32
                                                                                                                                                                                                                                                                                                                                                       Sequence 1593, Application US/09764877
Patent No. US20020147140A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 242
8.00
100.00%
100.00%
1.15%
                                                                                                             100.00%
100.00%
1.16%
ORGANISM: Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                 Percent Similarity:
Best Local Similarity:
```

1708 GCACGCAGGGGTACCAAGTGTTTGCGCAGGGGGCCCCGCGC 1749

```
Sequence 18, Application US/10237271

Fublication No. US20030096328A1

GENERAL INFORMATION

APPLICANT: THE BURNHAM INSTITUTE

APPLICANT: KRIDEL, Steven J.

APPLICANT: AXELROD, Funiko T.

TITLE OF INVENTION: SERINE/THREONINE HYDROLASE PROTEINS AND SCREENING ASSAYS

FILE REFERENCE: BUTNII00-1

CURRENT APPLICATION NUMBER: US 60/317,842

PRIOR APPLICATION NUMBER: US 60/317,842

PRIOR APPLICATION NUMBER: US 60/317,842

PRIOR FILING DATE: 2001-09-06

NUMBER OF SEQ ID NOS: 19

SOFTWARE: Patentin version 3.1

SEQ ID NO 18

TENGTH: 166

TYPE: PRIOR THE OFFICE THE 
                                                                                                                                                                                      US-09-824-647-16 (1-2095) x US-09-925-301-1558 (1-109)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative:
Mismatches:
Indels:
                          Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-824-647-16 (1-2095) x US-09-934-465-11 (1-151)
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: APO-2 LIGAND
FILE REFERENCE: 1166-22USO3
FURRENT PAPLICATION NUMBER: US/9/934,465
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: 08/584,031
PRIOR FILING DATE: 1996-01-09
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PATENTIN Ver: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
                                                                                           Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: MISC_FEATURE
LOCATION: (3)..(8)
FURER INFORMATION: Xaa is any Amino Acid
FEATURE:
                                                                                                                              Gaps:
                                                                                                                                                                                                                                             1734 CAGGGAGGCCCCGCGCTGGGACGC 1757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32 GlnGlyGlyProAlaLeuGlyArg 39
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 11, Application US/09934465
Patent No. US20020102233A1
                      100.008
100.008
1.158
10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
                   Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                         US-09-934-465-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -10-237-271-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-934-465-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..
№
.
                                                                                                                                                                                                                                                    ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (107)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-925-301-1558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1558, Application US/09925301
Patent No. US20020052308A1
GENERAL INFORMATION:
I TILE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA106
CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05882
PRIOR FILING DATE: 1909-03-12
PRIOR FILING DATE: 1999-03-12
                                                                                                                                                                         APPLICANT: Simmons, Cari
TITLE OF INVENTION: Malze Proteinase Inhibitor-Like
TITLE OF INVENTION: Polynucleotides and Methods of Use
FILE REFERENCE: 35718/239836
CURRENT APPLICATION NUMBER: US/10/039,836A
CURRENT FILING DATE: 2001-10-23
PRIOR APPLICATION NUMBER: 60/243,167
PRIOR FILING DATE: 2000-10-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-824-647-16 (1-2095) x US-10-039-836A-2 (1-97)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1455 GCAGTGCTGCCGATCCTCGCAGCA 1432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12 AlaValLeuAlaIleLeuAlaAla 19
                                                    Sequence 2, Application US/10039836A Publication No. US20030033532A1 GENERAL INFORMATION APPLICANT: Crane, Virginia APPLICANT: Simmons, Carl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (101)
OTHER INFORMATION: Xaa equals any
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 1694
SOFTWARE: PatentIn Ver. 2.
SEQ ID NO 1558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: SITE
LOCATION: (80)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JS-09-925-301-1558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
                   US-10-039-836A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-039-836A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ð
```

NAME/KEY: MISC_FEATURE

109

Length:

223

Alignment Scores:

```
US-09-824-647-16 (1-2095) x US-10-156-761-12579 (1-190)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                        Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                      US-09-824-647-16 (1-2095) x US-10-237-271-18 (1-166)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TILLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REPRENCE: 29-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: UP 2001-204089
PRIOR PILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: UP 2001-272697
PRIOR FILING DATE: 2001-05-30
                                                                                                                                                                                      Gaps:
; LOCATION: (32)..(56)
; OTHER INFORMATION: Xaa is any Amino Acid
US-10-237-271-18
                                                                                                                                                                                                                                                         1686 CTGTCCTGCTTCCGCTGCGC 1709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         936 AGGCCAGCCCCAGGCCCCCGA:913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49 ArgalaalaalaaroGlyProArg 56
                                                                                                                                                                                                                                                                                             78 LeuSerCysTrpLeuProLeuArg 85
                                                                                                                                                                                                                                                                                                                                                                      Sequence 12579, Application US/10156761 Publication No. US20030119018A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 48, Application US/10245103
Publication No. US20030068778A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Goddard, Audrey
Grimaldi, J. Christopher
Gurney, Austin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , ORGANISM: Streptomyces avermitilis
US-10-156-761-12579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Stephan, Jean-Phillippe
Watanbe, Colin
                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, UIN
APPLICANT: HORIKAWA, HIROSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.00%
100.00%
1.16%
                                                                                                                              100.00%
100.00%
1.15%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Filvaroff, Ellen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 12579
LENGTH: 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SHIBA, TADAYOSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Smith, Victoria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
                                                                                                                          Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                     RESULT 35
US-10-156-761-12579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alignment Scores:
                                                                              Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match:
                                                                                               Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ð
                                                                                                                                                                                                                                                                ð
```

```
ION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3630RLC112
CURRENT PAPLICATION NUMBER: 02/10/245,103
CURRENT FILING DATE: 2002-09-17
PRIOR PILING DATE: 2002-09-17
PRIOR PLILING DATE: 2002-07-18
PRIOR PLILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              - See File Wrapper or PALM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-824-647-16 (1-2095) x US-10-245-103-48 (1-192)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Remaining Prior Application data removed
NUMBER OF SEQ ID NOS: 116
SEQ ID NO 48
LENGTH: 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              794 TCTCCAAGGAGAACGCTACCACGG 817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 SerProArgArgThrLeuProArg 9
                                                                                                                                                                                                                                                                                                          R FILING DATE: 1998-03-27
R APPLICATION NUMBER: 60/086478
R FILING DATE: 1998-05-22
R PILING DATE: 1998-06-02
R FILING DATE: 1998-06-02
R APPLICATION NUMBER: 60/089801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 48, Application US/10245107
Publication No. US20030068779A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Goddard, Audrey
Grimaldi, J. Christopher
Gurney, Austin
Smith, Victoria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Stephan, Jean-Phillippe
Watanbe, Colin
Wood, William
                                                                                                                                                                                                                           FILING DATE: 1997-10-24
APPLICATION NUMBER: 60/065027
FILING DATE: 1997-11-10
APPLICATION NUMBER: 60/079689
                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/090689
                                                                                                                                                                                                     APPLICATION NUMBER: 60/063046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .00
100.00%
100.00%
1.15%
                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 1998-06-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: HOMO
US-10-245-103-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
Pred. No.:
```

```
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3630R1C98
                                                     PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR FILING DATE: 1998-06-24
PRIOR FILING DATE: 1998-06-24
PRIOR FILING DATE: 1998-06-25
PRIOR FILING DATE: 1998-06-25
PRIOR PLICATION NUMBER: 60/090689
PRIOR FILING DATE: 1998-06-25
PRIOR FILING DATE: 1998-06-25
PRIOR FILING DATE: 1998-06-15
PRIOR FILING DATE: 1998-06-15
PRIOR FILING DATE: 1998-06-15
PRIOR FILING DATE: 1998-06-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-824-647-16 (1-2095) x US-10-245-143-48 (1-192)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/245,771 CURRENT FILING DATE: 2002-09-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    794 TCTCCAAGGAGAACGCTACCACGG 817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 SerProArgArgThrLeuProArg 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/063046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 48, Application US/10245771
Publication No. US20030068781A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: 10/197942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 1997-10-24
APPLICATION NUMBER: 60/065027
FILING DATE: 1997-11-10
       60/087607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Goddard, Audrey
Grimaldi, J. Christopher
Gurney, Austin
Smith, Victoria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 60/059114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/079689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 1998-05-22
APPLICATION NUMBER: 60/087607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/086478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/090689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/089801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tephan,Jean-Phillippe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         002-07-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    998-06-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    998-03-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eaton, Dan
Filvaroff, Ellen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hang,2emin
                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Homo Sapien
US-10-245-143-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity: Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores
                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 192
                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Fong, Sherman
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE GAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-824-647-16 (1-2095) x US-10-245-107-48 (1-192)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3630R1C90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/245,143 CURRENT FILING DATE: 2002-09-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Remaining Prior Application data removed NUMBER OF SEQ ID NOS: 116 SEQ ID NO 48 LENGTH: 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        794 TCTCCAAGGAGAACGCTACCACGG 817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R APPLICATION NUMBER: 60/087607
R FILING DATE: 1998-06-02
R APPLICATION NUMBER: 60/089801
R FILING DATE: 1998-06-18
R APPLICATION NUMBER: 60/090557
R FILING DATE: 1998-06-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Filvaroff, Ellen
Goddard, Audrey
Grimaldi, J. Christopher
Gurney, Austin
Smith, Victoria
                                                 FILING DATE: 1997-10-24
APPLICATION NUMBER: 60/065027
                                                                                                                                                         APPLICATION NUMBER: 60/079689
FILING DATE: 1998-03-27
APPLICATION NUMBER: 60/086478
                            60/063046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-245-143-48
Sequence 48, Application US/10245143; Sequence 48, Application US/10245143; Publication No. US20030068780A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 10/197942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 2002-07-18
APPLICATION NUMBER: 60/059114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 1997-11-10
APPLICATION NUMBER: 60/079689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60/030683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/063046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stephan, Jean-Phillippe
Watanbe, Colin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/065027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2002-09-16
                                                                                                                                'ILING DATE: 1997-11-10
                                                                                                                                                                                                                                                                   998-05-22
1997-09-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 1998-06-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8.00
100.00%
100.00%
1.15%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 1998-03-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 1997-09-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 1997-10-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-245-107-48
                        PRIOR L
PRIOR PRIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..
Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR
```

Length: Matches: Conservative: Mismatches:

Indels:

us-09-824-647-16.std.rapb

```
APPLICANT: FONG, Sherman TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3630R1C70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Remaining Prior Application data removed - See File Wrapper or PALM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-824-647-16 (1-2095) x US-10-245-883-48 (1-192)
                                                 Conservative:
Mismatches:
Indels:
                                                                                                                                           US-09-824-647-16 (1-2095) x US-10-245-851-48 (1-192)
           Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/245,883 CURRENT FILING DATE: 2002-09-16
                                                                                                             Gaps:
                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 10/197942
PRIOR FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/059114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/063046
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/065027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RIOR FILING DATE: 1997-11-10
RIOR APPLICATION NUMBER: 60/079689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/086478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/087607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER: 60/090689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/090557
                                                                                                                                                                                                                                                                                                                                                                                                                          Goddard, Audrey
Grimaldi, J. Christopher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60/089801
                                                                                                                                                                                                                                                                                                   Sequence 48, Application US/10245883
Publication No. US20030068783A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Smith, Victoria
Stephan, Jean-Phillippe
Watanbe, Colin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/0
PRIOR FILING DATE: 1998-06-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      207
8.00
100.00%
1.00.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               998-06-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 1998-06-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         998-06-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     998-03-2
                                 8.00
100.00%
100.00%
1.15%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 116
SEQ ID NO 48
LENGTH: 192
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gurney, Austin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wood, William
                                       Score:
Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RIOR FILING DATE: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: HO
US-10-245-883-48
 Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                         10-245-883-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: FONG, Sherman
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3630R1C93

    See File Wrapper or PALM

; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 48
; LENGTH: 192
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-245-771-48
                                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                     US-09-824-647-16 (1-2095) x US-10-245-771-48 (1-192)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/245,851
CURRENT FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: 10/197942
PRIOR PILING DATE: 2002-07-18
PRIOR PELING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/063046
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063046
PRIOR FILING DATE: 1997-10-24
PRIOR FILING DATE: 1997-11-10
                                                                                                                                                                                                                                                                                 Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 1998-06-25
Remaining Prior Application data removed
NUMBER OF SEQ ID NOS: 116
SEQ IN 04 48
LENGTH: 192
                                                                                                                                                                                                                                                                                                   Gaps:
                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 60/079689
FILING DATE: 1998-03-27
APPLICATION NUMBER: 60/086478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PILING DATE: 1998-05-22
APPLICATION UNDERE: 60/087607
FILING DATE: 1998-06-02
APPLICATION NUMBER: 60/089801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/090689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60/090557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 48, Application US/10245851
Publication No. US20030068782A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Goddard, Audrey
Grimaldi, J. Christopher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stephan, Jean-Phillippe
Watanbe, Colin
Wood, William
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1998-06-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/
FILING DATE: 1998-06-24
                                                                                                                                                                                                                   8.00
100.00%
100.00%
1.15%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Smith, Victoria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gurney, Austin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hang, Zemin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Homo Sapien US-10-245-851-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eaton, Dan
                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                   Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                   ò
```

Length:
Matches:
Conservative:
Mismatches:
Indels:

```
APPLICATION NUMBER: 6/177118
FILING DATE: 2000-01-20
APPLICATION NUMBER: 6/179851
FILING DATE: 2000-02-02
APPLICATION NUMBER: 6/180921
FILING DATE: 2000-02-08
                            LICATION NUMBER: 60/138385
ING DATE: 1999-06-09
                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/145228
FILLING DATE: 1999-07-20
APPLICATION NUMBER: 60/145698
FILING DATE: 1999-07-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ILING DATE: 1999-08-17
ILING DATE: 1999-08-17
ILING DATE: 1999-08-20
PELICATION NUMBER: 60/151700
ILING DATE: 1999-08-31
                                                                  PLICATION NUMBER: 60/140653
                                                                             ILING DATE: 1999-06-22
PPLICATION NUMBER: 60/141037
                                                                                                                                          PPLICATION NUMBER: 60/144732
                                                                                                                                                                          ILING DATE: 1999-07-20
                                                                                                                                                                                                              APPLICATION NUMBER: 60/144790
                                                                                                                                                                                                                                                                                                                                                                        ILING DATE: 1999-08-03
PPLICATION NUMBER: 60/148188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LING DATE: 1999-08-17
PLICATION NUMBER: 60/149395
                                                                                                                                                                                                                                                                                                                                                              PPLICATION NUMBER: 60/146843
                                                                                                                                                                                                                                                                                                                                                                                                            ILING DATE: 1999-08-10
PPLICATION NUMBER: 60/148513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LICATION NUMBER: 60/151734
ING DATE: 1999-08-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LING DATE: 1999-10-29
PLICATION NUMBER: 60/170262
LING DATE: 1999-12-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PPLICATION NUMBER: 60/187202 ILING DATE: 2000-03-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PPLICATION NUMBER: 60/222695
ILING DATE: 2000-08-02
                                                                                                                                                                                                                                                                                                                          PPLICATION NUMBER: 60/146222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PLICATION NUMBER: 60/149327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PLICATION NUMBER: 60/162506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PLICATION NUMBER: 60/206330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60/206368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PLICATION NUMBER: 60/209832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CATION NUMBER: 60/229896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/235147
FILING DATE: 2000-09-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PLICATION NUMBER: 60/198587
LING DATE: 2000-04-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PPLICATION NUMBER: 60/199614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ICATION NUMBER: 60/218371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 60/230621
FILING DATE: 2000-09-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 60/232887
FILING DATE: 2000-09-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 60/261878 FILING DATE: 2001-01-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 60/261910
                                                                                                                                                                                                                               ILING DATE: 1999-07-20
                                                                                                                                                           999-07-20
                                                                                                                                                                                                                                                                                                                                         ILING DATE: 1999-07-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                     DATE: 1999-08-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LING DATE: 2000-06-05
                                                                                                                       ILING DATE: 1999-06-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LING DATE: 2000-05-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LING DATE: 2000-05-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  000-04-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LING DATE:
                                                 PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
                                                                                                                                                                                                                             PRIOR
                                                                                                                                                                                                                                                  PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
                                                                                                                                                                                                              PRIOR
                                                                                                                                                                                                                                                                                                                                                                             PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR
                                                                                                                                                                                                                                                                                                                                                                                         ITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ITLE OF INVENTION: ACIDS ENCODING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/10/237,535
794 TCTCCAAGGAGAACGCTACCACGG 817
                        URRENT AFFLICATION
URRENT FILING DATE: 2002-09-06
PRIOR APPLICATION NUMBER: 10/197942
                                                                                                                                                                                                                    Goddard, Audrey
Grimaldi, J. Christopher
Gurney, Austin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/119342
APPLICATION NUMBER: 60/119342
APPLICATION NUMBER: 60/119342
                                                                                                             Application US/10237535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60/063046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LICATION NUMBER: 60/065027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/106932
FILING DATE: 1998-11-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/059114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PPLICATION NUMBER: 60/079689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60/030689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LICATION NUMBER: 60/091358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/115554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/123957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 60/123972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/127372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60/086478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60/087607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LICATION NUMBER: 60/089801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60/090557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PPLICATION NUMBER: 60/091978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/099803
                                                                                                                                                                                                                                                                             Smith, Victoria
Stephan, Jean-Phillippe
Watanbe, Colin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/131271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATION NUMBER: 60/133459
                                                                                                                             FUDIICATION NO. US20030073188A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         998-06-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1998-07-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-60-8661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               998-06-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -09-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1999-03-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ILING DATE: 1999-03-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LING DATE: 1999-04-0
                                                                                                                                                                                                       lvaroff, Ellen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1999-04-2
                                                                                                                                                                                                                                                                                                                                                          Shang, Zemin
                                                                                                          Sequence 48,
   ð
                                    셤
```

8 07:45:14 2003

Tue Jul

ITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ITLE OF INVENTION: ACIDS ENCODING THE SAME ILE REFERENCE: P363QRIC11 URRENT APPLICATION NUMBER: US/10/238,183 PRIOR APPLICATION NUMBER: 60/119342
PRIOR PILING DATE: 1999-02-09
PRIOR PILING DATE: 1999-02-09
PRIOR FILING DATE: 1999-03-12
PRIOR FLING DATE: 1999-03-12
PRIOR PLING DATE: 1999-03-11
PRIOR PLING DATE: 1999-03-11
PRIOR PLING DATE: 1999-04-01
PRIOR PLING DATE: 1999-04-01
PRIOR PILING DATE: 1999-04-01
PRIOR PILING DATE: 1999-04-27
PRIOR PILING DATE: 1999-04-27
PRIOR PILING DATE: 1999-05-11
PRIOR PILING DATE: 1999-05-11
PRIOR PILING DATE: 1999-05-11
PRIOR PILING DATE: 1999-05-12
PRIOR PILING DATE: 1999-05-25
PRIOR PILING DATE: 1999-05-25 APPLICATION DATE: 1998-07-01
PILING DATE: 1998-07-01
APPLICATION NUMBER: 60/091978
APPLICATION NUMBER: 60/091978 RIOR APPLICATION NUMBER: 60/106932 RIOR FILING DATE: 1998-11-03 RIOR PILING DATE: 1999-01-12 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090689 APPLICATION NUMBER: 60/091358 FILING DATE: 1998-07-01 RIOR APPLICATION NUMBER: 60/099803 RIOR APPLICATION NUMBER: 10/197942 APPLICATION NUMBER: 60/087607 APPLICATION NUMBER: 60/089801 2 SerProArgArgThrLeuProArg RESULT 43
US-10-238-183-48
US-10-238-183-48
; Sequence 48, Application US/10238183
; Publication No. US20030073189A1
; GENERAL INFORMATION: Goddard, Audrey Grimaldi, J. Christopher Gurney, Austin Smith, Victoria Stephan, Jean-Phillippe Watanbe, Colin FILING Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: R APPLICATION NUMBER: 60/274399
R FILING DATE: 2001-03-09
R APPLICATION NUMBER: 60/280982
R FILING DATE: 2001-04-03
R APPLICATION NUMBER: 60/282129
R FILING DATE: 2001-04-04
R FILING DATE: 2001-04-04
R FILING DATE: 2001-04-04 CATION NUMBER: 10/081056 IG DATE: 2002-02-20 APPLICATION NUMBER: 10/119480 FILING DATE: 2002-04-09 IG DATE: 2001-11-30 CATION NUMBER: 10/052586 FILING DATE: 2001-08-06 APPLICATION NUMBER: 09/927796 FILING DATE: 2001-08-13 APPLICATION NUMBER: 09/931836 APPLICATION NUMBER: 09/941992 PPLICATION NUMBER: 09/709238 ILING DATE: 2000-11-08 FILING DATE: 2001-03-09 APPLICATION NUMBER: 09/872035 FILING DATE: 2001-06-01 FILING DATE: 2001-07-30 APPLICATION NUMBER: 09/924419 FILING DATE: 2001-08-09 APPLICATION NUMBER: 09/929404 PILING DATE: 1999-10-18 APPLICATION NUMBER: 09/423741 FILING DATE: 1999-11-10 APPLICATION NUMBER: 09/802706 APPLICATION NUMBER: 09/918585 APPLICATION NUMBER: 10/001054 PPLICATION NUMBER: 09/267213 ILING DATE: 1999-03-12 PPLICATION NUMBER: 09/380138 APPLICATION NUMBER: 09/403297 PPLICATION NUMBER: 60/290589 ILING DATE: 2001-05-09 PLICATION NUMBER: 09/380137 LING DATE: 2001-01-16
PLICATION NUMBER: 60/262150
LING DATE: 2001-01-16 PPLICATION NUMBER: 09/180997 ILING DATE: 1998-11-19 FILING DATE: 2001-01-16 APPLICATION NUMBER: 60/261939 APPLICATION NUMBER: 60/264395 FILING DATE: 2001-01-25 APPLICATION NUMBER: 60/267623 FILING DATE: 2001-02-09 2001-08-28 LING DATE: 2002-01-15 ILING DATE: 1999-08-25 LING DATE: 1999-08-25 Percent Similarity: Best Local Similarity: Query Match: Alignment Scores: PRIOR Score:

MBER: 60/090557

998-06-02

998-06-25

1998-09-10

60/059114

997-10-24

	•		
	•		
			·
385 653 037 732 758 790 228		51734 62506 70262 77118 79851 80921 87202 98587 99614	6368 9832 8371 2695 9896 0621 2887 5147 1878
7138 9 7140 2 7141 7144 0 7144 0 7144	17071777777	$\begin{bmatrix} 1 & 1 & 1 & 1 & 1 & 1 & 1 & 1 & 1 & 1 $	$\begin{array}{cccccccccccccccccccccccccccccccccccc$
σι σι σι σι σίσισί	7. 7. 6. 7. 7. 6. 7. 7. 6. 7. 7. 6. 7. 7. 6. 7. 7. 6. 7. 7. 6. 7. 7. 6. 7. 7. 6. 7. 7. 7. 7. 7. 7. 7. 7. 7. 7. 7. 7. 7.		00 00 00 00 00 00 00 00 00 00 00 00 00
NUMBER 1999-1 1999-1 1999-1 NUMBER NUMBER 1999-1 NUMBER 1999-1		MUMBER: 1999-10 WUMBER: 1999-11 WUMBER: 2000-05 WUMBER: 2000-05 WUMBER: 2000-05 WUMBER: 2000-06 WUMBER: 2000-07 WUMBER: 2000-06 WUMBER: 2000-07	NUMBER: 000000000000000000000000000000000000
** ** ** ** ** **			
CATION G DATE CATION G DATE G DATE CATION		ATION	ATION ATION DATE: DATE: ATION DATE: DATE: ATION ATION DATE: ATION DATE: ATION
- C) (0 C)		APPLICATION APPLICATION APPLING DATE APPLICATION APPLICATION APPLICATION FILING DATE APPLICATION FILING DATE APPLICATION ELLING DATE	
	APP PILL PILL PILL PILL PILL PILL PILL P	APP FILL FILL APP FILL FILL FILL FILL	APP FILL FILL FILL APP FILL FILL FILL APP FILL APP
PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR	PRIOR	PRIOR	PRIOR

Length:
Matches:
Conservative:
Mismatches:
Indels: US-09-824-647-16 (1-2095) x US-10-238-183-48 (1-192) PRIOR APPLICATION NUMBER: 09/872035
PRIOR FILING DATE: 2001-06-01
PRIOR FILING DATE: 2001-06-01
PRIOR PELING DATE: 2001-07-30
PRIOR PELING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: 09/924419
PRIOR PELING DATE: 2001-08-06
PRIOR PELING DATE: 2001-08-09
PRIOR FILING DATE: 2001-08-19
PRIOR FILING DATE: 2001-08-13
PRIOR PELING DATE: 2001-08-13
PRIOR PELING DATE: 2001-08-13
PRIOR PELING DATE: 2001-08-16
PRIOR APPLICATION NUMBER: 09/94192
PRIOR PELING DATE: 2001-08-28
PRIOR PELING DATE: 2001-08-28
PRIOR PELING DATE: 2001-08-28
PRIOR PELING DATE: 2001-08-28
PRIOR PELING DATE: 2001-08-04
PRIOR PELING DATE: 2001-08-04
PRIOR PELING DATE: 2001-13-00
PRIOR PELING DATE: 2002-01-15
PRIOR PELING DATE: 2002-01-15
PRIOR FILING DATE: 2002-01-15
PRIOR FILING DATE: 2002-02-20
PRIOR FILING DATE: 2002-02-20
PRIOR FILING DATE: 2002-02-20
PRIOR FILING DATE: 2002-02-20
PRIOR FILING DATE: 2002-02-20 R APPLICATION NUMBER: 09/802706
R FILING DATE: 2001-03-09
R APPLICATION NUMBER: 09/872035
R APPLICATION NUMBER: 09/918585
R APPLICATION NUMBER: 09/918585 PLICATION NUMBER: 60/262150 LING DATE: 2001-01-16 LING DATE: 2001-01-10
PELICATION NUMBER: 60/264395
TIME NATE: 2001-01-25 APPLICATION NUMBER: 09/423741 FILING DATE: 1999-11-10 APPLICATION NUMBER: 09/709238 FILING DATE: 2000-11-08 PPLICATION NUMBER: 60/274399 LLING DATE: 2001-03-09 FILING DATE: 2001-04-03 APPLICATION NUMBER: 60/282129 APPLICATION NUMBER: 60/282199 FILING DATE: 2001-04-04 APPLICATION NUMBER: 60/290589 FILING DATE: 2001-05-09 APPLICATION NUMBER: 09/380137 FILING DATE: 1999-08-25 LING DATE: 2001-01-25 PLICATION NUMBER: 60/266421 APPLICATION NUMBER: 60/267623 APPLICATION NUMBER: 60/280982 APPLICATION NUMBER: 09/267213 APPLICATION NUMBER: 09/380138 APPLICATION NUMBER: 09/403297 LICATION NUMBER: 09/180997 2001-02-02 1999-10-18 2001-04-04 1999-08-2 1998-11-3 999-03-Percent Similarity: Best Local Similarity: Alignment Scores: Query Match: Pred. No.: score:

à

```
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-824-647-16 (1-2095) x US-10-238-370-48 (1-192)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps:
                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/238,370 CURRENT FILING DATE: 2002-09-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Remaining Prior Application data removed NUMBER OF SEQ ID NOS: 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search completed: July 7, 2003, 16:04:38 Job time : 104 secs
                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 10/197942
FILID DATE: 2002-07-18
APPLICATION NUMBER: 60/059114
FILING DATE: 1997-09-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 60/063046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/065027
FILING DATE: 1997-11-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/079689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60/086478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: .60/087607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 60/089801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60/090557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1998-06-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         998-06-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 1997-10-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 1998-05-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.00%
100.00%
1.15%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 1998-06-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 1998-03-
                                                                                                                                                                                                                                 FILE REFERENCE: P3630R1C10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-238-370-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3630R1C15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-824-647-16 (1-2095) x US-10-238-283-48 (1-192)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/238,283 CURRENT FILING DATE: 2002-09-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     794 TCTCCAAGGAGAACGCTACCACGG 817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SerProArgArgThrLeuProArg 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 48, Application US/10238370; Publication No. US20030073191A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 10/197942
PRIOR FILLING DATE: 2002-07-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 1998-03-27
APPLICATION NUMBER: 60/086478
                                                                                                                                                                                    Goddard, Audrey
Grimaldi, J. Christopher
Gurney, Austin
Smith, Victoria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/063046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/065027
FILING DATE: 1997-11-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PPLICATION NUMBER: 60/079689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60/030689
Application US/10238283
o. US20030073190A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CATION NUMBER: 60/059114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60/089801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/087607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60/090557
                                                                                                                                                                                                                                                                                               Stephan, Jean-Phillippe
Watanbe, Colin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       998-05-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               998-06-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.00%
100.00%
1.15%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 1997-09-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         998-06-2
                                                                                                                                                       llvaroff, Ellen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 1998-00
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Remaining Prior Applicati
NUMBER OF SEQ ID NOS: 116
SEQ ID NO 48
LENGTH: 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ILING DATE: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-238-370-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-238-283-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPRIOR PRIOR PRIOR PRIOR PRIOR ALL PRIOR 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ð
```

```
(without alignments)
6245.011 Million cell updates/sec
                                                                                                                                                                                                              July 7, 2003, 15:47:40 ; Search time 64.5 Seconds
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                     OM nucleic - protein search, using frame_plus_n2p model
                                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                    283224 seqs, 96134422 residues
                                                                                                                                                                                                                                                                                                                   6.0 , Delext
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                               US-09-824-647-16
694
                                                                                                                                                                                                                                                              Xgapop 60.0
Ygapop 60.0
Fgapop 6.0
                                                                                                                                                                                                                                                                                                    Fgapop
Delop
                                                                                                                                                                                                                                                 OLIGO
                                                                                                                                                                                          Perfect score:
                                                                                                                                                                                                                                                 Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                        Word size:
                                                                                                                                                                                                              Sequence:
                                                                                                                                                                                                                                                                                                                                                       Searched:
                                                                                                      Run on:
```

Post-processing: Listing first 45 summaries

Command line parameters:
-MODEL-frame+_n2p.model -DEV-xlp
-Q-/cgn2_1/USFTO_spool/US09824647/runat_07072003_154719_26049/app_query.fasta_1.2247
-Q-/cgn2_1/USFTO_spool/US09824647/runat_07072003_154719_26049/app_query.fasta_1.2247
-DB-FRT_3 -QFWT-fastan -SUFFIX-std.rpr -MINMATCH-0.1 -LOOPCL-0 -LOOPEXT-0
-UNITS-blts -START-1 -END-1 -MATRIX-01190 -TRANS-human40.cdi -LIST-45
-DOCALIGN-200 -THR_SCORE-quality -THR_MIN-1 -ALIGN-45 -MODE-LOCAL -OUTFWT-pto
-NORM-ext -HERSIZIZE-500 -MINIMEN-0 -MAXLEN-200000000
-USER-US09824647_eCG-1_1_108_frund_10772003_154719_26049 -NCPU-6 -ICPU-3
-NO_MMAP -LARGEQUERY -NEG_SCORES-0 -WAIT -DSPBLOCK-100 -LONGLOG
-DEV_TIMEOUT-120 -WARN_TIMEOUT-30 -THRRADS-1 -XGAPOP-60 -XGAPEXT-60 -FGAPOP-6
-FGAPEXT-7 -YGAPOP-60 -YGAPEXT-60 -DELOP-6 -DELOF-6 Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	granulin precursor	epithelin/granulin	epithelin/granulin	acrogranin - quine	antimicrobial pept	o	gene u'shaped prot	variant surface ql	hypothetical prote	variant surface ql	hypothetical profe		_	
				-			-							
,												•		•
a	GYHU	C38128	B38128	I48141	A44794	S75525	T13850	C32986	E25161	S07326	H64481	E83560	T15585	E71530
80	-	~	7	~	7	~	7	7	N	~	~	~	7	~
Query Match Length DB	593	589	589	591	46	633	1191	7.1	93	115	135	143	150	171
Query Match	58.5	4.6	4.6	3.7	1.3	1.3	1.3	1.2	1.2	1.2	1.2	1.2	1.2	1.2
Score	406	32	32	26	6	б	σ	80	æ	æ	æ	æ	æ	80
Result No.	-	7	М	7	w	9	c 7	0 8	გ ე	c 10	c 11	c 12	c 13	14
_														

conserved hypothet hypothetical prote		surface antigen CD	probable cytochrom	retrovirus-related	transgription regu	uraci P-DNA glycosy	hypothetical prote	CCHH finger protei	probable C2H2-type	acetyl-CoA carboxy	aldehyde dehydroge	gene MAC25 protein	prostacyclin-stimu	hypothetical prote	probable DNA inver	geranyltranstransf	protein T22H2.6 [1	primosomal protein	hypothetical prote	hypothetical prote	6-phosphofructokin	lipopolysaccharide	protein F23N19.17	endo-1,4-beta-gluc	. NOL1/NOP2/sun fami	agaE protein (impo	oxidoreductase Atu	potassium channel	variant surface gl
														-	-														
														•					`\$										
	_		_	_				_		_				_		_	_		`. _	_		٠.		_		_	٠.		~
A81687 T08793	809789	A40738	F75267	F44490	C75611	H82525	T28695	S55884	B96686	T06600	AC3527	152825	S50031	A83299	T31146	F83139	E87929	AH3282	T25138	T25137	S74694	AC0972	H96652	G69230	C95163	H98243	AD3042	T43394	VMUT7R
77	.0	~	H	~	~	7	~	7	7	7	~	7	~	7	7	7	7	~	7	~	-	~	~	7	7	~	~	~	7
178 181	188	193	229	245	253	256	256	259	260	262	271	277	282	293	293	295	318	334	345			374	387	394	434	442	442	461	467
~ ~	~	~	~	~	~	~	~	~	~	~	~	~	~	~	~	~	~	~	~	~	~	~	~	~	~	~3	7	~	~
	-	ä	Ä	-	-	H	-	4	H	4	-	-	H	-	ä	-	-	ä	-	H	-	-	-	-	H	-	-	H	H
m m		~	<u>~</u>	~		_	- m	_	_	_	~ ~	~	~	~		_	_	_	<u>~</u>	&	_	m	<u>~</u>	œ	œ	<u>~</u>	~	~	m
		_	_	_	_	_	_	_	_	_	_	_	_	_	_	_		_	_	~		_	_	_	_	_	_	_	_
15	17	18	19	20	71	22	23	24	25	56	27	28	29	30	31	32	33	34	35		37	38	39	40	41	42	43	44	45
	O				ပ	ပ		ပ	O	ပ	ပ်				ပ	O		O			O	U	O		U	ņ		ပ	O

ALIGNMENTS

N;Alternate names: epithelin
N;Contains: granulin A; granulin B; granulin C; granulin D; granulin E; granulin I
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: JO-Sep-1992 *Sequence_revision 03-May-1996 *text_change 08-Dec-2000
C;Accession: JC1284, A38128; A38118; A36698; B36698; C36698; D36698; A56873
R;Bhandari, V.; Bateman, A. A; Residues: 1-593 <BHA>
R; Plowman, G.D.; Green, J.M.; Neubauer, M.G.; Buckley, S.D.; McDonald, V.L.; Todan J. Biol. Chem. 267, 13073-13078, 1992.
A;Title: The epithelin precursor encodes two proteins with opposing activities on A;Reference number: A38128; MUID:92317004; PMID:1618805 Biochem. Biophys. Res. Commun. 188, 57-63, 1992 A;Title: Structure and chromosomal location of the human granulin gene. A;Reference number: JC1284; MUID:93038704; PMID:1417868 granulin precursor [validated] - human Status: preliminary Molecule type: mRNA Residues: 1-593 <PLO> A; Molecule type: DNA ; Accession: A38128 A; Accession: JC1284

RiBhandari, V.; Palfree, R.G.E.; Bateman, A.
Proc. Natl. Acad. Sci. U.S.A. 89, 1715-1719, 1992
A;Title: Isolation and sequence of the granulin precursor cDNA from human bone max Reference number: A38118; MUID:92179253; PMID:1542665
A;Accession: A38118 ross-references: GB:X62320; NID:g31192; PIDN:CAA44196.1; PID:g31193 A; Molecule type: mRNA

A; Residues: 11-06, 'R', 408-433,'G', 435-453,'G', 455-459,'Q', 461-546,'A', 548-566,'R', A; Cross-references: GB: M75161; NID: 9183612; PIDN: AAA58617.1; PID: 9183613
A; Note: this sequence has been revised in reference JC1284
B; Bateman, A.; Belcourt, D.; Bennett, H.; Lazure, C.; Solomon, S.
Blochem. Blophys. Res. Commun. 173, 1161-1168, 1990
A; Title: Granulins, a novel class of peptide from leukocytes.
A; Reference number: A36698; MUD: 91097544; PMID: 2268320

140 492

372

160

```
N.Alternate names: acrogramin; PC-cell-derived growth factor C;Species: Mus musculus (house mouse) C;Species: Mus musculus (house mouse) C;Date: 10-Jul-1992 *sequence_revision 10-Jul-1992 *text_change 20-Aug-1999 C;Accession: C381286; S32503; 199468; A46705 **
S;Plowman, G.D.; Green, J.M.; Neubauer, M.G.; Buckley, S.D.; McDonald, V.L.; Todaro J. Biol. Chem. 267, 13073-13078, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GATGTGAAATGTGACATGGAGGTGAGCTGCCCAGATGGCTATACCTGCTGCCGTCTACAG 912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     281 AspvallysCysAspWetGluValSerCysProAspGlyTyrThrCysCysArgLeuGln 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAGGTGCCCTGGATGGAGAGACCCCCAGCTCACCTCAGCCTGCCAGACCCACAGCCTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTCACGTCTGGGGGGTGGGCTGTCCCAATCCCAGAGGCTGTCTGCTGCTCGGACCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               261 LeuSerLysGluAsnAlaThrThrAspLeuLeuThrLysLeuProAlaHisThrValGly
CCCACGGGCACCCACCCCTGGCAAAGAAGCTCCCTGCCCAGAGGACTAACAGGGCAGTG
                                                                                                                                                                                                                                                                                                                                                                   GTGGCTGCCATCCAGTGCCCTGATAGTCAGTTCGAATGCCCGGACTTCTCCACGTGCTGT
                                                                                                     A GTAATGGTCGATGCTCGTGGGGGGTGCTGCCCCATGCCCCAGGCTTCCTGCTGTGAAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAGCACTGCTGCCCCCAG 1230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GlunisCysCysProGlu 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               epithelin/granulin precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           853
                                                                                                                                                                                                                                                                                                                191
                                                                                                                                                                                                                                                                                                                                                                                                     181
                                                                                                                                                                                                                                                                                                                                                                                                                                                 613
                                                                                                                                                                                                                                                                                                                                                          553
                                                                                                                                                                                                                        141
                                                                                                                                                                                                                                                                    193
    313
                                                101
                                                                                         373
                                                                                                                                                                                 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ŏ
                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                 õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                          Š
                                                                                                                          ලි
                                                                                                                                                                                 à
                                                                                                                                                                                                                        셤
                                         8
                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A/CrossTeterenues.

A/Introns: 46/3; 88/3; 117/1; 154/3; 200/1; 236/3; 279/1; 311/3; 393/3; 471/3; 548/3

A/Introns: 46/3; 88/3; 117/1; 154/3; 200/1; 236/3; 279/1; 311/3; 393/3; 471/3; 548/3

A/Introns: 46/3; 88/3; 117/1; 154/3; 200/1; 236/3; 279/1; 311/3; 393/3; 471/3; 548/3

C. Superfamily: granulin

E/E-17/Domain: signal sequence #status predicted <SIG>
E/IB-59/Product: granulin #status predicted <GRO>
E/IB-59/Product: granulin #status experimental <GRP>
E/IB-44/Product: granulin # fstatus experimental <GRP>
E/IB-41/Product: granulin # fstatus experimental <GRP>
E/IB-36/Product: granulin # fstatus experimental <GRP>
E/A42-496/Product: granulin # fstatus experimental <GRP>
E/A42-496/Product: granulin # fstatus predicted <GRD>
E/E-173/Product: granulin # fstatus predicted <GRD>
E/E-173/Product # granulin # fstatus #
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCCAGTTGCTGCCCCTTCCCAGAGGCCGTGCCATGCGGGGATGGCCATCACTGCTGCCCCA 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCAGATGGTCAGTTCTGCCCTGTGGCCTGCTGCTGGACCCCGGAGGAGCCAGCTACAGC 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGCTGCCGTCCCCTTCTGGACAAATGGCCCACAACACTGAGCAGGCATCTGGGTGGCCCC 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: protein
A; Residues: 281-36 CBAT>
A; Note: this protein was purified and characterized as granulin A
A; Accession: B3669
A; Molecule type: protein
A; Residues: 206-218, 'H', '220-233 CBAZ>
A; Molecule type: protein was purified and characterized as granulin B
A; Molecule type: protein
A; Residues: 364-367, 'X', 369-385, 'H', 387-396 CBA3>
A; Note: this protein was purified and characterized as granulin C
A; Accession: D36698
A; Molecule type: protein
A; Residues: 342-446, 'XDTSS', 456-458, 'DG' CBA4>
A; Molecule type: protein
A; Residues: 442-446, 'XDTSS', 456-458, 'DG' CBA4>
A; Residues: 442-446, 'XDTSS', 456-458, 'DG' CBA4>
A; Residues: A; Bagshawe, R.D.; Coles, B.: Read, D.; Taylor, M.
A; Residues: A; Bagshawe, R.D.; Coles, B.: Read, D.; Taylor, M.
A; Reference number: A56873; MUID:93229246; PMID:8471426
A; Reference number: A56873; MUID:93229246; PMID:8471426
A; Residues: 281-283, 'X', 285-289, 'S', 291-295 CKAR>
A; Residues: Sequence extracted from NCBI backbone (NCBIP:129524)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gene: GDB:GRN
Cross-references: GDB:136006; OMIM:138945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (1-593)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Asn)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-824-647-16 (1-2095) x GYHU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;368/Binding site: carbohydrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  406.00
100.00%
100.00%
58.50%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score:
```

1092

360

1152

380

1212

400

셤

à

g

à a δ g

ŏ

g

ò

1032

340

320

972

852

280

792 260

220

200 672

612

ŝ

tissue distribution,

589 32 0 0 0 0

```
R;Baba, T.; Hoff, H.B. Mol. 1993 Mol. Reprod. Dev. 34, 133-243, 1993 A;Title: Acrogranin, an acrosomal cysteine-rich glycoprotein, is the precusor A;Reference number: 148141; MUID:93228994; PMID:8471244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C.Species: Cavia porcellus (guinea pig)
C.Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 20-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1396 GGGAGCTGGCCTGCTGCCAGTTGCCCCATGCTGTGTGCTGCGCAGGATCGCCAGCACTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   442 GATGGCTCCTGGGGGTGCTGCCCCATGCCCCAGGCTTCCTGCTGTGAAGACAGGGTGCAC
                                                                                                                                                                          A; Molecule type: protein
A; Residues: 279-307, SB',310-324, 'T',326,'X',328,'Q' < BAT>
A; Residues: 279-307, SB',310-324,'T',326,'X',328,'Q' < BAT>
B; Bhandari, V.; Glaid, A.; Bateman, A.
Endocrinology 133, 2662-2689, 1993
A; Title: The complementary deoxyribonucleic acid sequence, tissue distrib
A; Reference number: 153272; MUID: 94062640; PMID: 8243292
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: "RRM
A; Molecule type: "RRM
A; Residues: 1-200,'S', 203-388,'M', 390-589 < RES>
A; Cross-references: GB: M97750; NID: 9204223; PIDN: AAA16903.1; PID: 9204224
C; Superfamily: granulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:M86735; NID:g191234; PIDN:AAA37030.1; PID:g191235
C;Superfamily: granulin
                                 R;Bateman, A.; Belcourt, D.; Bennett, H.; Lazure, C.; Solomon, Blochem. Blophys. Res. Commun. 173, 1161-1168, 1990
A;Title: Granulins, a novel class of peptide from leukocytes. A;Reference number: A36698, MUID:91097544; PMID:2268320
A;Accession: E36698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1456 TGCCCGGCTGGCTACACCTGCAACGTGAAGGCTCGA 1491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             480 CysProAlaGlyTyrThrCysAsnValLySAlaArg 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-591 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-824-647-16 (1-2095) x.B38128 (1-589)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-824-647-16 (1-2095) x I48141 (1-591)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        502 TGCTGTCCGCACGGTGCC 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               acrogranin - guinea pig (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.37e-17
26.00
100.00%
100.00%
3.75%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32.00
100.00%
.ty: 100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: 148141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Accession: I48141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ð
                                                                                                                                                                                                                                                                                                                A.Molecule type: DNA
A.Residues: 18-48, L., 351-589 <BAB>
A.Residues: 18-48, L., 351-589 <BAB>
R.Baba, T.; Hoff, H.B.
Nol. Reprod. Dev. 34, 233-243, 1993
A.Title: Acrogranin, an acrosomal cysteine-rich glycoprotein, is the precusor of the grown and the status: I48141; MUID: 9328994; PMID: 8471244
A.Reference number: 149141; MUID: 9328994; PMID: 8471244
A.Recession: 149468
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Molecule type: mRNA
A.Molecule type: mRNA
A.Molecule type: mRNA
   epithe
                                                                                  A; Wolecule type: mRNA
A; Residues: 1-589 <PLO>
A; Residues: 1-589 <PLO>
A; Cross. 1-589 <PLO>
A; Cross. 1-580 <PLO>
A; Cross. GB: X62321; NID: 950851; PIDN: CAA44197.1; PID: 950852
B; Baba, T.; Nemoto, H.; Watanabe, K.; Aral, Y.; Gerton, G.L.
FEBS Lett. 322, 89-94, 1993
A; Title: Expoi/intron organization of the gene encoding the mouse epithelin/granulin pred A; Reference number: $32503; MUID: 93245991; PMID: 8482392
A; Accession: $32503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: protein
A; Residues: 18-19, 'X', 21-25, 'X', 27-29, 'XX', 32; 'XXX', 119-127;152-154, 'DXK', 158-161, 'X', 16
C; Superfamily: granulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               epithelin/granulin precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Jul-1992 #sequence_revision 10-Jul-1992 #text_change 20-Aug-1999
C;Accession: B38128; A36199; B36199; B36699; B35672
R;Plowman, G.D.; Green, J.M.; Neubauer, M.G.; Buckley, S.D.; McDonald, V.L.; Todaro, G.J.
A;Title: The epithelin precursor encodes two proteins with opposing activities on epithe
A;Reference number: A38128; MUID:92317004; PMID:1618805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-589 <PLC>
A; Residues: 1-589 <PLC>
A; Cross-references: GB:X62322; NID:g56108; PIDN:CAA44198.1; PID:g56109
A; Cross-references: GB:X62322; NID:g56108; DIDN:CAA44198.1; PID:g56109
B; Shoyab, M.; NcDonald, V.L.; Byles, C.; Todaro, G.J.; Plowman, G.D.
Proc. Natl. Acad. Sci. U.S.A. 87, 7912-7916, 1990
A; Title: Epithelins 1 and 2: isolation and characterization of two cysteine-rich growth-A; Reference number: A36199; MUID:91045907; PMID:2236009
A; Rocession: A36199
A; Molecule type: protein
A; Residues: 280-300 <SHO>
A; Accession: B36199
A; Molecule type: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Residues: 1-550,"L", 252-253, VV, 255-349, LL', 351-401, 'SA', 404-589 <RES>
A; Cross-references: GB:M86736; NID:g191766; PIDN:AAA37191.1; PID:g191767
R; Zhou, J.; Gao, G.; Crabb, J.W.; Serrero, G.
J. Blol. Chem. 268, 10863-10869, 1993
A; Title: Purification of an autocrine growth factor homologous with mouse epithelin A; Reference number: A46705; MUID:99266526; PMID:8496151
A;Title: The epithelin precursor encodes two proteins with opposing activities on A;Reference number: A38128; MUID:92317004; PMID:1618805
A;Accession: C38128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1396 GGGAGCTGGGCCTGCTGCTGCTTGCCCCATGCTGTGTGCTGCGAGGATCGCCAGCACTGC 1455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         589
00
00
00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1456 TGCCCGGCTGGCTACACCTGCAACGTGAAGGCTCGA 1491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       480 CysProAlaGlyTyrThrCysAsnValLySAlaArg 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (1-589)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-824-647-16 (1-2095) x C38128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32.00
100.00%
100.00%
4.61%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9e-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
```

οţ

591 0 0 0

RESULT

```
A; Description: acts as a transregulator of achaete and scute in the dorsal region of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein trak - Salmonella typhimurium plasmid pED208 (fragment)
C;Species: Salmonella typhimurium
C;Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 30-Sep-1993
                                                                                                                                                                                                                                                A; Cross-references: EMBL: Y12322; NID:e1169964; PID:e1169965; PIDN:CAA72991.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Trypanosoma equiperdum
C;Date: 27-Feb-1990 #sequence_revision 27-Feb-1990 #text_change 26-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  variant surface glycoprotein 20 BC1 RF2 - Trypanosoma equiperdum (fragment)
              C;Species: Drosophila melanogaster
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 17-Nov-2000
C;Accession: T13850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Thon, G.; Baltz, T.; Elsen, H. Genes Dev. 3, 1247-1254, 1989
A;Title: Antigenic diversity by the recombination of pseudogenes.
A;Reference number: A32986; MUD:90006746; PMID:2792762
gene u-shaped protein - fruit fly (Drosophila melanogaster)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11191
9
0
0
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                780000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
.Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative:
Mismatches:
Indels:
                                                                                           R; Haenlin, M.

Submitted 'to the EMBL Data Library, April 1997
A; Reference number: 217795
A; Accession: T13850
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule preliminary; translated from A; Residues: 1-1191 < HAE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-71 < THO>
A;Cross-references: GB:X17158
C; Superfamily: variant surface glycoprotein
C; Reywords: glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1632 GCCCTGTCGGTTGTCTCGGCAGCA 1609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Accession: E25161
R; Finlay, B.B.; Frost, L.S.; Paranchych, W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-824-647-16 (1-2095) x T13850 (1-1191)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-824-647-16 (1-2095) x C32986 (1-71)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58 AlaLeuSerValValSerAlaAla 65
                                                                                                                                                                                                                                                                                                                             Cross-references: FlyBase: FBgn0003963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84.9
8.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5.45
9.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1,318
                                                                                                                                                                                                                                                                                                                                                                                                   C; Keywords: zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: C32986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Accession: C32986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
                                                                                                                                                                                                                                                                                                       Gene: u-shaped
                                                                                                                                                                                                                                                                                                                                                            C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-633 <KAN>
A;Cross-references: EMBL:D90911; GB:AB001339; NID:g1653083; PIDN:BAA18086.1; PID:d101881
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R; Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sensory transduction histidine kinase sll1228 - Synechocystis sp. (strain PCC 6803) N;Alternate names: protein sll1228 C;Species: Synechocystis sp. A;Variety: PCC 6803 A;Variety: PCC 6803 C;Date: 25-Apr-1997 *sequence_revision 25-Apr-1997 *text_change 08-Oct-1999 C;Accession: 575525
                                                                                                                                         A.Fitle: Identification of eNAP-1, an antimicrobial peptide from equine neutrophils. A; Reference number: A44794; MUID:92347972; PMID:1639474
       antinicrobial peptide eNAP-1 - horse (fragment)
C;Species: Equus caballus (domestic horse)
C;Date: 24-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 17-Nov-1995
C;Accession: A44794, A40833
C;Accession: M.A.; Harwig, S.S.; Cullor, J.S.; Hughes, J.P.; Lehrer, R.I.
R;Couto, M.A.; Harwig, S.S.; Cullor, J.S.; Hughes, J.P.; Lehrer, R.I.
Infect. Immun. 60, 3065-3071, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F:420-531/Domain: response regulator homology <RRH>
F:468/Binding site: phosphate (Asp) (covalent) #status predicted
                                                                                                                                                                                                                                                                                      A;Experimental source: neutrophils
A;Note: sequence extracted from NCBI backbone (NCBIP:109730)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0000
                                                                                                                                                                                                                                                                                                                                                                                                          $ 6000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Reference number: S74322; MUID:97061201; PMID:8905231
A; Accession: S75525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1573 TGTGGGGAAGGACACTTCTGCCATGAT 1599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Superfamily: response regulator homology Reywords: phosphoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-824-647-16 (1-2095) x S75525 (1-633)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-824-647-16 (1-2095) x A44794 (1-46)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.00%
100.00%
1.30%
                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.00%
100.00%
1.30%
                                                                                                                                                                                                                                           A; Molecule type: protein
A; Residues: 1-46 <COU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                         ;Superfamily: granulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                        A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
                                                                                                                                                                                                Accession: A44794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Start codon: GTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
```

RESULT

ð

Query Match:

ò

```
A;Cross-references: GB:AE004503; GB:AE004091; NID:99946553; PIDN:AAG04068.1; GSPDE A;Experimental source: strain PAO1 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Artitle: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic
A; Reference number: A82950; MUID:20437337; PMID:10984043
                                                                                                           A; Cross-references: GB:U67586; GB:L77117; NID:g1592096; PIDN:AAB99470.1; PID:g1592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, .; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein PA0679 [imported] - Pseudomonas aeruginosa (strain PA01) C;Species: Pseudomonas aeruginosa C;Species: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
                                A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-135 <BUL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein C24A3.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T15585
                                                                                                                                                              A;Nap position: FOR1427020-1427427
A;Start codon: GTG
C;Superfamily: Methanococcus jannaschil hypothetical protein MJ1457
                                                                                                                                                                                                                                                                                            135
0
0
0
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted to the EMBL Data Library, November 1995
A; Description: The sequence of C. elegans cosmid C24A3
A; Reference number: Z18373
A; Accession: T15585
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-150 cFRV>
                                                                                                                                                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1458 GCAGCAGTGCTGGCGATCCTCGCA 1435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                144 GGGACGCAGCAGCTGTAGCTGGC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-824-647-16 (1-2095) x E83560 (1-143)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-824-647-16 (1-2095) x H64481 (1-135)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58 GlyThralaAlaAlaValAlaGly 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76.4
8.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                            77.1
8.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                  1.168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.168
                                                                                                                                                                                                                                                                                                                 Score:
Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary
A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Accession: E83560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: E83560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
             A; Accession: H64481
                                                                                                                                                                                                                                                                      Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Gene: PA0679
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match:
                                                                                                                                           C; Genetics:
                                                                                                                                                                                                                                                                                                    ..
Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score:
                                                                                                                                                                                                                                                                                                 Pred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                variant surface glycoprotein AnTat 1.8 precursor - Trypanosoma brucei (fragment)
C;Species: Trypanosoma brucei
C;Species: Trypanosoma brucei
C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 31-Jan-2000
C;Accession: 807326; A17609
R;Matthyssens, G.; Michiels, F.; Hamers, R.; Pays, E.; Steinert, M.
A;Title: Two variant surface glycoproteins of Trypanosoma brucei have a conserved C-term A;Reference number: A17609; MUID:82013622; PMID:7278981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A.Molecule type: mRNA
A.Residues: 1-115 cMATHS
A.Residues: 1-115 cMATHS
A.Cross-references: EMBL:J01227; NID:g162397; PIDN:AAA30292.1; PID:g162398
A.Kross-references: EMBL:J01227; NID:g163397; PIDN:AAA30292.1; PID:g162398
A.Note: the authors translated the codon GCT for residue 53 as Ser
C; Superfamily: variant surface glycoprotein
C; Keywords: blocked carboxyl end; glycoprotein; lipoprotein; membrane protein; phosphati
F:192/Product: variant surface glycoprotein (clone Antal 1.8) (fragment) #status predict
F:93-115/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F:42/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:92/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Asp) (in mature form)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Accession: H64481
R; Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, R; Bult, C.J.; White, O.; Olsen, G.J.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A. Science 273, 1058-1073, 1956
A; Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.A; Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii A; Reference number: A64300; MUID: 96337999; PMID: 8688087
J. Bacteriol. 168, 990-998, 1986
A;Title: Nucleotide sequence of the traYALE region from IncFV plasmid pED208.
A;Reference number: A91828; MUID:87056998; PMID:2877970
A;Accession: E2561
A;Accession: E2561
A;Accession: A;Accession: A64078
A;Residues: 1-93 <FIN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein MJ1457 - Methanococcus jannaschii
C;Species: Methanococcus jannaschii
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   115
8
0
0
                                                                                                                                                                                                                                                                                              00000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                            Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                  Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1289 AGTCCAGCCACGATCTCGCTTCCT 1266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1632 GCCCTGTCGGTTGTCTCGGCAGCA 1609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-824-647-16 (1-2095) x S07326 (1-115)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (1-93)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26 SerProAlaThrIleSerLeuPro 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-824-647-16 (1-2095) x E25161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                               100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                  ..168
                                                                                                                                                                                                                                                                                              81.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
                                                                                                                                                                                                                   A; Genome: plasmid
                                                                                                                                                                                                                                                                    Aliqnment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                               Query Match:
DB:
                                                                                                                                                                                           Gene: trak
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                Genetics:
                                                                                                                                                                                                                                                                                            red. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        H64481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                å
```

```
uypornetical protein UL26 - human cytomegalovirus (strain AD169)
C; Species: human cytomegalovirus, human herpesvirus 5
A;Note: host Homo sapiens (man)
C;Date: 07-5ep-1990 #sequence_revision 07-5ep-1990 #text_change 21-Jan-2000
C;Accession: S09789
R;Chee, M.S.; Bankier, A.T.; Beck, S.; Bohni, R.; Brown, C.M.; Cerny, R.; Horsnell, M.; Barrell, B.G.
Curr. Top. Microbiol. Immunol. 154, 125-169, 1990
A;Title: Analysis of the protein-coding content of the sequence of human cytomegalox A;Reference number: S09749; MUID: 90269039; PMID: 2161319
A;Status. .....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:X17403; NID:959591; PIDN:CAA35425.1; PID:959631
A;Note: this sequence was submitted to the EMBL Data Library, December 1989
C;Superfamily: human cytomegalovirus hypothetical protein UL26
                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Homo sapiens (man)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 13-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-188 <CHE>
                                                                                                                                                                                                                                                                                                                                                                                                                              C; Accession: T08793
R; Koehrer, K.; Beyer, A.; Mewes, H.W.; Gassenhuber, J.; Wiemann, Bubmitted to the Protein Sequence Database, May 1999
A; Reference number: 216468
A; Accession: T08793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Wolecule type: mRWA
A;Residues: 1-181 <KOE>
A;Cross-references: EMBL:AL050173
A;Experimental source: adult uterus; clone DKFZp586F0422
                                                                                                                                                                                                                                                                                                                                                         hypothetical protein DKFZp586F0422.1 - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches:
Conservative:
Mismatches:
Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels:
                                                                                             Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1847 TCTGCTCAGGCCTCCCTAGCACCT 1870
                                                                                                                                                                                                          US-09-824-647-16 (1-2095) x T08793 (1-181)
                                                                                                                                                                   US-09-824-647-16 (1-2095) x A81687 (1-178)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SeralaGinAlaSerLeuAlaPro 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.00%
100.00%
1.15%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73.3
8.00
100.00%
100.00%
1.16%
  73.9
8.00
100.00%
100.00%
1.15%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity:
Query Match:
                                       Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Genetics:
A;Note: DKFZp586F0422.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No.:
         ..
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Residues: 1-178 <TET>
Cross-references: GB:AE002326; GB:AE002160; NID:g7190614; PIDN:AAF39412.1; PID:g719061
Experimental source: strain Nigg (MoPn)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Accession: A81687
R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis Mopn and Chlamydia pneumoniae AR39.
A;Reference number: A81500; MUID:20150255; PMID:10684935
    A;Cross-references: EMBL:D40424; NID:91065542; PID:91065544; PIDN:AAA81456.1; CESP:C24A3
C;Genetics:
A;Gene: CESP:C24A3.5
A;Introns: 88/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein CT303 - Chlamydia trachomatis (serotype D, strain UW3/Cx)
C;Species: Chlamydia trachomatis
C;Species: Chlamydia trachomatis
C;Species: Chlamydia trachomatis
C;Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 08-Oct-1999
C;Accession: E71530
R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell, Science 282, 754-759, 1998
A;Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia track, Reference number: A71570; MUID:99000809; PMID:9784136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;Accession: E71530
;Status: preliminary
;Molecule type: DNA
;Residues: 1-171 <ARN>
;Cross-references: GB:AE001303; GB:AE001273; NID:q3328718; PIDN:AAC67896.1; PID:q332871
;Experimental source: serotype D, strain UW-3/Cx
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               - Chlamydia muridarum (strain Nigg)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          conserved hypothetical protein TCO577 [imported] - Chlamydia muridarum (stre
C;Species: Chlamydia muridarum, Chlamydia trachomatis MoPn
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 11-May-2000
                                                                                                                                                 0000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                        Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1125 CTGTCCCTCCGATACCTGCTG 1148
                                                                                                                                                                                                                                                                                                                                                                                       109 AlaProArgSerSerHisGlnPro 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-824-647-16 (1-2095) x E71530 (1-171)
                                                                                                                                                                                                                                                                                                                    US-09-824-647-16 (1-2095) x T15585 (1-150)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCACCGCGTTCCAGCCACCAGCCC 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74.4
8.00
100.00%
100.00%
1.15%
                                                                                                                                                    75.9
8.00
100.00%
100.00%
1.16%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                      Percent Similarity:.
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: A81687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alignment Scores:
Pred. No.:
                                                                                                                             Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Gene: TC0577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Genetics:
A;Gene: CT303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Duery Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
```

181 8 0 0 0

88 0000 0000

US-09-824-647-16 (1-2095) x S09789 (1-188)

Aliqument Scores

```
C; Species: Popillia japonica (Japanese beetle)
C; Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 01-Dec-2000
C; Accession: F44490; Add42
R; Burke, W.D; Eickbush, D.G; Xiong, Y.; Jakubczak, J.; Eickbush, T.H.
Mol. Biol. Evol. 10, 163-185, 1993
A; Title: Sequence relationship of retrotransposable elements R1 and R2 within and A; Reference number: A44490; MUID:93196484; PMID:8383793
A; Accession: F44490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             retrovirus-related reverse transcriptase homolog - Japanese beetle retrotransposc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transcription regulator, IclR family - Deinococcus radiodurans (strain R1) (:Species: Deinococcus radiodurans (c.Species: Deinococcus radiodurans (c.Species: Deinococcus radiodurans (c.Spate: Olobec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000 (c.Speciesion: 075611 (c.S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:L00944; NID:g160749; PID:g160750
A;Note: sequence extracted from NCBI backbone (NCBIP:127240)
R;Jakubczak, J.L.; Burke, W.D.; E10kbush, T.H.
R;Jakubczak, J.L.; Burke, W.D.; E10kbush, T.H.
A;Title: Retrotransposable elements R1 and R2 interrupt the rRNA genes of A;Reference number: A40442; MUID:91195337; PMID:1849649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-245 <BUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             245
0 0 0 0
0 0 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   229
8
0
0
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (1-229)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1494 CTGCGAGAAGGAAGTGGTCTCTGC 1517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-824-647-16 (1-2095) x F44490 (1-245)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-824-647-16 (1-2095) x F75267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71.2
8.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.00%
100.00%
1.15%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <JAK>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 175-191 <
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local S
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score:
                                                                                                                                                                                                                                                                    National Control of the control of control 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R.J.;
C.; Ma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Molecule type: DNA A,Residues: 1-229 <MHI>
A,Residues: 1-229 <MHI>
A,Residues: GB:AE002078; GB:AE000513; NID:g6460306; PIDN:AAF12028.1; PID:g646036
A,Experimental source: strain R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        묩.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: A40738
A; Molecule type: mRNA
A; Residues: 1-153, V7, 155-193 <GOO>
A; Cross-references: GB-L08096; NID:g307127; PIDN:AAA36175.1; PID:g307128
A; Experimental source: B cells
A; Note: sequence extracted from NCBI backbone (NCBIN:131664, NCBIP:131665)
C; Genetics:
A; Gnetics:
A; Gross-references: GDB:139157
A; App position: 19p13-19p13-19p13
C; Keywords: B-cell; glycoprotein; surface antigen; T-cell; transmembrane protein
C; Keywords: B-cell; glycoprotein; surface antigen; T-cell; transmembrane protein
F; 21-38/Domain: transmembrane #status predicted <EMT>
F; 39-193/Domain: extracellular #status predicted <EMT>
F; 39-193/Domain: extracellular #status predicted <EMT>
F; 31-10/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J.D.; Dodson,
T.; Zalewski,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans A:Reference number: A75250; MUID:20036896; PMID:10567266 A:Accession: P75267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probable cytochrome c4 - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Decies: Dana-2000 $sequence_revision 17-Mar-2000 $text_change 17-Mar-2000
C;Accession: F75267
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Do, M.; Shen, M.; Vanarthevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zale Science 286, 1571-1577, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
1212 GTGGTCCGAGCAGCAGACAGCCTC 1189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1734 CAGGGAGGCCCCGCGCTGGGACGC 1757
                                                  101 ValValArgAlaAlaAspSerLeu 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-824-647-16 (1-2095) x A40738 (1-193)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76 GlnGlyGlyProAlaLeuGlyArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.00%
100.00%
1.15%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8
                                                                                                                                                                                                                                           surface antigen CD70 - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 19
F75267
                                                                                                                                                           RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ŏ
```

most in

```
probable C2H2 type zinc finger protein F15E12.19 [imported] - Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Accession: S55884
R; Tague, B.W.; Goodman, H.M.
Plant Mol. Biol. 28, 267-279, 1995
Plant Mol. Biol. 28, 267-279, 1995
A; Title: Characterization of a family of Arabidopsis zinc finger protein cDNAs. A; Reference number: S55881; MUID:95322589; PMID:7599312
A; Recession: S55884
                                                                                                                                                                                                                                                                                                                                                                                         A; Cross-references: EMBL: AL023496; NID: e1292348; PID: e1292362; PIDN: CAA18912.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
                                                                                                                                                       CCHH finger protein 4 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A;Residues: 1-259 <TAG>
A;Cross-references: GB:L39647; NID:g790678; PIDN:AAA87300.1; PID:g790679
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       256
0
0
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-824-647-16 (1-2095) x S55884 (1-259)
                                         1544 CTACGGGCCAGGAAGGTGGCAGGC 1521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-824-647-16 (1-2095) x T28695 (1-256)
JS-09-824-647-16 (1-2095) x H82525 (1-256)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Genetroc.
A;Map position: 1
C;Keywords: DNA binding; zinc finger
C;Keywords: Zinc finger CCHH motif
                                                                 69.9
8.00
100.00%
1.16%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8.00
100.008
1.158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-256 <PAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No.:
                                                                                                                                  RESULT 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ŏ
                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             uracil-DNA glycosylase XF2692 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 %sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
C;Date: 18-Aug-2000 %sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
R;Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequent Nature 406, 151-157, 2000
A;Feigerence number: A02515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A, Authors: Perreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, W.L.; Remper, B.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigrenado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, B.A.; Matcukuma, A.Y.; Marck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Murtins, E.M.; Matcukuma, A.Y.; Monck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Murtins, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palnieri, D.M.; Rodrigues, V.; Rosa, A.J. de M.; de Solva, V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak A, Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silvai, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Zhibako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Cross-references: GB:AE004075; GB:AE003849; NID:99107929; PIDN:AAF85489.1; GSPDB:GN001
A; Experimental source: strain 9a5c
        Σ
                                                                                                                                                                                      A;Cross-references: GB:AE001862; GB:AE001825; NID:g6460468; PIDN:AAF12212.1; PID:g64605d
A;Experimental source: strain R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S. submitted to GenBank, June 2000
  , M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
                                                                       A.Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1. A;Reference number: A75250; MUID:20036896; PMID:10567266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            255
0
0
0
0
                                                                                                                                                                                                                                                                                                                                                                        253
0
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-824-647-16 (1-2095) x C75611 (1-253)
                                                                                                                                                                                                                                                                                          A;Map position: 2
C;Superfamily: acetate operon repressor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: XF2692
C;Superfamily: uracil-DNA glycosylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.00%
                                                                                                                                                                                                                                                                                                                                                                            70.1
8.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.16%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70
8.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Reference number: A59328
A; Contents: annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-256 <SIM>
                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Status: preliminary
                                                                                                                                                   Status: preliminary
                                                                                                                                                                    Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: H82525
                                                                                                                         Accession: C75611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
                                                                                                                                                                                                                                                                        A; Gene: DRA0152
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No.:
                                                                                                                                                                                                                                                         C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                   ..
9
                                                                                                                                                                                                                                                                                                                                                                                                      Score:
```

ð

1.168 Indels 1.168 Indels 1.169 Gaps: 2 Gaps: 3.09-824-647-16 (1-2095) x T06600 (1-262) 1404 CCACCTCCCACCCTGCTCGGCA 1381 161 ProAlaProThrLeuAlaArgAla 168 1.11	53382.1; PID:	t Similarity: 100.00% ocal Similarity: 100.00% Match: 2 2 824-647-16 (1-2095) x AC3527 (1-2 2021 ACAGGGTCCACTGAAACGGGGAGG	152825 gene MAC25 protein - human C;Specles: Homo sapiens (man) C;Specles: Homo sapiens (man) C;Specles: Homo sapiens (man) C;Date: 02-Jul-1996 #text_change 05-Nov-1999 C;Accession: 152825 R;Murphy, M.; Pykett, M.J.; Harnish, P.; Zang, K.D.; George, D.L. Cell Growth Differ. 4, 715-722, 1993 A;Title: Identification and characterization of genes differentially expressed in A;Reference number: 152825; MuID: 94059820; PMID: 7694637 A;Accession: 152825; MuID: 94059820; PMID: 7694637 A;Accession: 152825; MuID: 94059820; PMID: 7694637 A;Residues: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-277 <-RES. A;Cross-references: GB:L19182; NID: 9307150; PIDN: AAA16187.1; PID: 9307151	C; Genetics: A; Genetics: C; Superfamily: Kazal proteinase inhibitor homology C; Superfamily: Kazal proteinase inhibitor homology F; 104-156/Domain: Kazal proteinase inhibitor homology (KPI8> Alignment Scores: 69.2 Length: 277 Score: 8.00 Matches: 8 Percent Similarity: 100.00% Mismatches: 0 Best Local Similarity: 100:00% Mismatches: 0 Owery Match: 2 DB: Gaps: 0
C; Accession: B96686 R; Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Hulzar, L. ansen, N.F.; Hughes, B.; Hulzar, L. Nature 408, 816-820, 2000 A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Rowley, J.; Sakano, H. A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Ker, M.; Roun, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A; Reference and analysis of chromosome 1 of the plant Arabidopsis. A; Reference and analysis of chromosome 1 of the plant Arabidopsis. A; Reference and analysis of chromosome 1 of the plant Arabidopsis. A; Reference number: A86141; MUID:21016719; PMID:11130712 A; Residues: 1-260 cSTO- A; Cross-references: GB: AE005173; NID:g11038470; PIDN: AAG27749.1; GSPDB: GN00141 C; Genetics: A; Map position: 1	Alignment Scores: Fred. No.: 8.00 Matches: 8.00	70 7	A; Status: translated from GB/EMBL/DDBJ A; Molecule type: mRNA A; Molecule type: mRNA A; Residues: 1-262 (ANE) A; Residues: 1-262 (ANE) A; Residues: 1-262 (ANE) A; Residues: 1-262 (ANE) A; Reperimental source: strain Resnik C; Genetics: A; Gene: accB-1 A; Gene: accB-1 A; Gene: accE-1 A	C;Function: ABCC> A;Description: blotin carboxyl carrier chain is responsible for binding of blotin A;Perthway: fatty acid blosynthesis C;Superfamily: blotin carboxyl carrier protein; lipoyl/blotin-binding homology C;Scywords: blotin metabolism; chloroplast; fatty acid blosynthesis; ligase C;Scywords: blotin metabolism; chloroplast) #status predicted <tnp> F:1-47/Domain: transit peptide (chloroplast) #status predicted <tnp> F:48-262/Product: acetyl-CoA carboxylase, blotin carboxyl carrier chain #status predicted Alignment Scores: B:00 Matches: Score: Best Local Similarity: 100.00\$ Mismatches: 0 Best Local Similarity: 100.00\$</tnp></tnp>

```
C; Accession: T31146
R; Romine, M.F.; Stillwell, L.C.; Wong, K.K.; Thurston, S.J.; Sisk, E.C.; Sensen, C.W submitted to the EMBL Data Library, July 1998
A; Description: Complete sequence of a 184 kb catabolic plasmid from Sphingomonas aro A; Reference number: 220992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cjaccession: F83139
R;Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larblg, K.; J. Junay, S.; Olson, M.V.
Mature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:AE004821; GB:AE004091; NID:g9950236; PIDN:AAG07430.1; GSPDB:
A;Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic A; Reference number: A82950; MUID:20437337; PMID:10984043
A; Accession: F83139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              geranyltranstransferase PA4043 [imported] - Pseudomonas aeruginosa (strain PAOI)
C.Species: Pseudomonas aeruginosa
C.Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
                                                                                                                                                                                                                                                                                        A; Cross references: EMBL: AF079317; NID: 93378261; PID: 93378287; PIDN: AAD03870.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     c;Species: Caenorhabditis elegans
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
                                                C; Species: Sphingomonas aromaticivorans
C; Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 11-Jan-2000
                             - Sphingomonas aromaticivorans plasmid pNL1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                295
0 0 0 0
                                                                                                                                                                                                                                                                                                                                                                                                                                293
0
0
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Caenorhabditis elegans
                                                                                                                                                                                                     A; Accession: T31146
A; Status: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: DNA
A; Residues: 1-293 < ROW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                  _
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTGGCTCGGGCAGCAGGTTCCGCC 1369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LeualaargalaalaGlySerala 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-824-647-16 (1-2095) x F83139 (1-295)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JS-09-824-647-16 (1-2095) x T31146 (1-293)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein T22H2.6 [imported] - Caenorspecies: Caenorpabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68.5
8.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                     68.6
8.00
100.00%
1.16%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-295 <STO>
A; Cross-references: GB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity:
                                                                                                                                                                                                                                                                                                                                                  A; Genome: plasmid pNL1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Gene: 1S; PA4043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       144
                                                                                                                                                                                                                                                                                                                                                                           A; Note: orf181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genetics:
                                                                                                                                                                                                                                                                                                                                  Genetics:
31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein PA2778 [imported] - Pseudomonas aeruginosa (strain PAO1)
hypothetical protein PA2778 [imported] - Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: A83299
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br Adman, S.; Yuan, X.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J. Lory, S.; Olson, M.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathd A; Reference number: A82950; MUID:20437337; PMID:10984043
A; Reference number: A8299
A; Accession: A83299
A; Status: prelimnary
A; Molecule type: DNA
A; Residues: 1-293 <STO>A; Residues: 1-293 <STO>A; Experimental source: strain PA01
C; Genetics:
A; Experimental source: strain PA01
C; Genetics:
A; Genetics:
                                                                                                                                                                                                                                                                 R; Yamauchi, T.; Umeda, F.; Masakado, M.; Isaji, M.; Mizushima, S.; Nawata, H. Biochem. J. 303, 591-598, 1994
A; Title: Purification and molecular cloning of prostacyclin-stimulating factor from seru A; Reference number: S50031; NUID:95071263; PMID:7980422
                                                                                                                                                                            prostacyclin-stimulating factor - human
C:Species: Homo sapiens (man)
C:Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 28-May-1999
                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: mRNA
A;Residues: 1-282 <YAN>
A;Cross references: GBs.55725; NID:g861520; PIDN:AAB32370.1; PID:g861521
A;Cross references: GBs.575725; NID:g861520; Superfamily: Kazal proteinase inhibitor homology
F;104-156/Domain: Kazal proteinase inhibitor homology <KPI8>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E 0 0 0 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1006 AAGGGTACCTGTGAACAGGGGCCC 1029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCAGCTACAGCTGCTGCCGTCCCC 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          157 ProAlaThrAlaAlaAlaValPro 164
                                                    1006 AAGGGTACCTGTGAACAGGGGCCC 1029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           153 LysGlyThrCysGluGlnGlyPro 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-824-647-16 (1-2095) x A83299 (1-293)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-824-647-16 (1-2095) x S50031 (1-282)
                                                                              LysGlyThrCysGluGlnGlyPro 160
         US-09-824-647-16 (1-2095) x I52825 (1-277)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.00%
100.00%
1.15%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69
8.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .15%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68.6
8.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                       Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
                                                                                                  153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ð
```

CESP: T22H2.6b

```
C; Accession: $74694
R; Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyaji
o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.;
DNA Res. 3, 109-136, 1996
A; Title: Sequence analysis of the genome of the unicellular cyanobacterium Synech
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Phosphofructokinase (EC 2.7.1.11) pfkA-2 - Synechocystis sp. (strain PCC 6803) Alternate names: protein sll1196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:281595; PIDN:CAB54304.1; GSPDB:GN00019; CESP:T22H2.6a
A;Experimental source: clone T22H2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein T22H2.6a - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T25137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
                                                                                                             A;Cross-references: EMBL:281595; PIDN:CAB54305.1; GSPDB:GN00019; A;Experimental source: clone T22H2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                               Conservative:
Mismatches:
                                          A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-345 <MIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Lennard, N.
submitted to the EMBL Data Library, November 1996
A;Reference number: Z19985
A;Accession: T25137
                                                                                                                                                                                                                                                                                               Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                            Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GlyCysCysProMetProAsnAla 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGCTGCTGCCCAATGCCCAACGCC 723
                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-824-647-16 (1-2095) x T25138 (1-345)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-824-647-16 (1-2095) x T25137 (1-358)
                                                                                                                                                                                                                                                                                               66.9
8.00
100.00%
100.00%
1.15%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.008
100.008
1.158
                                                                                                                                                                                                     A; Map position: 1
A; Introns: 93/3; 232/3; 314/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Introns: 93/3; 232/3; 314/3
A; Reference number: 219985
A; Accession: T25138
                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Residues: 1-358 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
                                                                                                                                                                               A; Gene: CESP:T22H2.6b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gene: CESP:T22H2.6a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
                                                                                                                                                                                                                                                                            Alignment Scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    119
                                                                                                                                                                                                                                                                                                                                                                                            Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match:
                                                                                                                                                          Genetics:
                                                                                                                                                                                                                                                                                                  Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37
                                                                                                                                                                                                                                                                                                                              Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score:
                                                           A; Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog A; Reference number: A75000; MUID:9969613; PMID:9851916
A; Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_ele A; Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and A; Accession: E87929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ribelvecchio, V.G.; Rapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, J. Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess Proc. Natl. Acad. Sci. US.A. 99, 443-448, 2002
A;Ittle: The genome sequence of the facultative intracellular pathogen Brucella melitens A;Reference number: AD3252; PMID:11756688
                                                                                                                                                                                                                                                A; Cross-references: GB:chr_I; PIDN: CABO4752.1; PID: 93880056; GSPDB: GN00019; CESP: T22H2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:AE008917; PIDN:AAL51427.1; PID:917982134; GSPDB:GN00190
A;Experimental source: strain 16M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Species: Brucella melitensis
Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
Accession: AH3282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Species: Caenorhabditis elegans
.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  primosomal protein N' [imported] - Brucella melitensis (strain 16M)
                                                                                                                                                                                                                                                                                                                                                                                       334
0 0 0 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein T22H2.6b - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
Conservative:
Mismatches:
Indels:
                   anonymous, The C. elegans Sequencing Consortium.
clence 282, 2012-2018, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Lennard, N. submitted to the EMBL Data Library, November 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        531 CAGGICGCAGAAGCCACCGIGCGG 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            700 GGCTGCTGCCCAATGCCCAACGCC 723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                305 GlnValAlaGluGlyThrValArg 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-824-647-16 (1-2095) x E87929 (1-318)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-824-647-16 (1-2095) x AH3282 (1-334)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79 GlyCysCysProMetProAsnAla 86
                                                                                                                                                                                                                                                                                                                                                                                                                                100.00%
100.00%
1.15%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.00%
100.00%
1.16%
                                        Science 282, 2012-2018,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-334 <KUR>
                                                                                                                                                                           A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-318 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Accession: AH3282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Accession: T25138
                                                                                                                                                                                                                                                                                                                A; Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Map position: I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genetics:
Gene: BMEI0245
                                                                                                                                                                                                                                                                     Genetics:
Gene: T22H2.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 34
                                                                                                                                                                                                                                                                                                                                                                                                               Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ð
```

```
Nature 408, 816-820, 2000
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, B.; Kin
C.A.; Lil, J.H.; Lil, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzi
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tall
A; Authors: Salzberg, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Reference number: A86141; MUID: 21016719; PMID: 11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Accession: G69230
C;Acce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      endo-1,4-beta-glucanase related protein - Methanobacterium thermoautotrophicum (str
C;Species: Methanobacterium thermoautotrophicum
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gross-references: GB:AE000871; GB:AE000666; NID:g2622069; PIDN:AAB85473.1; PID:g2
A;Experimental source: strain Delta H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                          A; Cross-references: GB: AE005173; NID: 96630455; PIDN: AAF19543.1; GSPDB: GN00141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VOLI/NOP2/sun family protein [imported] - Streptococcus pneumoniae (strain C.Species: Streptococcus pneumoniae C.Species: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       394
0
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    387
0
0
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-824-647-16 (1-2095) x G69230 (1-394)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (1-387)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    465 GGGCAGCACCCCCAGGAGCCATC 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Map position: 1
C;Superfamily: aspartate aminotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-824-647-16 (1-2095) x H96652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65.6
8.00
100.00%
100.00%
1.15%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No.: 65.8
Score: 8.00 00 percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 1.16%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATH
                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: pNA
A; Residues: 1-387 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                   A; Accession: H96652
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Start codon: TTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Residues: 1-394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Gene: F23N19.17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Gene: MTH977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Species: Salmonella enterica subsp. enterica serovar Typhi
A; Note: this species has also been called Salmonella typhi
C; Species: Salmonella enterica subsp. enterica serovar Typhi
A; Note: this species has also been called Salmonella typhi
C; Date: 00: Nov-2001 #sequence_revision 09-Nov-2001 #text_change 27-Nov-2001
C; Ccession: AC0972
R; Parkhili, J; Dougan, G; James, K.D; Thomson, N.R; Pickard, D; Wain, J; Churcher, th, T; Connerton, P; Croin, A; Davis, P; Davies, R.M; Dowd, L; White, N.; Parrar, S; Moule, S; O'Gaora, P.
Nature 413, 848-852, 2001
A; Authors: Parry, C; Quail, M; Rutherford, K; Simmonds, M; Skelton, J; Stevens, K.; A; Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov A; Reference number: AB0502; PMID:11677608
A; Accession: AC0972
A; Residues type: DNA
A; Residues: 1-374 cPARA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein F23N19:17 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
S;Accession: H96652
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              - Salmonella enterica subsp. ent
                                                                                                                                                                                         A;Cross-references: EMBL:D90901; GB:AB001339; NID:g1651897; PIDN:BAR16845.1; PID:g165191
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cross-references: GB:AL513382; PIDN:CAD03271.1; PID:g16504892; GSPDB:GN00176; Genetics:
                                                                                                                                                                                                                                                                                                                      C;Superfamily: 6-phosphofructokinase; 6-phosphofructokinase 1 homology C;Reywords: 91ycolysis; phosphotransferase F;7-313/Domain: 6-phosphofructokinase 1 homology <6PF>
      A;Reference number: S74322; MUID:97061201; PMID:8905231
A;Accession: S74694
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-361 <KAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          374
0
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lipopolysaccharide core biosynthesis protein [imported]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: waau
C;Superfamily: probable hexosyltransferase ytxN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCTGCTGACATTATCACAGGGGAC 1102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1152 TTGGCAGCAGGTATCGGAGGAGGG 1129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-824-647-16 (1-2095) x AC0972 (1-374)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   364 AlaAlaAspileileThrGlyAsp 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-824-647-16 (1-2095) x S74694 (1-361)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66.1
8.00
100.00%
100.00%
1.16%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66.5
8.00
100.00%
1.00.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
                                                                                                                                                                                                                                                                                                     A; Gene: pfkA-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gene: waag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 39
H96652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No.:
                                                                                                                                                                                                                                                                      Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ð
```

셤 à

TIGR4)

```
variant surface glycoprotein 7 precursor - Trypanosoma brucei rhodesiense (fragmer
N;Alternate names: metacyclic variable antigen; VSG.
C;Species: Trypanosoma brucei rhodesiense
C;Date: 28-Feb-1986 #sequence_revision 28-Feb-1986 #text_change 17-Nov-2000
                                                                       ater, E.W.

A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; PMID:11743193
A;Accession: AD3042
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-442 <KUR>
A;Residues: 1-442 <KUR>
A;Cross-references: GB.AE008689; PIDN:AAL44754.1; PID:g17742390; GSPDB:GN00187
A;Experimental source: strain C58 (Dupont)
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Accession: A03393
K; Lenardo, M.J.; Rice-Ficht, A.C.; Kelly, G.; Esser, K.M.; Donelson, J.E. Proc. Natl. Acad. Sci. U.S.A. 81, 6642-6646, 1984
A; Title: Characterization of the genes specifying two metacyclic variable antigen A; Reference number: A94011; MUID:85038570; PMID:6593722
A; Accession: A03393
A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      potassium channel chain n2P18 homolog - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jan-2000
C;Accession: 143394
R;Kunkel, M.T.; Salkoff, L.
submitted to the EMBL Data Library, August 1998
A;Pescription: Potassium channels in C. elegans.
A;Reference number: 222479
                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA
A;Residues: 1-461 <KUN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Cross-references: EMBL: AF083650; PIDN: AAC32861.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1125 GCTGCTGACATTATCACAGGGGAC 1102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        409 AlaAlaAspIleIleThrGlyAsp 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (1-442)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-824-647-16 (1-2095) x T43394 (1-461)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-824-647-16 (1-2095) x AD3042
                                                                                                                                                                                                                                                                                                                                           A; Map position: linear chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                   64.5
8.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64.1
8.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                            Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
                                                                                                                                                                                                                                                                                                                       A; Gene: Atu3952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match:
                                                                                                                                                                                                                                                                                                  C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AD3042

oxidoreductase Atu3952 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
C;Accession: AD3042
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
               Ritetelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heidon, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, nson, T.; Hickey, E.K.; Holt, I.E. Science 293, 498-56, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae. A;Reference number: A95000; MUID:21357209; PMID:11463916
A;Accession: C95163
A;Authors: Loftus B.D.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A;Reference number: A97359; PMID:11743194
A;Accession: H98243
                                                                                                                                                                                                                                                               A;Residues: 1-434 <KUR>
A;Cross-references: GB:AE005672; PIDN:AAK75500.1; PID:g14972890; GSPDB:GN00164; TIGR:SP4
A;Experimental source: strain TIGR4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            agaE protein [imported] - Agrobacterium tumefaciens (strain C58, Cereon)
(Species: Agrobacterium tumefaciens
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 11-Jan-2002
C;Accession: H98243
R;Goodher, B.; Hinkle, G; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2333-2338, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Cross-references: GB: AE007870; PIDN: AAK89474.1; PID: 915159342; GSPDB: GN00170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 80000
4
                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1125 GCTGCTGACATTATCACAGGGGAC 1102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             409 AlaAlaAspileileThrGlyAsp 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-824-647-16 (1-2095) x H98243 (1-442)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-824-647-16 (1-2095) x C95163 (1-434)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Map position: linear chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                       64.6
8.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64.5
8.00
100.00%
1.00.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-442 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
C; Accession: C95163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gene: AGR L 1801
                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                  A; Gene: SP1402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match:
                                                                                                                                                                                                                                                                                                                                           Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ð
```

A; Residues: 1-467 <LEN>
C; Superfamily: variant surface glycoprotein
C; Superfamily: variant surface glycoprotein; lipoprotein; phosphatidylinositol linkag
C; Superfamils: blocked carboxyl end; glycoprotein; lipoprotein; phosphatidylinositol linkag
F; 1-27/Domain: signal sequence (fragment) *status predicted <SIG>
F; 28-444/Product: variant surface glycoprotein 7 (fragment) *status predicted <MAT>
F; 445-467/Domain: carboxyl-terminal propeptide *status predicted <CTP>
F; 108, 252, 416/Binding site: carboxyl-trane(amidated carboxyl end (Asp) (in mature form

Alignment Scores:
Alignment Scores:
Bred. No.:
Score:
Brecent Similarity:
Best Local Similarity:
Best Matches:
Bes

US-09-824-647-16 (1-2095) x VMUT7R (1-467)

Search completed: July 7, 2003, 15:51:20 Job time: 91.5 secs

homo sapien cercopithec arabidopsis

fugu rubrip

trypanosoma

trypanosoma rattus norv mus musculu

homo sapien mycobacteri

enterococcu rattus norv

homo sapien caenorhabdi homo sapien

petromyzon

trypanosoma bradyrhizob

trypanosoma

methanopyru rhizobium s

streptomyce halobacteri bos taurus

drosophila

```
LMI.2_CAEEL
SMS_PETMA
6H9A_HUMAN
RS27_METKA ·
EXOX_RHISN
SSIC_STRHY
CLP3_DROME
                                              DGT1_CERAE
UAP1_ARATH
VSA1_TRYBB
VS16_TRYBB
YCP7_BRAJA
                                                                                                                                            Alad Homan
YS50_MYCTU
ALYS_ENTFA
T2D5_RAT
AAT4_ARATH
RRA_FUGRU
VSG7_TRYBR
DGT1_HUMAN
                                                                                                                                                                                                                                                                                         GVI2_HALN1
MOTI_BOVIN
YDG5_SCHPO
                                                                                                                                                                                            ROXN_HUMAN
                                                                                                                      EST3_RAT
ES22_MOUSE
                                                                                                                                                          uuuuu000000000
                                                                              7, 2003, 15:47:40; Search time 35 Seconds (without alignments) 4965.309 Million cell updates/sec
                                                                                                                            US-09-824-647-16
694
1 cgcaggcagaccatgtggac.....ataaagtttgtcactttctt 2095
                                                                                                                                                                                                                                                                                                      225614
           GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

    protein search, using frame_plus_n2p model

                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                     112892 seqs, 41476328 residues
                                                                                                                                                                                         Xgapop 60.0 , Xgapext (Ygapop 60.0 , Ygapext Pgapop 6.0 , Fgapext Delop 6.0 , Delext
                                                                                                                                                                                                                                                                                                                              seq length: 0 seq length: 2000000000
                                                                                 July
                                                                                                                                                                                OLIGO
                                                                                                                             Title:
Perfect score:
Sequence:
                                                                                                                                                                              Scoring table:
                                                                                                                                                                                                                                                                                                                           Minimum DB :
Maximum DB :
                                                        OM nucleic
                                                                                                                                                                                                                                                                             Word size:
                                                                                                                                                                                                                                                     Searched:
                                                                                Run on:
```

ALIGNMENTS

Post-processing: Listing first 45 summaries

Control of	J H		OC Mammalla; Butherla; Primates; Catarrhini; Hominidae; Homo. OX NCBI_TaxID=9606; RN [1] RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.	 	KL Proc. Natl. Acad. Sci. U.S.A. 89:1/12-1/19(1992). RN [2] RP REVISIONS, SEQUENCE FROM N.A. RX MEDIJINF#9403704. DubMed=141788.		_	RP SEQUENCE FROM N.A. RC TISSUE-Kidney; RX MEDI.NE-92317004: PubMed-1618805:			
Troccorna, marking through a summaring	Command line parameters:	Database : SwissProt_40:*	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	Result Query No. Score Match Length DB ID Description	1 406 58.5 593 1 GRN_HUMAN P28799 h granulins 2 32 4.6 588 1 GRN_RAT P23785 r granulins 3 32 4.6 589 1 GRN_MOUSE P28798 mus musculus	3.7 591 1 GRN_CAVPO P28797 1.3 46 1 ENA1_HORSE P80930	115 1 VSA8_TRYBB P06017 135 1 YE57_METUA Q58852	1.5.5	8 1.2 212 1 KTHY_HUMAN P23919 8 1.2 245 1 PO11_POPJA 003276	8 1.2 262 1 BCCP_SOYBN Q42783 8 1.2 269 1 CIT2_MOUSE 035740 8 1.2 296 1 CRK_XENIA P87378	1.2 334 1 EFB1_CHICK 073612 1.2 361 1 K6PF_SYNY3 P72830 1.2 401 1 NPT4_HUMAN 000476

```
406.00
100.00%
100.00%
58.50%
                                                        Percent Similarity;
Best Local Similarity;
Query Match:
Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       253
                                                                                                                                                                                                                      13
                                                                                                                                                                                                                                                                                                                                                                                            133
                                                                                                                                                                                                                                                                                                                                                                                                                                       41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19
                                                 Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ğ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                  원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            음
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ç
                                                                                                                                                                                                                      Š
                                                                                                                                                                                                                                                                                                          ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstationthe European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseélsb-sib.ch).
                                                                                                                                                                                                    MEDLINE-91097544; PubMed-2268320;

MEDLINE-91097548, PubMed-2268320;

MEDLINE-91097548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GLCNAC. . .) (POTENTIAL)
(GLCNAC. . .) (POTENTIAL)
(GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00799; GRANULINS; 7.
Cytokine; Repeat; Glycoprotein; Signal; Alternative splicing;
Polymorphism.
    Yu W., Gibbs R.A.;
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                     Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /FTId=VAR_003445.
S -> H (IN REF. 6).
W -> H (IN REF. 6).
4E402BDB16DE2819 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GLCNAC. .
                                                                                                                                                                                  OF 206-233; 281-336; 364-396 AND 442-447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
ACROGRANIN.
PRRAGRANULIN .
GRANULIN 1.
GRANULIN 3.
GRANULIN 3.
GRANULIN 6.
GRANULIN 6.
GRANULIN 7.
N-LINKED (GLC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M75161; AAA58617.1; ALT_SEQ. EMBL; X62320; CAA44196.1; --
EMBL; AF055008; AAC09359.1; --
EMBL; BC000324; AAH00324.1; --
EMBL; BC010577; AAH10577.1; --
PIR; A38118; GYMU.
PIR; D36698; D36698.
PIR; JG1284; JG1284.
Genew; HGNC:4601; GRN.
                                                                        (ISOFORMS 1 AND Lung;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000118; Granulin.
Pfam; PF00396; granulin; 7.
SMART; SM00277; GRAN; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ¥
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      747
7113
7179
261
336
7417
7496
7573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      236
265
368
530
531
454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ¥¥;
                                                                          SEQUENCE FROM N.A. TISSUE-Cervix, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         219
386
593 A
                                                                                                                       Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genew; HGNC:4
MIM; 138945;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
VARSPLIC
VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
CARBOHYD
                                                                                                                                                                [6]
SEQUENCE (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PEPTIDE
PEPTIDE
PEPTIDE
PEPTIDE
PEPTIDE
PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHAIN
```

```
220
                                                                                                                                                                                                                                                                                                                                                                                                   260
                                                                                                                                                                                                                                                                                                       612
                                                                                                                                                                                                                                                                                                                                  672
                                                                                                                                                                                                                                                                                                                                                            732
                                                                                                                                                                                                                                                                                                                                                                         240
                                                                                                                                                                                                                                                                                                                                                                                      792
                                                                                                                                                                                                                                                                                                                                                                                                                 852
                                                                                                                                                                                                                                                                                                                                                                                                                              280
                                                                                                                                                                                                                                                                                                                                                                                                                                           912
                                                                                                                                                                                                                                                                                                                                                                                                                                                        300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   320
                                                                                                                                                                                                                                                               160
                                                                                                                                                                                                                                                                             552
                                                                                                                                                                                                                                                                                         180
                                                                                                                                                                                                                                                                                                                    200
                                                                                                                                                                                                                                                 GITATGGICGAIGGCICCIGGGGGIGCIGCCCCCAIGCCCCAGGCIICCIGCIGTGAAGAC 492
                                                                                                                                                                                 100
                                                                                                                                                                                              372
                                                                                                                                                                                                           120
                                                                                                                                                                                                                        432
                                                                                                                                                                                                                              192
                                                                                                                                          252
                                                                                                                                                                    312
                                                                                     132
                                                                                                                                                      80
                                                                                                  40
                                                                                                                             9
                                                           72
                                                                       20
                                                                                                                                                                                                                                                                                                                                                                                     GATGTGAAATGTGACATGGAGGTGAGCTGCCCAGATGGCTATACCTGCTGCTGCTACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGGGTGCACTGCTGTCCGCACGGTGCCTTCTGCGACCTGGTTCACACCCGCTGCATCACA
                                                                                                                                                                                                                                                                                    TCGGGGGCCTGGGGCTGCTGCCCTTTTACCCAGGCTGTGTGCTGTGAGGACCACATACAC
                                                                                                                                                                                              GTGGGTGCCATCCAGTGCCCTGATAGTCAGTTCGAATGCCCGGACTTCTCCACGTGCTGT
                                                                                                              TGCTGCCGTCCCCTTCTGGACAAATGGCCCACAAAAGACTGAGCAGGCATCTGGGTGGCCCC
                                                                                                                      TGCCAGGTTGATGCCCCACTGCTGTGCCGGCCACTCCTGCATCTTTACCGTCTCAGGGACT
                                                                                                                                                ATGTEGACCCTGGTGAGCTGGGTGGCCTTAACAGCAGGGCTGGTGGCTGGAACGCGGTGC
593
406
0
0
Length:
Matches:
Conservative:
Mismatches:
Indels:
                                              US-09-824-647-16, (1-2095) x GRN_HUMAN (1-593)
                                  Gaps:
```

```
EPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                  SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                   CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GRN_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score:
Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a
                                                                                                1092
                                                                                                                                                                                 1152
                                                                                                                                                                                                                                                                CTCACGTCTGGGGAGTGGGGCTGCTGTCCAATCCCAGAGGCTGTCTGCTGCTCGGACCAC 1212
                                      TGCTGTCCCGCGGGGTTTACGTGTGACACGCAGAAGGGTACCTGTGAACAGGGGCCCCAC
                                                                                                CAGGTGCCCTGGATGGAGAAGGCCCCAGCTCACCTCAGCCTGCCAGACCCAAGCCTTG
                                                                                                                                                                               AAGAGAGATGTCCCCTGTGATAATGTCAGCAGCTGTCCCTCCTCCGATACCTGCTGCCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plowman G.D., Green J.M., Neubauer M.G., Buckley S.D., McDonald V.L., Todaro G.J., Shoyab M.;

"The epithelin precursor encodes two proteins with opposing activities on epithelial cell growth.";
J. Biol. Chem. 267:13073-13078(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .;
G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1991 (Rel. 20, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Granulins precursor (Acrognain) [Contains: Granulin 1 (Granulin Granulin 2 (Granulin B); Granulin 3 (Granulin B) (Epithelin 2);
Granulin 4 (Granulin A) (Epithelin 1); Granulin 5 (Granulin C);
Granulin 6 (Granulin D); Granulin 7 (Granulin E)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-91045907; PubMed-2236009; Shoyab M., McDonald V.L., Byles C., Todaro G.J., Plowman G.D.; Shoyab M., McDonald V.L., Byles C., Todaro G.J., Plowman G.D.; "Epithelins 1 and 2: isolation and characterization of two cysteine-rich growth-modulating proteins."; Proc. Natl. Acad. Sci. U.S.A. 87:7912-7916(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    d sequence, tissue
of the rat granulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND SEQUENCE OF 204-259 AND 278-334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         588 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bhandari V., Glaid A., Bateman A.;
"The complementary deoxyribonucleic acid
distribution, and cellular localization o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        precursor.*;
Endocrinology 133:2682-2689(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Kidney;
MEDLINE-92317004; PubMed-1618805;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Kidney;
MEDLINE-94062640; PubMed-8243292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-91097544; PubMed-2268320;
                                                                                                                                                                                                                                                                                                                                               CAGCACTGCTCCCCCAG 1230
                                                                                                                                                                                                                                                                                                                                                                   401 GlnHisCysCysProGln 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 204-225 AND 279-299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 278-328.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Bone marrow;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID-10116;
                                                                                                1033
                                                                                                                                                                                                                     361
                                                                                                                                                                                                                                                              1153
                                                                                                                                                                                                                                                                                                       381
                                                                                                                                                                                                                                                                                                                                             1213
                                                       321
                                                                                                                                                                                 1093
                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                    GRN_RAT
                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11D
DPT JDD BB DDB BB DD BB DD
              ò
                                                     셤
                                                                                              ð
                                                                                                                                      a
                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                              ä
                                                                                                                                                                                                                                                                                                     음
                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                               à
```

```
1396 GGGAGCTGGGCCTGCTGCCCCATGCTGTGTGTGCTGCGGAGGATCGCCACCTGC 1455
                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            459 GlySerTrpAlaCysCysGlnLeuProHisAlaValCysCysGluAspArgGlnHisCys
                                                                                                                                                                                                                                                                                                                                                                                                                    ACROGRANIN.
GRANULIN 1.
GRANULIN 2.
GRANULIN 3.
GRANULIN 4.
GRANULIN 5.
GRANULIN 7.
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
THEN 5.
THEN 5.
THEN 5.
THEN 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi;
Sclurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Granulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-0CT-1994 (Rel. 30, Last sequence update)
1-0CT-2001 (Rel. 40, Last annotation update)
Granulins precursor (Acrogrania) [Contains: Granulin 1; Gra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           113D434F7E099B31 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     $88
32
0
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1456 TGCCCGCTGCCTACACCTGCAACGTGAAGGCTCGA 1491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -> T (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           589 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels:
GRANULINS ARE DISULFIDE BRIDGED.
                                                                                                                                                          or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-824-647-16 (1-2095) x GRN_RAT (1-588)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [1]
SEQUENCE FROM N.A.
MEDLINE-93245991; PubMed-8482392;
                                                                                                                                                                                                                                                                                                  InterPro; IPR000118; Granulin. Pfam; PF00396; granulin; 7. SMART; SM00277; GRAN; 7. PR0SITE; PS00799; GRANULINS; 7. Cytokine; Repeat; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Rel. 24, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MW.
                                                                                                                                                                                                EMBL; M97750; AAA16903.1; -. EMBL; X62322; CAA44198.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.49e-22
32.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.00%
100.00%
4.61%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                       PIR; A36199; A36199.
PIR; B36199; B36199.
PIR; E36698; E36698.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ¥,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GRN_MOUSE
P28798;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PEPTIDE
PEPTIDE
PEPTIDE
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONFLICT
CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ARBOHYD
```

```
Alignment Scores:
                                                         (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PEPTIDE
                                                                                                                                                                                  Gerton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENA1_HORSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score:
合
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ð
                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1396 GGGAGCTGGCCCTGCTGCTGCTGCTCTGTGTGTGTGCGCGAGGATCGCCAGCACTGC 1455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           460 GlySerTrpAlaCysCysGlnLeuProHisAlaValCysCysGluAspArgGlnHisCys 479
                                                                    TISSUE-Kiddey;
MEDLINE-92317004; PubMed-1618805;
MEDLINE-92317004; PubMed-1618805;
MEDLINE-92317004; PubMed-1618805;
Plowman G.D., Green I.M., Neubauer M.G., Buckley S., McDonald V.L.,
Todaro G.I., Shoyab M.;
Todaro G.I., Shoyab M.;
The epithelin precursor encodes two proteins with opposing
activities on epithelial cell growth.";
J. Biol. Chem. 267:13073-13078 (1992)
-1- FUNCTION: GRANULINS HAVE POSSIBLE CYTOKINE-LIKE ACTIVITY. THEY MAY
PLAY A ROLLE IN INTELAMMATION, WOUND REPAIR, AND TISSUE REMODELING.
-1- TISSUE SPECIFICITY: UBLOUITOUS.
-1- PTM: GRANULINS ARE DISULFIDE BRIDGED.
                                                                                                                                                                                                                                                                                                                                                                                                                    ACROGRAMIN.
GRANULIN 1.
GRANULIN 3.
GRANULIN 4.
GRANULIN 5.
GRANULIN 6.
GRANULIN 7.
N-LINKED (GLCNAC. . . ) (POTENTIAL).
 Baba T., Nemoto H., Watanabe K., Arai Y., Gerton G.L.; "Exon'intron organization of the gene encoding the mouse epithelih/gramulin precursor (acrogramin)."; FEBS Lett. 322:89-94(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -> R (IN REF. 2).
1DE8229C413CB787 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        589
0
0
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1456 TGCCCGGCTGCCTACACCTGCAACGTGAAGGCTCGA 1491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          480 CysproalaglyTyrThrCysAsnValLysAlaArg 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ž
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels:
                                                                                                                                                                                                                                                                                                     EMBL; D16195; BAA03736.1; --
EMBL; M66736; AAA37191.1; --
EMBL; X62321; CAA44197.1; --
EMBL; X62321; CAA4197.1; --
InterPro; IPR000118; Granulin.
Pfam; PF00396; granulin; 7.
PROSITE; SMO077; GRAN; 7.
PROSITE; PS00799; GRANULINS; 7.
CYTOKINE; Repeqt; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-824-647-16 (1-2095) x GRN_MOUSE (1-589)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ı
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ž
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.49e-22
32.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              350
63458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2414
2493
2568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GRN_CAVPO
P28797;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                 PEPTIDE
PEPTIDE
PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PEPTIDE
PEPTIDE
PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHY
                                                                                                                                                                                                                                                                                                                                                                                                               SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 4
GRN_CAVPO
                                                                                                                                                                                                                                                                                                                                                                                                                         CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score:
   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to licensediab-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 *Acrogramin, an acrosomal cysteine-rich glycoprotein, is the precursor of the growth-modulating peptides, granulins, and epithelins, and is expressed in somatic as well as male germ cells.*; who. Reprod. Dev. 34:233-243(1993).

-I- FUNCTION: GRANULINS HAVE POSSIBLE CYTOKINE-LIKE ACTIVITY. THEY MAY PLAY A ROLE IN INFLAMMATION, WOUND REPAIR, AND TISSUE REMODELING.

-I- TISSUE SPECIFICITY: UBIQUIFIDE BRICGED.
01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Granulins precursor (Contains: Granulin 1; Granulin 2; Granulin 3; Granulin 4; Granulin 5; Granulin 6; Granulin 7]
                                                                                                                                                          Cavia porcellus (Guinea pig).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.

NCBI_TaxID=10141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL).
                                                                                                                                                                                                                                                                                                                         MEDLINE-93228994; PubMed-8471244;
Baba T., Hoff H.B. III, Nemoto H., Lee H., Orth J., Arai Y.,
Gerton G.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GRANULIN 7.
N-LINKED (GLCNAC. . .) (P
EE7C9FC8F21CB8A1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       591
0
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GRANULIN 1.
GRANULIN 2.
GRANULIN 3.
GRANULIN 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-824-647-16 (1-2095) x GRN_CAVPO (1-591)
                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., AND SEQUENCE OF 4-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GRANULIN 5.
GRANULIN 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACROGRANIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M86735; AAA37030.1; -.
InterPro; IPR000118; Granulin.
Pfam; PF00396; granulin; 7.
SMART; SM00277; GRAN; 6.
PROSITE; PS00799; GRANULINS; 6.
Cytokine; Repeat; Signal; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.05e-16
26.00
100.00%
100.00%
3.75%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          502 TGCTGTCCGCACGGTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ¥,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   439
```

ស

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
01-MAY-1992 (Rel. 22, Last annotation update)
Variant surface glycoprotein ANTAT 1.8 (VSG) (Fragment).
Trypanosoma brucei brucei.
BUKATYOLE: EUGlenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBI_TAXID-5702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLUIAR LOCATION: Attached to the membrane by a GPI-anchor. A SOLUBLE FORM IS RELASED FROM RUPTURED CELLS BY THE ACTION OF A PI-PLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                conserved C-terminus. ;
Nature 293:230-233(1981).
-1- FUNCTION: VSG FORMS A COAT ON THE SURFACE OF THE PARASITE. THE
TYPANOSOME EVADES THE IMMUNE RESPONSE OF THE HOST BY EXPRESSING
                                                                                                                                                                                                                                                                         Infect. Immun. 60:3065-3071(1992).
-1- FUNCTION: HAS ANTIMICROBIAL ACTIVITY AGAINST GRAM-NEGATIVE AND
GRAM-POSITIVE BACTERIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SERIES OF ANTIGENICALLY DISTINCT VSGS FROM AN ESTIMATED 1000
                                                                                                                                                                                         TISSUE-Neutrophils;
MEDLINE-92347972; PubMed-1639474;
Couto A.M., Harwig S.S.L., Cullor J.S., Hughes J.P., Lehrer R.I.;
"Identification of eNAP-1, an antimicrobial peptide from equine
                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-82013622; PubMed-7278981;
Matthyssens G., Michiels F., Hamers R., Pays E., Steinert M.;
"Two variant surface glycoproteins of Trypanosoma brucel have a
                                                                                                                                                                                                                                                                                                                                                                                                                                             2171934C15265862 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4
0
0
                                                                                                                                                                                                                                                                                                                      -1- SIMILARITY: SEEMS TO CORRESPONDS TO GRANULIN 7. Interpro; IPR000118; Granulin. Pfam; PF00396; granulin; 1. SMART; SM00277; GRAN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative:
Mismatches:
                            01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Antimicrobial peptide eNAP-1 (Fragment).
   46 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       115 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1573 TGTGGGGAAGGACACTTCTGCCATGAT 1599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-824-647-16 (1-2095) x ENA1_HORSE (1-46)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 CysGlyGluGlyHisPheCysHisAsp 12
                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00799; GRANULINS; PARTIAL.
   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                         4888 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.92
9.00
100.00%
100.00%
1.30%
 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                              Equus caballus (Horse).
                                                                                                                                                                                                                                                                                                                                                                                                                                           46 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity:
                                                                                                                                               NCBI_TaxID-9796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENES.
                                                                                                                                                                                                                                                           neutrophils."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VSA8_TRYBB
P06017:
ENA1_HORSE
P80930;
                                                                                                                                                                                                                                                                                                                                                                                                           Antibiotic.
                                                                                                                                                                                                                                                                                                                                                                                                                            NON_TER
SEQUENCE
                                                                                                                                                                             SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VSA8_TRYBB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      윱
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCCCCCCCCRRRRRWOOOBBAAAA
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
is not removed. Usage by and for commercial agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-JAL-1 / DSM 2661 / ATCC 43067;

MEDLINE-96337999; PubMed-8688087;

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Sutton G.G., Blake J.A., FltzGerald L.M., Clayton R.A., Gocayne J.D.,

Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

Scott J.L., Geoghagen M.S.M., Weidman J.E., Fuhrmann J.L., Nguyen D.,

Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Cotton M.D., Roberts K.M., Milth H.O., Woese C.R., Venter J.C.;

"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                      VARIANT SURFACE GLYCOPROTEIN ANTAT 1.8. HYDROPHOBIC, REMOVED DURING MATURATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: integral membrane protein (Potential).
                                                                                                 InterPro; IPR001812; Trypan_glycop.
Pfam; PF00913; Trypan_glycop; 1.
Glycoprotein; Antigen; Trypanosomiasis; GPI-anchor; Membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Archaea; Euryarchaeota; Methanococci; Methanococcales;
Methanocaldococcaceae; Methanocaldococcus.
NCBL_TaxID=2190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Aypothetical protein; Transmembrane; Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
E69A4F18B630A92D CRC64;
                                                                                                                                                                                                                         12761F33D1305C7E CRC64;
                                                                                                                                                                                                                                                                              115
8
0
0
0
0
                                                                                                                                                                                                                                                                                                Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Hypothetical protein MJ457.
                                                                                                                                                                                                                                                                                                                                 Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            135 AA.
                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                     Indels
modified and this statement is not remove
entities requires a license agreement (Se
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                      US-09-824-647-16 (1-2095) x VSA8_TRYBB (1-115)
                                                                                                                                                                                                                                                                                                                                                                     Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
                                                                                                                                                                                                           GPI-ANCHOR
                                                                                                                                                                                                                                                                                                                                                                                                                                        1632 GCCCTGTCGGTTGTCTCGGCAGCA 1609
                                                                                                                                                                                                                                                                                                                                                                                                                                                       102 AlaLeuSerValValSerAlaAla 109
                                                                                                                                                                     ( <1 92 VA
93 115 HY
6 92 92 GP
115 AA; 12530 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57 77 P
135 AA; 14508 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U67586; AAB99470.1; -. IIGR: MJ1457; -.
                                                                                                                                                                                                                                                                            48.5
8.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    273:1058-1073(1996)
                                                                 EMBL; J01227; AAA30292.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Methanococcus jannaschii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                     PIR; S07326; S07326.
                                                                                                                                                                                                                                                                                                                                 Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                Percent Similarity
                                                                                                                                                                                                                                                              Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REST_METUA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jannaschii.
                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRANSMEM
SEQUENCE
                                                                                                                                                        NON_TER
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Science
                                                                                                                                                                                                                                                                                                                                                 Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              058852;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MJ1457.
                                                                                                                                                                                         PROPEP
                                                                                                                                                                                                           CIPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YES7_METJA
                                                                                                                                                                                                                                                                                Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rigr;
                                                                                                                                                                                                                                                                                                  Score:
 STITION
```

..

ö

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long/ as its content is in no modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-007-1993 (Rel. 27, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last sequence update)
16-JUN-2002 (Rel. 41, Last sequence update)
16-JUN-2002 (Rel. 41, Last sequence update)
17-JUN-2002 (Rel. 41, Last sequence update)
17-JUN-2002 (Rel. 41, Last sequence update)
17-JUN-2002 (Rel. 41, Last sequence update)
18-JUN-2002 (Rel. 41, L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The cloning of CD70 and its identification as the ligand for CD27.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-93258810; PubMed-8387892; Goodwin R.G., Alderson M.R., Smith C.A., Armitage R.J., Vandenbos Goodwin R.G., Alderson M.R., Smith C.A., David-Smith T., Hennen K., Jerzy R., Tough T.W., Schoenborn M.A., David-Smith T., Hennen K., Falk B., Cosman D., Baker E., Sutherland G.R., Grabstein K.H., Farrah T., Giri J.G., Beckmann M.P.; *Molecular and biological characterization of a ligand for CD27 defines a new family of cytokines with homology to tumor necrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-94165470; PubMed-8120384;
Bowman M.R., Crimmins M.A., Yetz-Aldape J., Kriz R., Kelleher K.,
Herrmann S.;
                                                                                      Chee M.S., Bankier A.T., Beck S., Bohni R., Brown C.M., Cerny R., Horsnell T., Hutchison C.A. III, Kouzarides T., Martignetti J.A., Preddie E., Satchwell S.C., Tomlinson P., Weston K.M., Barrell B.C. "Analysis of the protein-coding content of the sequence of human cytomegalovirus strain AD169.";

Curr. Top. M.Crobiol. Immunol. 154:125-169(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-LINKED (GLCNAC. ..) (POTENTIAL).
57EA40349212FEBB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-824-647-16 (1-2095) x UL26_HCMVA (1-188)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
Betaherpesvirinae; Cytomegalovirus.
NCBI_TaxID=10360;
                                                                      SECUENCE FROM N.A.
MEDLINE-90269039; PubMed-2161319;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              136 136 1
188 AA; 21155 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X17403; CAA35425.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.00%
100.00%
1.16%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44.9
8.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cell 73:447-456(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; S09789; S09789.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TNF7_HUMAN ST
P32970; Q96J57;
01-OCT-1993 (Rel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo saptens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rissue-B-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local S
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
         This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseélsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kochrer K., Beyer A., Mewes H.-W., Gassenhuber J., Wiemann S.;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9F4831DCEB7DFF2A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human cytomegalovirus (strain AD169).
Viruses; dSDNA viruses, no RNA stage; Herpesviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181
8
0
0
0
0
                                                        135
0
0
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
Conservative:
Mismatches:
                                                                                               Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
Hypothetical protein UL26.
                                                                                                                                                                                                                                                                                                                                                                                                                             30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Hypothetical protein C2lorf25 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            188 AA
                                                                                                                                                                                                                                                                                                                                                                                          181 AA
                                                           Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-824-647-16 (1-2095) x CU25_HUMAN (1-181)
                                                                                                                                                                                                              US-09-824-647-16 (1-2095) x YE57_METJA (1-135)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1847 TCTGCTCAGGCCTCCCTAGCACCT 1870
                                                                                                                                                                       Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SerAlaGlnAlaSerLeuAlaPro 57
                                                                                                                                                                                                                                                         144 GGGACGCCAGCAGCTGTAGCTGGC 121
                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AL050173; CAB43307.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE 181 AA; 19799 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45.2
8.00
100.00%
100.00%
1.15%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genew; HGNC:1266; C2lorf25
Hypothetical protein.
                                                           47.3
8.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SECUENCE FROM N.A.
                                                                                                        Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Uterus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UL26_HCMVA
P16762;
                                                                                                                                                                                                                                                                                                                                                                    CU25_HUMAN
ID CU25_HUMAN
AC Q97426;
                                           Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20
                                                                                                                                                                                                                                                                                                       28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C210RF25
                                                                                                                                                   Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 9
UL26_HCMVA
                                                                    Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score:
                                                                                                                                                                                                                                                                                                                                                    RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SSSSSSSSSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ð
                                                                                                                                                                                                                                                                                                                                                                                               셤
```

Length:
Matches:
Conservative:
Mismatches:

Indels:

Gaps:

1189

193 AA

```
MEDLINE-91204436; PubMed-2017365;
Su J.Y., Sclafani R.A.;
                                                                                                                                                                                  5'-diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity:
                    SEQUENCE FROM N.A.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                         MIM; 188345;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Allqnment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PO11_POPJA
Q03276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match:
OB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PO11_POPJA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 12
                                                                                                                                                                                                                                                                                                                              DAR WEET THE SO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CSEEDAGES
 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                      CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                               N-LINKED (GLCNAC. . .) (POTENTIAL)
A-J. V (IN REF. 1)
P. S. V (IN REF. 1)
P. S. V (IN REF. 1)
                                                                                                                                                                                                                                                                                                                                                                    Cytokine; Transmembrane; Glycoprotein; Signal-anchor; Antigen.
                                                                                         SUBUNIT: Homotrimer (Probable).
SUBCELLULAR LOCATION: Type II membrane protein.
SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
                                                                                      (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR.1992 (Rel. 21, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL.1999 (Rel. 38, Last annotation update)
Thymidylate kinase (EC 2.7.4.9) (dTMP kinase)
HOMO sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   212 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-824-647-16 (1-2095) x TNF7_HUMAN (1-193)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1734 CAGGGAGGCCCCGCGCTGGGACGC 1757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GlnGlyGlyProAlaLeuGlyArg 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                               InterPro; IPR003637; TNF_7.
InterPro; IPR00478; TNF_family.
Pfam; PF00229; TNF_1.
ProDom; PD036400; TNF_7; 1.
 Immunol. 152:1756-1761(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                    154 2
21118 MW;
                                                                                                                                                                                                                                   EMBL; L08096; AAA36175.1; -. EMBL; S69339; AAB30121.1; -. EMBL; BC000725; AAB00725.1; -. PIR; A40738; A40738.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.00%
                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS50049; TNF_1; 1. PROSITE; PS50049; TNF_2; 1.
                                                                                                                                                                                                                                                                         Genew; HGNC:11937; TNFSF7.
MIM; 602840; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .15%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                             193
                                                                                                                                                                                                                                                                                                                                         SMART; SM00207; TNF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              193 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity:
                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
                                TISSUE-Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KTHY_HUMAN
P23919;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92
                                                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                    CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                          PRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KTHY_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score:
 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SCSSEPPR
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@lib-sib.ch).
                                                                                                                                                                                                  "Molecular cloning and expression of the human deoxythymidylate kinase gene in yeast.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Endonuclease] (Fragment).
Popillia japonica (Japanese beetle).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Retrovirus related Pol. polyprotein from type I retrotransposable element R1 [Contains: Reverse transcriptase (EC 2.7.7.49);
                                                                                                                           SEQUENCE FROM N.A.
MEDLINE-94246549; Pubmed-8024690;
Huang S.H., Tang A., Drisco B., Zhang S.Q., Seeger R., Li C.,
                                                                      3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfan: PF0223; Thymidylate_kin.
Pfan: PF0223; Thymidylate_kin: 1.
TIGRFAMS; TIGR00041; DIMP_kinase; 1.
PROSITE; P501331; THYMIDYLATE_KINASE; 1.
Transferase; Kinase; Nucleotide biosynthesis; ATP-binding.
NP_BIND 13 20 ATP (PROBABLE).
CONFLICT 31 CAAGHRA -> SRGPPP (IN REF. 1).
CONFLICT 58 58 Q -> K (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                    -i- PATHWAY: SYNTHESIS OF DITP FROM DIMP.
-i- SIMILARITY: BELONGS TO THE THYMIDYLATE KINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . -> SI (IN REF. 2).
E42876625E61D3CB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                245 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-824-647-16 (1-2095) x KTHY_HUMAN (1-212)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                              Nucleic Acids Res. 19:823-827(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  105 GCAGCAGGCCACAGGGCAGAACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           184 i
23902 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X54729; CAA38528.1; -. EMBL; L16991; AAA21719.1; -. PIR; X26845. S26845. HSSP; POG972; ITWK. Genew; HGNC:3061; DTYMK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.00%
100.00%
1.16%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44.1
8.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           183
212 AA;
```

```
RANSIT
                                                                                                                                                                                                                BINDING
                                                                                                                                                                                                                                                                                                 Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        domain.
                                                                                                                                                                                                                                                          ..
Q
                                                                                                                                                                                                                                                                                                                                                                                         RESULT 14
CIT2_MOUSE
                                                                                                                                                                                             CHAIN
                                                                                                                                                                                                                                                                   Score
ð
                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMED outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE-93196484; PubMed-8383793;
MEDLINE-93196484; PubMed-8383793;
Burke W.D., Elckbush D.G., Xiong Y., Jakubczak J.L., Elckbush T.H.;
"Sequence relationship of retrotransposable elements R1 and R2 within and between divergent insect species.";
Mol. Biol. Evol. 10:163-185(1993).
-!- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Biotin carboxyl carrier protein of acetyl-CoA carboxylase, chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
Insecta; Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
Scarabaeiformia; Scarabaeidae; Rutelinae; Popillia.
                                                                                                                                                                                                                                   Transferase; RNA-directed DNA polymerase; Transposable element;
                                                                                                                                                                                                                                                                 REVERSE TRANSCRIPTASE.
NUCLEIC ACID-BINDING ENDONUCLEASE.
44D5C5C55E0D6166 CRC64;
                                                                                                                                                                                                                                                                                                                   245
0
0
0
                                                                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         262 AA.
                                                                                                                                                                                                                                                                                                                                                            Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                          US-09-824-647-16 (1-2095) x POII_POPJA (1-245)
                                                                                                                                                                                                                                                                                                                                                                       Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                             1494 CTGCGAGAAGGAAGTGGTCTCTGC 1517
                                                                                                                                                                                                                                                                                                                                                                                                                        168 LeuArgGluGlySerGlyLeuCys 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                            Hydrolase; Nuclease; Endonuclease.
                                                                                                                                                                                                                                                                105 RE
245 NU
28406 MW;
                                                                                                                                                                                                              EMBL; L00944; AAA29783.1; -.
                                                                                                                                                                                                                                                                                                                   43.1
8.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                           1.158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glycine max (Soybean).
                                                                                                                                                                                                                          F44490; F44490.
                                                                                                                                                                                                                                                                                      245 AA;
                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     precursor (BCCP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID-3847;
                  NCBI_TaxID=7064;
                                                                                                             (DNA)(N)
                                                                                                                                                                                                                                                                                                          Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BCCP_SOYBN
                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   042783;
                                                                                                                                                                                                                                                                                                                                                            Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCB-1.
                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                      :
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOYBN
                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
                                                                                                                                                                                                                                                                                                                              Score
ò
                                                                                                                                                                                                                                                                                                                                                                                                                               셤
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseéisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gene 204:235-241(1997).

-!- FUNCTION: Interferes with the binding of transcription factors

-!- FUNCTION: Interferes with the binding of transcription factors

HIF-la and STAT2 to p300/CBP (By similarity).

-!- SUBCHINIT: Binds to the p300/CBP CHI region (By similarity).

-!- SUBCHINITAR LOCATION: Nuclear.

-!- ALTERNATIVE PRODUCTS: 4 isoforms; 1 (shown here), 2, 3 and 4; are produced by alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM 3).
MEDILTE-9804278; PubMed-944189;
SALOda T., Fenner M.H., Isselbacher K.J.;
"MSGI and its related protein MRGI share a transcription activating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    035740; 035741; 035742; 035743; 055198;
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last sequence update)
CDP/P0300-interacting transactivator 2 (MSG-related protein 1) (MRG1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Musaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-98202510; PubMed-9533950; Dubwoodle S.L.; Rodriguez T.R.; Beddington R.S.P.; Rodriguez T.R.; Beddington R.S.P.; Busgl and Mrgl, founding members of a gene family, show distinct patterns of gene expression during mouse embryogenesis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fatty acid biosynthesis; Biotin; Chloroplast; Transit peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BIOTIN CARBOXIL CARRIER PROTEIN
ACETYL-COA CARBOXILASE.
BIOTIN (BY SIMILARITY).
798273BD8B870F48 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7
0
0
0
0
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               269 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3 AND 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (1-262)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHLOROPLAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD; PRT; 26
035742; 035743; 055198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1404 CCAGCTCCCACCTGGCTCGGGCA 1381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Interpro; IPR001249; ACCOA_biotinCC.
Interpro; IPR001882; Biotin_attach.
Interpro; IPR000089; Biotin_lipoyl.
Pfam; PF00364; biotin_lipoyl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-824-647-16 (1-2095) x BCCP_SOYBN
                                                                                                                                                                                                                                          EMBL; U40666; AAB67836.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              227 B
                                                                                                                                                                                                                                                                                                                                                                                                                                        TIGRFAMS; TIGR00531; BCCP; 1. PROSITE; PS00188; BIOTIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00364; biotin_lipoy]; PRINTS; PR01071; ACOABIOTINCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42.6
8.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         dech. Dev. 72:27-40(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITED2 OR MRG1 OR MSG2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-C57BL/6 X DBA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         262 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                                                                                                                        P02905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CIT2 MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein)
```

σ

PR001452;

```
ProDom; PD002533; Ephrin; 1
                                        Pfam; PF00017; SH2; 1.
Pfam; PF00018; SH3; 1.
InterPro; IPR000980;
                            InterPro;
                                                                                                                                                                                                                                                                                                                         DOMAIN
DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   073612;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EFNB1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EFB1_CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DE PRESENTA DE PRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                       Nuclear protein; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDITHE=97180926; Pubmed=9029144; MAYER B.J., Kornbluth S.; MEVANE B.K., Lu W., Strum S.L., Mayer B.J., Kornbluth S.; Exans B.K., Lu W., Strum S.L., Mayer B.J., Kornbluth S.; Crk is required for apoptosis in Xenopus egg extracts."; EMED J. 16;230-241(1997).
-I- FUNCTION: REQUIRED FOR APOPTOSIS IN XENOPUS EGG EXTRACTS.-I- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
-I- SIMILARITY: CONTAINS 2 SH3 DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                     ASP/GLG-RICH (ACIDIC).
MISSING (IN ISOFORM 2).
MISSING (IN ISOFORM 3).
MISSING (IN ISOFORM 4).
7; AFACDDD5D7902A48 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
SH2/SH3 adaptor crk (Adapter molecule crk) (CRK2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          296 AA
-!- SIMILARITY: BELONGS TO THE CITED FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-824-647-16 (1-2095) x CIT2_MOUSE (1-269)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1231 GCTGGGGCAGCAGTGCTGGTGGT 1208
                                                                                                                                                                                                                                                                                                                                                                                            HIS-RICH.
GLY-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         186 AlaGlyGlySerSerAlaGlyGly 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28382 MW;
                                                                                                                                                                                                                                 EMBL; Y15163; CAA75432.1; -.
                                                                                                                                                                                                                                                                                                                       EMBL; U86445; AAC39945.1; -. MGD; MGI:1306784; Cited2.
                                                                                                                                                                                                                                                                                                 EMBL; Y15163; CAA75435.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U89774; AAB49698.1; -
HSSP; Q64010; 1CKA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.00%
100.00%
1.16%
                                                                                                                                                                                                                                                                                                                                                                         regulation;
                                                                                                                                                                                                                                                      EMBL; Y15163; CAA75433.1
EMBL; Y15163; CAA75434.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xenopodinae; Xenopus.
NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                       218
138
159
203
269 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                       Transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CRK_XENLA
P87378;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARSPLIC
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CRK_XENLA
ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               合
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseelsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'Reciprocal expression of the Eph receptor Cek5 and its ligand(s) in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a Wa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE-97223524; PubMed-9070326;
Holash J.A., Soans C., Chong L.D., Shao H., Dixit V.M.,
                                                                                                                                                                                                                                                                                                544F11F4A1F75A66 CRC64;
                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Ephrin-B1 precursor (CEK5 11gand) (CEL5-L).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              334 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-824-647-16 (1-2095) x CRK_XENLA (1-296)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         184 ArgProProSerSerProGlySer 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40 AGGCCACCCAGCTCACCAGGGTCC 17
                                                                                                                                                                                                                              SH2.
SH3 1.
SH3 2.
                                                                                                                                                  PROSITE; PS50001; SH2; 1.
PROSITE; PS50002; SH3; 1.
SH2 domain; SH3 domain; Repeat
DOMAIN 13 112 SI
                                                                                                                                                                                                                                                125 185 S
249 289 S
296 AA; 33409 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001799; Ephrin
Pfam; PF00812; Ephrin; 1.
PRINTS; PR00401; SH2DOMAIN.
PRINTS; PR00452; SH3DOMAIN.
ProDom; PD000066; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                       rercent Similarity: 100.008
Best Local Similarity: 100.008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U72394; AAC07986.1;
                                                  ProDom; PD000066; SH3; 1.
ProDom; PD000093; SH2; 1.
SMART; SM00252; SH2; 1.
SMART; SM00326; SH3; 2.
                                                                                                                                                                                                                                                                                                                                                                         41.8
8.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR01347; EPHRIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the early retina."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pasquale E.B.;
                                                                                                                                                                                                                                                                                                                                                     Aliqnment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EFB1_CHICK
```

96A83E05F318552C CRC64;

38588 MW;

361 AA;

```
Percent Similarity:
  SEQUENCE
                                                                                                                                                                                                         RESULT 18
NPT4_HUMAN
                                                      Score:
                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      s:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions."; DNR Res. 3:109-136(1996).
-!- CATALYTIC ACTIVITY: ATP + D-fructose 6-phosphate = ADP + D-fructose 1,6-bisphosphate.
-!- PATHWAY: KEY CONTROL STEP OF GLYCOLYSIS.
-!- PATHWAY: LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: BELONGS TO THE PHOSPHOFRUCTOKINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y., Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T., Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M., Tabata S.;
PROSITE; PS01299; EPHRIN; 1.
Developmental protein; Neurogenesis; Transmembrane; Glycoprotein;
Signal; Phosphorylation.
                                                                                                                    (POTENTIAL)
                                                                                         CYTOPLASMIC (POTENTIAL).

PDZ RECOGNITION MOTIF (POTENTIAL).

N-LINKED (GLCNAC. . ) (POTENTIAL).

48AF556EPED56CD5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                         15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
6-phosphofructokinase (EC 2.7.1.11) (Phosphofructokinase)
                                                                 EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synechocystis sp. (strain PCC 6803).
Bacteria; Cyanobacteria; Chrococcales; Synechocystis.
                                                                                                                                                                    334
0
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PRO0465; PPK; 1.
PRINTS; PR00476; PHERCTKINASE.
PRODOM; PD000707; Ppfruckinase; 1.
PROSITE; PS00433; PHOSPHORRUCTOKINASE; 1.
Kinase; Trönsferase; Glycolysis; Complete proteome.
                                                                                                                                                                    Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                  361 AA.
                                                                                                                                                                                                                        Indels:
                                                                                                                                                                                                                                                             US-09-824-647-16 (1-2095) x EFB1_CHICK (1-334)
                                                                                                                                                                                                                                     Gaps:
                                                                                POTENTIAL.
                                         POTENTIAL.
                                                        EPHRIN-B1
                                                                                                                                                                                                                                                                                        GGTCGATGGCTCCTGGGGGTGCTG 461
                                                                                                                                                                                                                                                                                                    7 GlyArgTrpLeuLeuGlyValLeu 14
                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nterPro; IPR000023; Ppfruckinase.
                                                                                          334 CX
334 PI
135 N-
36858 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; D90901; BAA16845.1; -.
                                                                                                                                                                     41.1
8.00
100.00%
100.00%
                                                                                                                                                                                                                        .158
                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                             (Phosphohexokinase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                334 AA;
                                                                                                                                                                                                            Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=1148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PFKA OR SLL1196
                                                      26
232
253
253
332
135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P06998;
                                                                                                                                                                                                Percent Similarity:
                                                                                                                                                          Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                 K6PF_SYNY3
P72830;
                                                                                                                    CARBOHYD
                                                                                TRANSMEM
                                                                                                                                                                                                                         Query Match:
                                                      CHAIN
                                             SIGNAL
                                                                                            DOMAIN
                                                                                                         DOMAIN
                                                                                                                                                                         Pred. No.:
                                                                                                                                                                                                                                                                                                                                          RESULT 17
                                                                                                                                                                                    Score
                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                셤
     SPETFFFF
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@fib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-97294057; PubMed-9149941;

REUGHY D.A., Krommal G.S., Lee V.K., Mintier G.A., Quintana L.,

Ruddy D.A., Krommal G.S., Lee V.K., Mintier G.A., Quintana L.,

Domingo R. Jr., Meyer N.C., Irrinki A., McClelland E.E., Fullan A.,

Mapa F.A., Moore T., Thomas W., Loeb D.B., Harmon C., Tsuchihashi Z.,

Wolff R.K., Schatzman R.C., Feder J.N.;

"A 1.1-Mb transcript map of the hereditary hemochromatosis locus.";

Genome Res. 7:441-456(1997).

-I FUNCTION: MAY BE INVOLVED IN ACTIVELY TRANSPORTING PHOSPHATE

INTO CELLS VIA NA+ COTANSPORT (BY SIMILARITY).

-I SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transport; Symport; Sodium transport; Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                  15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
2001um-dependent phosphate transport protein 4 (Sodium/phosphate cotransporter 4) (Na(+)/PI cotransporter 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL)
                                                                                                 54.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LINKED (GLCNAC. . .) (P
52359B2091948285 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               401
8
0
                    361
0
0
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative:
                                                           Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                  401 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
                    Length:
Matches:
                                                                                                          Indels:
                                                                                                                                                                        US-09-824-647-16 (1-2095) x K6PF_SYNY3 (1-361)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                 Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL
                                                                                                                                                                                                              1152 TTGGCAGCAGGTATCGGAGGAGGG 1129
                                                                                                                                                                                                                                     193 LeuklahlaGlyIleGlyGlyGly 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44051 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39.9
8.00
100.00%
                    40.6
8.00
100.00%
100.00%
1.16%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U90545; AAB53423.1; -Genew; HGNC:10931; SLC17A3.
                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                    Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MIM: 604216;
Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores
                                                                                                                                                                                                                                                                                                                                                       NPT4_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FRANSMEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FRANSMEM
```

```
윱
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDINE-21016719; PubMed-11130712;

MEDLINE-21016719; PubMed-11130712;

MEDLINE-21016719; PubMed-11130712;

MEDLINE-21016719; PubMed-11130712;

MEDLINE-21016719; PubMed-11130712;

MEDLINE-21016719; PubMed-11130712;

MINTEO O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

MINTEO O., Alonso J., Conway A.R., Creasy T.H., Dewar K.,

MEDLING M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

MEDLING M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

MEDLIN P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,

MEDLI J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,

MEDLIN T., Liu S.X., Liu Z.A., Liu J.H., Li Y.-P.,

MEDLI J.E., Marziali A.,

MILItscher J., Miranda M., Nguyen M., Nguren M., Nguren M., Nguren M., Nguren M., Nguren M., Rooney T., Rowley D.,

Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

MEDLI Y. W. G., Fraser C.M., Vorsterlun, Yosotskia V.S., Walker M.,

M. D., Yu G., Fraser C.M., Vorster J.C., Davis R.W.;

"Sequence and analysis of chromosome I of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1- FUNCTION: IMPORTANT FOR THE METABOLLSM OF AMINO ACIDS AND KREBS-CYCLE RELATED ORGANIC ACIDS. IN PLANTS, IT IS INVOLVED IN NITROGEN METABOLLSM AND IN ASPECTS OF CARBON AND ENERGY METABOLLSM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATALYTIC ACTIVITY: L-aspartate + 2-oxoglutarate = oxaloacetate +
                                                                                                                                                                                                                                                                                                              Arabidopsis thallana (Mouse-ear cress).

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAUTION: Ref.2 sequence differs from that shown due to erroneous gene model prediction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: HOMODIMER (BY SIMILARITY).
SUBCELLULAR LOCATION: Cytoplasmic (Potential).
SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schultz C.J., Coruzzi G.M.; "The aspartate aminotransferase gene family of Arabidopsis encodes isoenzymes localized to three distinct subcellular compartments.";
                                                                                                                                                                                                                                  15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Aspartate aminotransferase, cytoplasmic isozyme 2 (EC 2.6.1.1)
   000
 Mismatches:
                                                                                                                                                                                                                                                                                (Transaminase A).
ASP4 OR AT1G62800 OR F23N19.17 OR F23N19_26.
                                                                                                                                                                                        403 AA.
                   Indels:
                                                               US-09-824-647-16 (1-2095) x NPT4_HUMAN (1-401)
                                  Gaps:
                                                                                                              281 ProserSerAlaLeulleValSer 288
                                                                                                                                                                                       PRT;
                                                                                             CCATCCAGTGCCCTGATAGTCAGT
                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-cv. Columbia; TISSUE-Leaf;
MEDLINE-97201829; PubMed-7894512;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -1- COFACTOR: PYRIDOXAL PHOSPHATE
                                                                                                                                                                                                     P46646; 098169;
01-NOV-1995 (Rel. 32, Created)
15-UNN-2002 (Rel. 41, Last seq
15-JUN-2002 (Rel. 41, Last and
   100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 408:816-820(2000).
                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plant J. 7:61-75(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AMINOTRANSFERASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            L-qlutamate.
                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=3702;
                                                                                                                                                                                  AAT4_ARATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 thaliana.
                   Query Match:
                                                                                                                                                        RESULT 19
AAT4 ARATH
                                                                                            ò
                                                                                                                                                                                                       셤
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
  commercial
                   entities requires a license agreement (See http://www.lsb-slb.ch/announce/or send an email to license@lsb-slb.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -1- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN, A DNA-BINDING DOMAIN AND A C-TERMINAL SPEROID-BINDING DOMAIN.
-1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.
NR1 SUBFAMILY.
                                                                                                                                                                                                                             -i- SUBCELLULAR LOCATION: Nuclear.
-i- ALTERNATIVE PRODUCTS: 2 ISOFORMS; ALPHA-1 (SHOWN HERE) AND ALPHA-2; ARE PRODUCED BY ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -1- FUNCTION: THIS IS A RECEPTOR FOR RETINOIC ACID. THIS METABOLITE HAS PROFOCUED EFFECTS ON VERTEBRATE DEVELOPMENT. RETINOIC ACID IS A MORPHOGEN AND IS A POWERFUL TERATOGEN. THIS RECEPTOR CONTROLS CELLS FUNCTIONS BY DIRECTLY REGULATING GENE EXPRESSION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chatterjee K.K.; rand characterization of the retinoic acid receptor-alpha gene in the Japanese pufferfish, F. rubripes."; Gene 236:315-323(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; NCBL_TaxID-31033;
and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wentworth J.M., Schoenfeld V., Meek S., Elgar G., Brenner S.,
                                                                                                                                                                           186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fugu rubripes (Japanese pufferfish) (Takifugu rubripes)
ģ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 403
00
00
00
00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Retinoic acid receptor alpha (RAR-alpha).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          447 AA.
  modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-824-647-16 (1-2095) x AAT4_ARATH (1-403)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  465 GGGCCACCCCCAGGAGCCATC 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              169 GlyAlaAlaProProGlyAlaIle 176
                                                                                                                                                                                         InterPro; IPR004839; Aminotransf1/2.
                                                                                                                                    AC007190; AAF19543.1; ALT_SEQ P00508; 7AAT.
                                                                                                                                                                                                               IPR000796; Asptransf_sub. IPR004838; NHtransf_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-99384012; PubMed-10452951;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rercent Similarity: 100.008
Best Local Similarity: 100.008
Query Match: 1.168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39.9
8.00
                                                                                                          EMBL; U15035; AAA79372.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RRA_FUGRU
Q9W5Z3; Q9W5Z4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
                                                                                                                                                                                                                     InterPro;
InterPro;
                                                                                                                                                                HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 20
```

```
Trypanosomiasis; GPI-anchor; Membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE-98434592; PubMed-9756920;
                                                                                                                                                                                            49963 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF059202; AAC63997.1;
                                                                                                                                                                                                                                                                          8.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HGNC:2843; DGAT1
                                           88
444
467
1108
252
416
444
  Antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
                                                                                                                                                                                       467 AA;
                                                                                                                                                                                                                                                                                                                    Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID-9606;
      Glycoprotein;
NON_TER
NON_CONS 8
                                                                                                                                                                                                                                                                                                  Percent Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MIM; 604900;
                                                                                                                                                                                                                                     Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DGT1_HUMAN
075907;
                                                                                                        CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRANSMEM
                                                                                                                                                                                         SEQUENCE
                                                                   CHAIN
                                                                                                                                                                        LIPID
                                                                                                                                                                                                                                                             Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GT1_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   THE TANK DEATH OF THE PRINCIPLE OF THE P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a
          SELLELEES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LIGAND-BINDING.
MAGKGNPVPGPHLNGFPVPTYSYFFPHMLGSLSPPALPGLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ISGYSTPSPAT -> MYESVDVVGLNPSPNPFLAMETYNQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIJINE-85038570; PubMed-6593722;
Lenardo M.J., Rice-Ficht A.C., Kelly G., Esser K.M., Donelson J.E.;
Characterization of the genes specifying two metacyclic variable
antigen types in Trypanosoma brucei rhodesiense.";
Proc. Natl. Acad. Sci. U.S.A. 81:6642-6646(1984)
-!-FUNCTION: VGG FORMS A CORT ON THE SURFACE OF THE PARASITE. THE
TYPANOSOME BYADES THE IMMUNE RESPONSE OF THE HOST BY EXPRESSING
A SERIES OF ANTIGENICALLY DISTINCT VSGS FROM AN ESTIMATED 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
11-DEC-1998 (Rel. 37, Last annotation update)
Variant surface glycoprotein 7 (VSG 7) (Metacyclic variable antigen)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -1- SUBCELLUTAR LOCATION: Attached to the membrane by a GPI-anchor. A SOLUBLE FORM IS RELASED FROM RUPTURED CELLS BY THE ACTION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RGCLIPEKGLVPGAPHPYSTSIRNQHWNGSNHS (IN
                                                                                                                                                                                                                                                                                                                                                                    PROSITE: PSO0031; NUCLEAR RECEPTOR; 1. Receptor; Transcription regulation; DNA-binding; Nuclear protein; Zinc-finger; Multigene family; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFORM ALPHA-2).
E00630F720B1508D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              447
8
0
0
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEAR RECEPTOR-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    467 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (1-447)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MODULATING
             to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C4-TYPE.
C4-TYPE.
                                                EMBL; AJ012382; CAB96754.1; --
EMBL; AJ012380; CAB96754.1; JOINED.
EMBL; AJ012381; CAB43979.1; --
EMBL; AJ012380; CAB43979.1; JOINED.
EMBL; AJ012378; CAB43870.1; --
EMBL; AJ012379; CAB43871.1; --
EMBL; AJ012379; CAB43871.1; --
                                                                                                                                                                                                    interPro; IPR000536; Hormone_rec_lig.
interPro; IPR001628; Znf_C4steroid.
                                                                                                                                                                                                                                                                                   PRINTS; PROD047; STROIDFINGER.
ProDom; PD000035; Znf_C4steroid; 1.
SMART; SM00430; HOLI; 1.
SMART; SM00399; ZnF_C4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD; PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HINGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-824-647-16 (1-2095). x RRA_FUGRU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Trypanosoma brucei rhodesiense
                                                                                                                                                                                                                                              Pfam; PF00104; hormone_rec; 2. Pfam; PF00105; zf-C4; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49532 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39.3
8.00
100.00%
100.00%
1.16%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PI-PLC.
PIR; A03393; VMUT7R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     447 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=31286;
                 email
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VSG GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Fragments).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VSG7_TRYBR
P02898;
                     an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA_BIND
ZN_FING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZN_FING
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VARSPLIC
                 or send
                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VSG7_TRYBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         triacylglycerol.
-!- PATHWAY: Central role in the metabolism of cellular diacylglycerol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           acyl
InterPro: IPR002688; ACAT.
Pfam; PF01800; ACAT; 1
Pfam; PF01800; ACAT; 1
Pransferase; Acyltransferase; Transmembrane; Endoplasmic reticulum.
TRANSMEM 104 124
POTENTIAL.
TRANSMEM 10 150
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -1- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Manmalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           reticulum (By similarity).
SIMILARITY: BELONGS TO THE STEROL O-ACYLTRANSFERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          - COA +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Diglyceride
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -1- CATALYTIC ACTIVITY: Acyl-CoA + 1,2-diacylglycerol
                                                                                                                                                      GPI-ANCHOR.
3A4805AFFBECA686 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-CCT-2001 (Rel. 40, Created)
16-CCT-2001 (Rel. 40, Last sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
Diacyllycerol o-acyltransferase 1 (EC 2.3.1.20)
acyltransferase) (ACAF related gene product 1).
DGATION DGAT OR AGRPI.
                                                                                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          488 AA
                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-824-647-16 (1+2095) x VSG7_TRYBR (1-467)
                                                                                                                                                                                                                                                                                                                                                                                 Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1632 GCCCTGTCGGTTGTCTCGGCAGCA 1609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       454 AlaLeuServälvalSerAlaAla 461
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -1- PATHWAY: Central role in the metabolism of cellular diacylglycerol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Joyce C.W., Davis M.A., Anderson R.A., Rudel L.L.;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Catalyzes the terminal and only committed step in
triacylglycerol synthesis by using diacylglycerol and fatty acyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transmembrane; Endoplasmic reticulum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cercopithecus aethiops (Green monkey) (Grivet).
Wakaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Cercopithecus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  reticulum (By similarity).
-i- SIMILARITY: BELONGS TO THE STEROL O-ACYLTRANSFERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CATALYTIC ACTIVITY: Acyl-CoA + 1,2-diacylglycerol = CoA +
                                                                                                                                                                                                                                                                                                                                                                                                     16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Diacylglycerol O-acyltransferase 1 (EC 2.3.1.20) (Diglyceride
                                                                                                       12E34BA7478ABA1F CRC64;
                                                                                                                                                               Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                             491 AA.
                                                                                                                                                                                                          Indels:
                                                                                                                                                  Length:
                                                                                                                                                                                                                                                    JS-09-824-647-16 (1-2095) x DGT1_HUMAN (1-488)
                                                            POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                             Gaps:
                                POTENTIAL.
                                               POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
POTENTIAL.
POTENTIAL.
   POTENTIAL
                    POTENTIAL
                                                                                                                                                                                                                                                                                POTENTIAL.
                                                                                         POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF236018; AAF98557.1; -.
InterPro; IPR002688; ACAT.
Pfam; PF01800; ACAT; 1.
                                                                                                         55252 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Acyltransferase;
                                                                                                                                            38.7
8.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COA as substrates.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        triacylglycerol.
                                           332
406
428
453
488 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                           Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  acyltransferase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9534;
                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DGAT1 OR DGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ransferase;
                                                                                                                                 Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                           DGT1_CERAE
Q9GMF1;
                                                          TRANSMEM
TRANSMEM
TRANSMEM
SEQUENCE
TRANSMEM
TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSMEM
TRANSMEM
TRANSMEM
TRANSMEM
                                            TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRANSMEM
                                                                                                                                                                                                          Query Match:
                                                                                                                                                  :.
9
                                                                                                                                                                                                                                                                                                                                                            DGT1_CERAE
                                                                                                                                                                                                                                                                                                                                              RESULT 23
                                                                                                                                                                Score:
                                                                                                                                                                                                                                                                                   à
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseélsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 402:761-768(1999).
-1- CATALYTIC ACTIVITY: UTP + N-acetyl-alpha-D-glucosamine 1-phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-CV. Columbia;
MEDLINE-20083487; PubMed-10617197;
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,
Moffat K.S., Cronin L.A., Shen M., Pal G., Van Aken S., Umayam L.,
Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
Goodman H.M., Somerville C.R., Copenhaver G.P., Freuss D.,
Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                 15-UUL-1999 (Rel. 38, Created)
15-UUL-1999 (Rel. 38, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Probable UDP-N-acetylglucosamine pyrophosphorylase (EC 2:7.7.23).
AT2G35020 OR F1913.25.

    diphosphate + UDP-N-acetyl-D-glucosamine.
    -1- PATHWAY: UDP-GlcNAc biosynthesis from Fru-6-P; fourth (last)

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.",
                                                                                                             30
                    POTENTIAL.
BFD3683453D588DB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72C0F2DCF15ACAD7 CRC64;
                                                                                                                         Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AC004238; ARCOGOS 18, UDPGP.
InterPror. IRRO05618; UDPGP.
InterPror. Prof. 1.
Fransferase; Nucleotidyltransferase.
133 BINDING SITE FOR I
                                                                                                                                                                                                                                                                                                                                                        PRT; 502 AA.
                                                                                         Length:
Matches:
                                                                                                                                                              Indels:
                                                                                                                                                                                                             US-09-824-647-162 (1-2095) x DGT1_CERAE (1-491)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY).
                                                                                                                                                                            Gaps:
   POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL
                                                                                                                                                                                                                                                              15 ThrGlySerArgProSerSerHis 22
                                                                                                                                                                                                                                              1417 ACTGGCAGCAGGCCCAGCTCCCAC
                                      55643 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55759 MW;
                                                                                 38.7
8.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                STANDARD;
   451
476
431
456
491 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     137
144
502 AA;
                                                                                                                        Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID-3702;
                                                                      Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                  UAP1_ARATH
O64765;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Venter J.C.
TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACT_SITE
ACT_SITE
SEQUENCE
                                      SEQUENCE
                                                                                                                                                            Query Match:
                                                                                                                                                                                                                                                                                                                                     UAP1_ARATH
                                                                                                                                                                                                                                                                                                                   RESULT 24
```

Alignment Scores: Pred. No.:

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ilenserial.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ጀ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 270-344 FROM N.A.
MEDILINE-86028178; PubMed-4053185;
Bays E., Bouard S., Pays A., van Assel S., Dupont F., Aerts D.,
Huet-Duviller G., Gomes V., Richet C., Degand P., van Meirvenne N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor. A SOLUBLE FORM IS RELASED FROM RUPTURED CELLS BY THE ACTION OF
                                                                                                                                                                                                                                             13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Variant surface glycoprotein AnTaT 1.1 precursor (VSG) (Expression-Inned copy) (ELC).
Trypanosoma brucei brucei.
                                                                                                                                                                                                                                                                                                                                                                                                   MEDIINE-84028590; PubMed-6313354; Michiels F., Matthyssens G., Kronenberger P., Pays E., Dero B., van Assel S., Darrille M., Cravador A., Steinert M., Ramers R.; Gene activation and re-expression of a Trypanosoma brucei variant surface alveoratem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Steinert M., Pays E.;
programming of antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-82013622; PubMed-7278981;
Matthyssens G., Michiels F., Hamers R., Pays E., Steinert M.;
"Two variant surface glycoproteins of Trypanosoma brucei have
80000
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                     503 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          van der Werf A., van Assel S., Aerts D., "Telomere interactions may condition the expression in Trypanosoma brucel.";
                                              Indels:
                                                                                         US-09-824-647-16 (1-2095) x UAP1_ARATH (1-502)
                                                                Gaps:
                                                                                                                        242 TCTCAGGGACTTCCAGTTGCTGCC 265
                                                                                                                                      82 SerGinGlyLeuProValalaAla 89
                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-90214610; PubMed-2323332;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1-416 FROM N.A.
 8.00
100.00%
100.00%
1.15%
                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBO J. 9:1035-1040(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       surface glycoprotein.";
EMBO J. 2:1185-1192(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wature 293:230-233(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    conserved C-terminus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-EATRO 1125;
                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                   Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=5702;
                                                                                                                                                                                                                                      026722;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Steinert M.;
                                                                                                                                                                                                                        VSA1_TRYBB
P06015; Q26
                                                Query Match:
                                                                                                                                                                                         RESULT 25
VSA1_TRYBB
```

EMBL; X01843; CAA25971.1;

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseélsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; S09640; S09640.
InterPro; IPR001812; Trypan_glycop.
Pfam; PF00913; Trypan_glycop; 1.
Glycoprotein; Antigen; Trypanosomiasis; Signal; GPI-anchor; Membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-AUG-1987 (Rel. 05, Last sequence update)
01-MAY-1992 (Rel. 22, Last annotation update)
Variant surface glycoprotein ILTAT 1.3 precursor (VSG).
Trypanosoma brucei brucei.
Eukaryota; Eugenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rice-Picht A.C., Chen K.K., Donelson J.E.;
Sequence homologies near the C-termini of the variable surface glycoproteins of Trypanosoma brucei.";
Nature 294:33-57(1981).
-!- FUNCTION: VSG (PSH).
-!- FUNCTION: VSG PORMS A COAT ON THE SURFACE OF THE PARASITE. THE TYPANOSOME EVADES THE IMMUNE RESPONSE OF THE HOST BY EXPRESSING A SERIES OF ANTIGENICALLY DISTINCT VSGS FROM AN ESTIMATED 1000
                                                                                  Trypanosomiasis; GPI-anchor; Membrane; Signal.
                                                                                                      VARIANT SURFACE GLYCOPROTEIN ANTAL 1.1. HYDROPHOBIC, REMOVED DURING MATURATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUCCELLUIAR LOCATION: Attached to the membrane by a GPI-anchor. A SOLUBLE FORM IS RELASED FROM RUPTURED CELLS BY THE ACTION OF
                                                                                                                                              BY SIMILARITY.

BY SIMILARITY.

N-LINKED (GLCNAC. . . ) (POTENTIAL).

N-LINKED (GLCNAC. . . ) (POTENTIAL).

GPI-ANCHOR.
                                                                                                                                                                                                                                    -> P (IN REF. 2).
-> V (IN REF. 2).
-> K (IN REF. 3).
38541B93F6DF46C6 CRC64;
                                                                                                                                                                                                                                                                                                                             503
0
0
0
0
                                                                                                                                                                                                                                                                                                                                                          Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    503 AA.
                                                                                                                                                                                                                                                                                                                                              Matches:
                                                                                                                                                                                                                                                                                                                               Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-824-647-16 (1-2095) x VSAL_TRYBB (1-503)
                                                                                                                                                                                                                                                                                                                                                                                       Indels:
                                                                                                                                                                                                                                                                                                                                                                                                        Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              1632 GCCCTGTCGGTTGTCTCGGCAGCA 1609
EMBL; X15817; CAA33809.1; -.
EMBL; M12005; AAA30162.1; -.
EMBL; J01213; AAA30280.1; -.
PIR; S07174; VMUT1B.
InterPro; IPR001812; Trypan_glycop.
Pfam; PF00913; Trypan_glycop: 1.
Glycoprotein; Antigen; Trypanosomiasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            490 AlaLeuSerValValSerAlaAla 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05, Created)
05, Last sequ
                                                                                                                                                                                                                                          KKZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; J01221; AAA30288.1; -.
                                                                                                                                                                                                                                                                                     ₹
                                                                                                                                                                                                                                                                                                                          38.5
8.00
100.00%
100.00%
1.16%
                                                                                                                                                                                                                                                                                     52814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                      480
503
172
209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-AUG-1987 (Rel.
13-AUG-1987 (Rel.
01-MAY-1992 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID-5702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VSG GENES
                                                                                          Glycoprotein;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                               Percent Similarity
                                                                                                                                                                                                                                                                                                                    Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VSI6_TRYBB
P06014;
                                                                                                                                                                                                                                                                       CONFLICT
                                                                                                                                                                                                                  CARBOHYD
                                                                                                                                                                                                                                          CONFLICT
                                                                                                                                                      DISULFID
                                                                                                                                                                 DISULFID
                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                 CARBOHYD
                                                                                                                                                                                                                                                           CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                           Query Match:
                                                                                                                                     PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 26
VSI6_TRYBB
                                                                                                                                                                                                                                                                                                                                      ..
Q
                                                                                                                          CHAIN
                                                                                                                                                                                                                              LIPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <u>-</u>
                                                                                                                                                                                                                                                                                                                                                    Score:
                                                                                                                                                                                                                                                                                                                                      _{\text{Pred}}
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tully R.E., van Berkum P., Lovins K.W., Keister D.L.;
*Identification and sequencing of a cytochrome P450 gene cluster from Bradyrizobium alponicum.*;
Blochim. Blophys. Acta 1398-243-255(1998).
-1- SIMILARITY: CONTAINS 2 PFTB REPEATS.
         VARIANT SURFACE GLYCOPROTEIN ILTAT 1.3 HYDROPHOBIC, REMOVED DURING MATURATION BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Bradyrhizobium group; Bradyrhizobium.
                                                                      N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-USDA 110;
Tully R.E., Keister D.L.;
"Cloning and mutagenesis of a cytochrome P-450 locus from
Bradyrhizoblum japonicum that is expressed anaerobically and
symbiotically.";
                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical 55.4 kDa protein in CYP117 3'region (ORF7).
                                                                                                                70144D8B0408AA9A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8C0660A0C7AFBCE5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                        Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Appl. Environ. Microbiol. 59:4136-4142(1993)
                                                                                                                                                                                                                                                                                                                                                                                  516 AA
                                                                                                                                                            Length:
Matches:
                                                                                                                                                                                                                                                            US-09-824-647-16 (1-2095) x VSI6_TRYBB (1-503)
                                                                                                  GPI-ANCHOR
                                                                                                                                                                                                                                    Gaps:
                                                                                                                                                                                                                                                                                            1632 GCCCTGTCGGTTGTCTCGGCAGCA 1609
                                                                                                                                                                                                                                                                                                          490 AlaLeuSerValValSerAlaAla 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PFTB 1.
PFTB 2.
                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-98322110; PubMed-9655913;
                                                                                                                                                                                                                                                                                                                                                                                                             (Rel. 35, Created)
(Rel. 35, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               443 P
                                                                                                                   Ĕ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein; Repeat. REPEAT 45 86
                                                                                                                                                                                     100.00%
100.00%
1.16%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38.4
8.00
100.00%
100.00%
                                                                                                                54618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U12678; AAC28895.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bradyrhizobium japonicum
                                                                                                                                                           38.5
8.00
                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            401 4
516 AA;
                                                                                                  480
503 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                    Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WCBI_TaxID=375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-USDA 110
                                                                                                                                                                                      Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
                                                                                                                                            Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                YCP7_BRAJA
045221;
                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1997
01-NOV-1997
                                                                    CARBOHYD
CARBOHYD
LIPID
                                         DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                SEQUENCE
                            ROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REPEAT
                                                                                                                                                                                                                                                                                                                                                     RESULT 27
83333333
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VSG GENES.
-1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
A SOLUBLE FORM IS RELASED FROM RUPTURED CELLS BY THE ACTION OF A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Glycoprotein; Antigen; Trypanosomiasis; GPI-anchor; Membrane; Signal.
                                                                                                                                                                                                                                                                                              Trypanosoma brucel brucel.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma
NCBL_TaxID=5702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VARIANT SURFACE GLYCOPROTEIN ILTAT 1.23
                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Variant specific glycoprotein of Trypanosoma brucei consists of two domains each having an independently conserved pattern of cysteine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYDROPHOBIC, REMOVED DURING MATURATION.
N-LINKED (GLCNAC. . ) (POTENTIÁL).
N-LINKED (GLCNAC. . ) (POTENTIÁL).
N-LINKED (GLCNAC. . . ) (POTENTIÁL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. Mol. Biol. 221:823-835(1991).
-!- FUNCTION: YGG FORMS A COAT ON THE SURFACE OF THE PARASITE. THE
- TYPANGSOME EVADES THE IMMURE RESPONSE OF THE HOST BY EXPRESSING
A SERIES OF ANTIGENICALLY DISTINCT VSGS FROM AN ESTIMATED 1000.
                                                                                                             ist.
                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-ISOlate MIAG 206;
MEDLINE-92046037; PubMed-1942032;
Carrington M., Miller N., Blum M.L., Roditi I., Wiley D.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GPI-ANCHOR (BY SIMILARITY).
EED0D72C919396E6 CRC64;
                                                                                                                                                                                                                                                              15-DEC-1998 (Rel. 37, Last annotation update)
Variant surface glycoprotein ILTAT 1.23 precursor (VSG).
   00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative:
Mismatches:
                                                                                                                                                                                           532 AA.
                                                                                                                                                                                                                        01-MAY-1992 ((Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches:
                                                     US-09-824-647-16 (1-2095) x YCP7_BRAJA (1-516)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-824-647-16 (1-2095) x VSI3_TRYBB (1-532)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2056 CAAACACCCCTGTGGATAGGGAAA 2033
                                                                                                       X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X56768; CAA40087.1; -. PIR; S18448; S18448.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.00%
100.00%
1.16%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56778
1.16%
                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         511
532 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                         Purner M.J.;
                                                                                                                                                                                        VSI3_TRYBB
P26328;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          residues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match:
   Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CIPID
                                                                                                                                                                           VSI3_TRYBB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred.
```

RESULT

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                        "Cloning and sequencing of rat liver carboxylesterase ES-3 (egasyn)."; Biochem. Biophys. Res. Commun. 203:1404-1411(1994).
-!- FUNCTION: INVOLVED IN THE DETOXIFICATION OF XENOBIOFICS AND IN THE ACTIVATION OF ESTER AND AMIDE PRODRUGS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BY SIMILARITY.

LIVER CARBOXYLESTERASE 3.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

N-LINKED (GLCNAC. . . ) (POTENTIAL).
                           01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-UNH-2002 (Rel. 41, Last annotation update)
Liver carboxylesterase 3 precursor (EC 3.1.1.1) (Carboxyesterase ES-3)
(PI 5.5 esterase) (ES-HTEL).
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                    -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                       -i- CATALYTIC ACTIVITY: A carboxylic ester + H(2)0 - an alcohol + a
                                                                                                                                                                                                                                                                                                                                     -1- SUBCELLULAR LOCATION: Microsomal membrane, lumen of endoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00135; COesterase; 1.
PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
PROSITE; PS00441; CARBOXYLESTERASE_B_2; 1.
Glycoproteal; Hydrolase; Serine esterase; Endoplasmic reticulum; signal; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LINKED (GLCNAC. . .) (P
1E14D66DF089B86F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  561
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ź
561 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-824-647-16 (1-2095) x EST3_RAT (1-561)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR002018; CarbesteraseB.
InterPro; IPR000379; Ser_estrs_site.
                                                                                                                                                                                                STRAIN-Sprague-Dawley; TISSUE-Liver;
MEDLINE-95032008; PubMed=7945287;
Robbi M., Beaufay H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X81395; CAA57158.1; -. HSSP; P21836; 1MAA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.00%
100.00%
1.15%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37.9
8.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
STANDARD;
                                                                                                                                                                                                                                                                                                                             carboxylic anion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ä.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity:
                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                     NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similari
                                                                                                                                                                                                                                                                                                                                                          reticulum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ES22_MOUSE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACT_SITE
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..
₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 30
 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWIS Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE-92147141; PubMed-1783403;
Ovnic. M., Swaink R.T., Fletcher C., Zhen L., Novak E.K., Baumann H.,
Heintz N., Ganschow R.E.,
"Characterization and functional expression of a cDNA encoding egasyn
(esterase-22); the endoplasmic reticulum-targeting protein of beta-
qlucuronidase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         glucuronidase.";
Genomics 11:956-967(1991).
-1- FUNCTION: INVOLVED IN THE DETOXIFICATION OF XENOBIOTICS AND IN
THE ACTIVATION OF ESTER AND AMIDE PRODRUGS.
-1- CATALYTIC ACTIVATY: A carboxylic ester + H(2)0 = an alcohol + a
064176;
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Liver carboxylesterase 22 precursor (EC 3.1.1.1) (Egasyn) (Esterase-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     carboxylic anion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PREVENT SECRETION FROM ER (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                    wus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PSO0122; CARBOXYLESTERASE B 1; 1.
PROSITE; PSO0941; CARBOXXLESTERASE B 2; 1.
Glycoprotein; Hydrolase; Serine esterase; Endoplasmic reticulum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LIVER CARBOXILESTERASE 22.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
PY SIMILARITY.
PREVENT SECRETION FROM ER (F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FIINKED (GLCNAC. . .) (PFBIA4367A0CCB2E3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-824-647-16 (1-2095) x ES22_MOUSE (1-562)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 250 ValAlaLeuThrAlaGlyLeuVal 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Interpretation of the properties of the properti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34 GTGGCCTTAACAGCAGGGCTGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61581 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; S80191; AAB21335.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37.9
8.00
100.00%
100.00%
1.15%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Signal; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      222
467
1117
285
562
80
276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MGD; MGI:95432; Es22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                562 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HWH
                                                                                                                                                                                                                                                                            NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               reticulum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
Pred. No.:
                                                                                                                                        (Es-22).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACT_SITE
ACT_SITE
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSP;
     ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
```

RESULT 31

```
[1]
SEQUENCE FROM N.A.
STRAIN-H37RV;
    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics. Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-95114877; PubMed-7815325; Schwinn D.A., Johnston G.I., Page S.O., Mosley M.J., Wilson K.H., Worman N.P., Campbell S., Fidock M.D., Furness L.M., Parry-Smith D.J., Peter B., Balley D.S.; Parry-Smith D.J., Peter B., Balley D.S.; addrenergic receptors: sequence corrections and direct comparison of human alpha-1 other species homologues."

J. Pharmacol. Exp. Ther. 272:134-142(1995).
                                                                                                                                                                                                                                    Bruno J.F., Whittaker J., Song J., Berelowitz M.; "Molecular cloning and sequencing of a CDNA encoding a human alpha lA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-94296402; PubMed-8024574;
Weinberg D.B., Trivedi P., Tan C.P., Mitra S., Perkins-Barrow A.,
Borkworki D., Strader C.D., Bayne M.;
"Clouing, expression and characterization of human alpha adrenergic
receptors alpha 1a, alpha 1b and alpha 1c.";
Blochem. Blophys: Res. Commun. 201:1296-1304(1994).
                                                                                                                                                                                                                                                                                                                                                                                                          oŧ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     THROUGH THE INPIGX OF EXTRACELLULAR CALCIUM.
-1- SUBCELLULAR LOCATION: Integral membrane protein.
-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                          Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                        "The alpha 1-adrenergic receptor that mediates smooth muscle contraction in human prostate has the pharmacological properties the cloned human alpha 1c subtype.":
MOI. Pharmacol. 45:703-708(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Minneman K.P., Murphy T.U.;
"Cloning of the human alpha 1d-adrenergic receptor and inducible expression of three human subtypes in SK-N-MC cells.";
Mol. Pharmacol. 47:977-985(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Placenta, and Prostate;
MEDLINE-95265059; PubMed-7746284;
Esbenshade T.A., Hirasawa A., Tsujimoto G., Tanaka T., Yano J.,
                                                   01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Alpha-1D adrenergic receptor (Alpha 1D-adrenoceptor) (Alpha-1A
                                                                                                                                                                                                                                                                                                                   TISSUE-Hippocampus;
MEDLINE-94239386; PubMed-8183249;
Forray C., Bard J.A., Wetzel J.M., Chiu G., Shapiro E., Tang
Lepor H., Hartig P.R., Weinshank R.L., Branchek T.A.,
                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                           lochem. Blophys. Res. Commun. 179:1485-1490(1991).
              572 AA.
            PRT;
                                                                                                                                                                                                         TISSUE-Hippocampus;
MEDLINE-92028892; PubMed-1656955;
                                        22, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M76446; AAA35496.1;
               STANDARD;
                                                                                                adrenergic receptor).
                                                                                                                                                                                                                                                               drenergic receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                        EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                             ADRAID OR ADRAIA.
                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                             uchowski C.;
           Alab_HUMAN
P25100;
                                        01-MAY-1992
Alad_HUMAN
```

```
S -> G (IN REF. 4).
KPPSAFREWRLLGPFRRPTTOLRAKVSSLSHKIRAGGAOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                PAVGGVPGGAGGGGVVGAGSGEDNRSSAGEPGSAGAGGD
VNG -> MAAALRSVMMAGYLSEWRTPTYRSTEMVQRLRM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AEAACAQRSEVEAVSLGVPHEVAEGATCQAYELADYSNLR
ETDI -> SHPAPSASGGCWGRSGDPRPSCAPKSPACRTR
                                                                                                                                                                                                                                                                                                                                                                                                                                    MTFRDLLSVSFEGPRPDSSAGGSSAGGGGGSAGGAAPSEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPPGARSAQRQRAPSAQRWRLCP (IN REF. 1).
                                                                                        3
                                                                                                  Premis Prototi 1.

PRINTS: PRO10217; GPCRRHODOPSN.

PROSITE: PS00237; GPROTEIN RECEP_F1_1; 1.

PROSITE: PS50262; G_PROTEIN_RECEP_F1_2; 1.

G_PROTEIN COUPLED RECEP_F1_2; 1.

G_PROTEIN COUPLED RECEPTOR: Transmembrane; Glycoprotein; Multigene family; Phosphorylation; Lipoprotein; Palmitate.

95

EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                         EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                    2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -> P (IN REF. 4).
EBEB134CF20A4988 CRC64;
                                                                                                                                                                                                                                                                                                                                     CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                              CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                          CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  572
8
0
0
0
0
                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                       PALMITATE (POTENTIAL).
POLY-ARG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EAVQUSTS (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Rel. 39, Created)
(Rel. 39, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               629 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
                                                                                                                                                                                                                                                                3 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                      (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL)
                                                                                                                                                                                                                                                                                           (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                   6 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-824-647-16 (1-2095) x AlAD_HUMAN (1-572)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                              IPR000276; GPCR_Rhodpsn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein Rv2850c.
RV2850c OR MT2916 OR MTCY24A1.07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            522 1
60462 MW;
  . . . . .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.00%
100.00%
1.16%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycobacterium tuberculosis.
AAB60351.1;
AAB59487.1;
                           S70782; AAB31163.2;
D29952; BAA06222.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37.8
8.00
                                                                 Genew; HGNC:280; ADRAID.
                                                                                                                                                                                                                       133
159
169
192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           522 5
572 AA;
                                                      JH0447; JH0447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                   134
170
170
193
233
252
                                                                                                                                                                                                                                                                                                                                                  349
374
381
406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31
489
                                                                               104219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-MAY-2000
15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 32
YS50_MYCTU
ID YS50_MYCTU
AC 005809;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAY-2000
                                                                                               InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONFLICT
                                                                                                                                                                                                                       DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                              DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CONFLICT
                                                                                                                                                                                                                                                                                                                                                                             TRANSMEM
DOMAIN
                                                                                                                                                                                                           RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                      PRANSMEM
                                                                                                                                                                                                                                                                                                                                                  RANSMEM
                                                                                                                                                                                                                                                                RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match:
                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  No.:
                          EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                          LIPID
```

Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus

```
NCBI_TaxID=10116;
            NCBI_TaxID=1351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match:
OB:
                                                                                                                                                                                                                                                                                                                                                                                                                                       SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 34
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                               [2]
SEQUENCE FROM N.A.
STRAIN-CDC 1551 / Oshkosh;
STRAIN-CDC 1551 / Aland D., Eisen J.A., Carpenter L., White O.,
Felschmann R.D., Alland D., Eisen J.A., Earning, Haft D., Hickey E.,
Feterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Folomay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Deloher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
Bishai W.,
            Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.Y., Eiglaneier K., Gas S., Barry C.E. Ili, Fekaia F., Bavlacok K., Basham D., Brown D., Chillingworth T., Connor R., Bavies R., Devlin K., Peltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Woule S., Murphy L., Oliver S., Osborne J., Quall M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence."
                                                                                                                                                                                                                                          Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                       01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Autolysin precursor (EC 3.2.1.-) (Peptidoglycan hydrolase)
(Beta-91ycosidase).
Enterococcus faecalis (Streptococcus faecalis).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F4ACB04E3E5B526F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             629
0
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               671 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-824-647-16 (1-2095) x YS50_MYCTU (1-629)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tuberculist; Rv2850c; --
InterPro; IPR000523; Wg_chelatse_chil.
InterPro; IPR002035; VWF_A.
PF001778; Wg_chelatase; 1.
SWART; SM00327; VWR; 1.
PROSITE; PS50234; VWFA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCCACAGGGTCCACTGAAACGGGG 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                      AE007116; AAK47242.1; ALT_FRAME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VWFA
   MEDLINE-98295987; PubMed-9634230;
                                                                                                                                                                                                                                                                                                                   frameshift in position 19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66986 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37.2
8.00
100.00%
100.00%
1.16%
                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; 295207; CAB08456.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                     Nature 393:537-544(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE 629 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rIGR; MT2916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALYS_ENTFA P37710;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALYS_ENTFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 33
   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEESTES
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
       MEDLINE-91368349; PubMed-1679432;
Beliveau C., Potvin C., Trudel J., Asselin A., Bellemare G.;
Beliveau C., Potvin C., Trudel J., Asselin A., Bellemare G.;
Beliveau C., Potvin C., Trudel J., Asselin A., Bellemare G.;
Cloning, sequencing, and expression in Escherichia coli of a Streptococcus facecalis autolysin.";
J. Bacteriol, 173:5619-5623 (1991).
I. Subcritol, HYDROLYZES THE CELL WALL OF E.FAECALIS AND
M.LYSODERTATIONS. NAY PLAY AN IMPORTANT ROLE IN CELL WALL GROWTH
AND CELL SEPARATION:
-: DOMAIN: LYSM REPEATS ARE THOUGHT TO BE INVOLVED IN PEPTIDOGLYCAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
17-JUN-2002 (Rel. 41, Last annotation update)
17-JUN-2002 (APFII80) (P80)
17-JUN-1809 (APFII80) (P80)
17-JUN-1809 (APFII80) (P80)
                                                                                                                                                                                                                                                                                               -1- SIMILARITY: BELONGS TO FAMILY 73 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             enzyme; Cell wall;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LYSM 5.
3458268C6C1A4A33 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    671
8
0
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  678 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hydrolase; Glycosidase; Bacteriolytic enzy
Cell division; Septation; Repeat; Signal..
SIGNAL 1 53 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (1-671)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LYSM 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LYSM 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-824-647-16 (1-2095) x ALYS_ENTFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    383 TCCAGTGCCCTGATAGTCAGTTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR002901; Amidase_4.
InterPro; IPR002482; LysM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70442 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Interpro; IPR002482; LysM.
Pfam; PF01476; LysM; 5.
Pfam; PF01832; Amidase_4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M58002; AAA67325.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36.9
8.00
100.00%
100.00%
1.15%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00047; LYZ2; 1. SMART; SM00257; LYSM; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; A38109; A38109.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    629
671 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Aliqnment Scores:
                                                                                                                                                                                                                                                                                       BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T2D5_RAT
Q63801;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                      -1- FUNCTION: TRIID IS A MULTIMERIC PROTEIN COMPLEX THAT PLAYS A CENTRAL ROLL IN MEDIATING PROMOTER RESPONSES TO VARIOUS ACTIVATORS AND REPRESSORS. BINDS TIGHTLY TO TAFIL-250 AND ALSO DIRECTLY INTERACTS WITH TAFIL-40.

-1- SUBMINT: FRIID IS COMPOSED OF TATA BINDING PROTEIN (TBP) AND A NUMBER OF TBP-ASSOCIATED FACTORS (TAFS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-20057165; PubMed-10591208; Dunham I., Hunt A.R., Collins J.E., Brusklewich R., Beare D.M., Clamp M., Smink L.J., Ainscough R., Aimelda J.P., Babage A.K., Bagguley C., Balley J., Barlow K.F., Bates K.N., Beasley O.P., Bayguley C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J., Burtli W.D., Button J., Carder C., Carter N.P., Chen Y., Clark G., Clept S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R., Conroy D., Corby N.R., Collie G.J., Cox A.V., Davis J.J., Dawson E., Dhami P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G., Bvans K.L., Fey J.M., Fleming K., French L., Garner A.A., Gilbert J.G., R., Goward M.E., Graffen D.V., Criffiths M.N.D., Hall C., Hall R.E., Hall-Tamlyn G., Heathcott R.W., Ho S., Holmes S.,
                        TISSUE-Testis;
MEDLINE-95394378; PubMed-7665101;
Kida S., Umehara T., Horikoshi M.;
"Three distinct regions in a rat TFIID subunit containing histone H4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ROXN_HUMAN STANDARD; PRT; 993 AA.
09UGR2; Q9UFW9; Q9UGQ9; Q9UGR0; Q9UGR1; Q9UK03; Q9HBB6;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
ROIN-2002 (Rel. 41, Last annotation update)
ROIN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                               Transcription regulation; Nuclear protein.
SEQUENCE 678 AA; 72713 MW; 92D7225E3B7CC171 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                   SIMILARITY: BELONGS TO THE TAFZE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-824-647-16 (1-2095) x T2D5_RAT (1-678)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1053 GGCCCCAGCTCACCTCAGCCTGCC 1076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           670 GlyProSerSerProGlnProAla 677
                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR004822; Histone_core.
InterPro; IPR004823; TFIID_TAF.
Pfam; PF02969; TAF; 1.
                                                                                                                                                                                                                                                                                                                                           EMBL; D49446; BAA08435.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.00%
100.00%
1.15%
                                                                             homology.";
Gene 161:303-304(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                        Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KIAA1031.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ROXN_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 35
ð
```

```
RA Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,
RA Laird G.K., Langford C.F., Leversha M.A., Lloyd C., Lloyd D.M.,
Martyn I.D., Mashrephi-Mohamadi M., Matthwa L.H., Mordin O.T.,
RA Morlay J., McLaren S., McMurray A.A., Milne S.A., Mortimore B.J.,
RA Colay J., McLaren S., McMurray A.A., Milne S.A., Mortimore B.J.C.T.,
RA Colail C.N., Pavitt R., Fearce A.V., Pearson D., Phillimore B.J.C.T.,
RA Scott C.E., Sehra H.K., Skuce C.D., Samley S., Smith M.L.,
RA Soderlund C., Spragon L., Steward C.A., Sulston J.E., Swanda R.M.,
Wall M., Walls M., Whiteley M.N., Willey D.L.,
Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,
Williams L., Rabaski R., Beck S., Rogers J., Shimizu N.,
RA Minoshima S., Kawasaki K., Sasaki T., Asakwas S., Rodo J.,
Shintani A., Shibuya K., Yoshizaki Y., Asakwas S., Rodo H.I.,
RA Porma A., Shibuya K., Yoshizaki Y., Asakwas S., Lewis S., Lin S.-P., Loh P., Walaj E., Nguyen T., Pan H.,
Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T.,
RA Dorma A., Shibuya K., Yoshizaki Y., Asakwas S., Lan H., Lao H.I.,
RA Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S.,
Ra Cordes M., Du'Z., Frilton L., Goela D., Graves T., Hawkins T.,
Rhan S., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S.,
Roseet P., Walker C., Wamsley A., Wohldmann P., Pepin K., Wilson J.,
Rhoth R., Johnson M., Mong A.C.C., Morrow B.E., Edelmann L.,
Bmanuel B.S., Shiauya H., Shonson M.I., Dumanski J.P., Peyrard M., Kedra D.,
Sercoussi E., Fransson I., Tapia I., Bruder C.E., O'Brien K.,
Wilkinson P., Bodenteich A., Hartman R., Ru X., Rhan A.S., Lane L.,
Wilkinson P., Naider C.P., O'Brien R.,
Wilkinson P., Naider C.P., William Y., Rhan A., Rattman R.,
Wilkinson P., Bodenteich A., Hartman R., Ru X., Rhan A.S., Lane L.,
Ruban R., Ruban R., Rattman R., Ruban R.,
Ruban R., Ruban R., Ruban R.,
Ruban R., Ruban R., Ruban R.,
Ruban R., Ruban R., Ruban R.,
Ruba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y., Nishikawa T., Nagai K., Sugano S., Aotsuka S., Yoshikawa Y., Makama T., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Sasaki N.; "NEDO human cDNA sequencing project."; Sasaki N.; Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kikuno R., Nagase T., Ishikawa K.-I., Hirosawa M., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
"pradiction of the coding sequences of unidentified human genes. XIV. The complete sequences of 100 new CDNA clones from brain which code for large proteins in vitro.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -i- SUBCELLULAR LOCATION: Nuclear (Probable).
-i- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; may be produced by alternative splicing.
-i- SIMILARITY: CONTAINS 2 TPR REPEATS.
-i- SIMILARITY: CONTAINS 1 C2H2-TYPE ZINC FINGER.
-i- SIMILARITY: CONTAINS 4 C3H1-TYPE ZINC FINGERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA Res. 6:197-205(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Roxan: a tetratricopeptide cellular protein interacting with rotavirus non-structural protein NSP3."; Thesis (2000), University of Paris XI, France.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The DNA sequence of human chromosome 22.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 38-993 FROM N.A. (ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1-780 FROM N.A. (ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-99397452; PubMed-10470851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1-208 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 402:489-495(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rissue=Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    indenbaum P.;
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseéisb-sib.ch).
                                                                                                                                                                                                                                                                    EGF-LIKE 15.
EGF-LIKE 16 (N-TERMINAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EGF-LIKE 11 (INCOMPLETE) .
EGF-LIKE 12.
                                                                                                                                                                                                                                                                                                                                                                                                              LAMININ N-TERMINAL (DOMAIN VI).
LAMININ N-TERMINAL (DOMAIN VI).
LAMININ BGF-LIKE 1.
LAMININ BGF-LIKE 2.
LAMININ BGF-LIKE 4.
LAMININ BGF-LIKE 5.
LAMININ BGF-LIKE 6.
LAMININ BGF-LIKE 7.
LAMININ BGF-LIKE 7.
LAMININ BGF-LIKE 10.
LAMININ BGF-LIKE 10.
LAMININ BGF-LIKE 11.
LAMININ BGF-LIKE 11.
LAMININ BGF-LIKE 11.
LAMININ BGF-LIKE 11.
LAMININ BGF-LIKE 12.
LAMININ BGF-LIKE 14.
LAMININ BGF-LIKE 15.
LAMININ BGF-LIKE 16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN IV.
EGF-LIKE 16 (C-TERMINAL)
EGF-LIKE 17.
SIMILARITY: CONTAINS 1 LAMININ DOMAIN IV. SIMILARITY: CONTAINS 5 LAMININ G-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EGF-LIKE 18
EGF-LIKE 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LAMININ G-LIKE 1.
LAMININ G-LIKE 2.
LAMININ G-LIKE 3.
LAMININ G-LIKE 4.
LAMININ G-LIKE 5.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LAMININ EGF-LIKE
LAMININ EGF-LIKE
LAMININ EGF-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LAMININ
                                                                                                                                                       WOITMLEP; NUBCL'3; CENOLID.
InterPro; IPR001886; LamNT.
InterPro; IPR001886; LamNT.
InterPro; IPR001034; Laminin_B.
InterPro; IPR001049; Laminin_B.
InterPro; IPR001791; Laminin_G.
Pfam; PR00052; laminin_B; 1.
Pfam; PP00054; laminin_G; 21.
Pfam; PP00054; laminin_G; 5.
Pfam; PP00055; laminin_G; 7.
                                                                                                                                                                                                                                                            FIGURE SECULO AGENTAL ANCELLI, PRODON; PRODON; PRODON; BGFLAMIN. PRODON; PRODON 21; Lamnin_B; SWART; SMOD180; EGE_Lam; 21. SWART; SMOD181; LamB; 1. SWART; SMOD181; LamB; 1. SWART; SMOD181; LamB; 1. SWART; SMOD185; LamNT; 1. PROSITE; PSO1024; EGF_1; 19. PROSITE; PSO1146; EGF_2; 4. PROSITE; PSO1146; LAMININ_TYPE PROSITE; PSO1025; LAM G_DOMAIN
                                                                                                                         EMBL; Z70286; CAA94293.1; -. HSSP; P02468; 1KLO.
                                                                                                                                               могтрер; К08С7.3; СЕ06136.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   461
506
554
                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                      CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                          SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OMAIN
    MISSING (IN ISOFORM 2).

NL -> LE (IN REF. 4).

R -> K (IN REF. 2).

GTSNGAGSIDDLET -> VGSGLMQPVSVYPL (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Berks M.;
Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: CONTAINS 1 LAMININ N-TERMINAL DOMAIN (DOMAIN VI).
-!- SIMILARITY: CONTAINS 21.5 LAMININ EGF-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                      3).

G -> A (IN REF. 2).

G -> V (IN REF. 2).

S -> F (IN REF. 1; CAB62495 AND 2).

W, B8le9e67772FFEIB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Laminin-like protein KO8C7.3 precursor.
KO8C7.3.
                                                                                                                                                                                                                                                         TPR 1.
TPR 2.
C3H1-TYPE 1.
C3H1-TYPE 2.
C3H1-TYPE 3.
C2H2-TYPE.
C3H1-TYPE 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-824-647-16 (1-2095) x ROXN_HUMAN (1-993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1437 CGAGGATCGCCAGCACTGCTCC 1460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 111577 MW;
                                      EMBL; AL035659; CAB62495.1; --
EMBL; AL035659; CAB62496.1; --
EMBL; AF18830; AR05541.1; --
EMBL; AR023849; BAB14701.1; --
EMBL; AR028954; BAA82983.1; --
INTERPO; IPR0001440; TPR.
InterPro; IPR000822; Zuf.CCH2.
InterPro; IPR000871; Znf.CCH2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34.7
8.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                  521
651
795
882
927
224
39
88
88
                                                                                                                                                                                                                                                                                                                                                                                                232
386
676
993 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alignment Scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LML2_CAEEL
Q21313;
                                                                                                                                                                                                                                                                                                                                                                                                            CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                      CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                                                                   DOMAIN
DOMAIN
REPEAT
ZN_FING
ZN_FING
ZN_FING
ZN_FING
ZN_FING
ZN_FING
VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                   CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 36
LML2_CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..
9
       셤
```

us-09-824-647-16.std.rsp

•			
	·		
•	•		
			<u>-</u> .
	•	•	
SIMILARITY		SIMILARITY	SIMILARITY
SIMILARITY	SIMILARITY	SIMILARITY	SIMILARITY SIMILARITY SIMILARITY SIMILARITY SIMILARITY SIMILARITY SIMILARITY SIMILARITY SIMILARITY SIMILARITY SIMILARITY SIMILARITY SIMILARITY SIMILARITY SIMILARITY SIMILARITY SIMILARITY
	NAME OF STREET O		
BY B			BY B
	•		
で485000445048010 8	000 000 000 000 000 000 000 000 000 00	- 4 ಬಐಲೂ	/4ñò4ii80b0b0b848b9ii984
444444444	00000000000000000000000000000000000000	14444 11444	1877 19094 19094 19094 1909 1970 1987 2000 2000 2003 2004 2004 2006 2006 2006 2006 2006
4 <i>0</i>		v / ര ത പ ധ ത ଠ ര ത യ പ 4 ര സ / റ റ വ യ :	100000000000000000000000000000000000000
	888 888 888 888 888 888 888 888 888 88	11444411111111111111111111111111111111	1880 1880 1980 1990 1990 1990 1990 2001 2037 2039 2086
999888888888888		99999999999999999	3888888888888888
SULFID SULFID SULFID SULFID SULFID SULFID SULFID SULFID SULFID SULFID SULFID SULFID SULFID SULFID SULFID	01501,210 01501,	15.01.610 15.010 15	DISGUEID
DISCULPTO	DISULETO DISTALETO		
		•	
មកក្តុក្សិត្តិក្រុង មានក្រុង			

```
MEDLINE-89008497; PubMed-2902094;
Andrews P.C., Pollock H.G., Elliott W.M., Youson J.H.,
Plisetskaya E.M.;
"Isolation and characterization of a variant somatostatin-14 and two
related somatostatins of 34 and 37 residues from lamprey (Petromyzon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Petromyzon marinus (Sea lamprey).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;

Petromyzontiformes; Petromyzontidae; Petromyzon.

NCBL_TaxID=7757;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         marinus).";
J. Biol. Chem. 263:15809-15814(1988).
-!- FUNCTION: SOMATOSTAIN INHIBITS THE RELEASE OF SOMATOTROPIN.
-!- FUNCTION: SOMATOSTAIN INHIBITS THE RELEASE OF SOMATOTROPIN.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: BELONGS TO THE SOMATOSTATIN FAMILY.
PIR, A32000; A32000.
InterPro; IPR004250; Somatostatin.
PF03002; Somatostatin; 1.
                                                                                                                                                                                                                                                                                                          (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                          (POTENTIAL).
(POTENTIAL).
(POTENTAL).
(POTENTIAL).
                                                                                                                                              (POTENTIAL)
                                                                                                                                                                                                                                  (POTENTIAL)
                                                                                                                        (POTENTIAL)
                                                                                                                                     (POTENTIAL)
                                                                                                                                                                       (POTENTIAL)
                                                                                                                                                                                                          (POTENTIAL)
                                                                                                                                                                                                                                                          (POTENTIAL)
                                                                                                                                                                                                                                                                      (POTENTIAL)
                                                                                                                                                                                                                                                                                   (POTENTIAL)
                                                (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Somatostatin-37 [Contains: Somatostatin-34; Somatostatin-14].
                                                                                                                                                                                                                                                                                                                                              INKED (GLCNAC. . . . 28E262DB5FF14BFA
                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
Indels:
                                     (GLCNAC
                                                 (GLCNAC
                                                             (GLCNAC
                                                                          (GLCNAC
                                                                                                 (GLCNAC
                                                                                                                         (GLCNAC
                                                                                                                                                            (GLCNAC
                                                                                                                                                                        (GLCNAC
                                                                                                                                                                                                                                                          (GLCNAC
                                                                                   (GLCNAC
                                                                                                                                                                                     (GLCNAC
                                                                                                                                                                                                            (GLCNAC
                                                                                                                                                                                                                                     (GLCNAC
                                                                                                                                                                                                                                                (GLCNAC
                                                                                                                                                                                                                                                                        (GLCNAC
                                                                                                                                                                                                                                                                                    (GLCNAC
                                                                                                            (GLCNAC
                                                                                                                                                 (GLCNAC
                                                                                                                                                                                                GDCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37 AA.
 SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-824-647-16 (1-2095) x LML2_CAEEL (1-3672)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-LINKED
                                                                                                                                                                      N-LINKED
N-LINKED
N-LINKED
N-LINKED
N-LINKED
                                                                                                                                                                                                                                                                                                                    N-LINKED
N-LINKED
N-LINKED
                                                                                                                                                                                                                                  N-LINKED
N-LINKED
                                                                                                                                                                                                                                                          N-LINKED
N-LINKED
                                                                                                                                                                                                                                                                                                                                                          404223
                                                                                                                                                                                                                                                                                                                                                                                             28.3
8.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                          3672 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE.
TISSUE-Pancreas;
                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMS_PETMA
P21779;
                                               CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                           CARBOHYD
CARBOHYD
DISGLFID
CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                  CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                      CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                          CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                   CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                       CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                  CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                          CARBOHYD
                                                                                                                                                                                                                        CARBOHYL
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match:
                                                                                                                                                                                                                                                                                                                                                                                              Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMS_PETMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
```

the contemporary and the least sector of the Charles and Charles a

```
RPS27E OR RPS27A OR. MK0418
          Methanopyrus kandleri.
                                      NCBI_TaxID-2320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID-394;
                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EXOX_RHISN
P14185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18
                                                                                                                                                                                                                                                                                                                                                                                              Query Match:
                                                                                                                                                                                                                                                                                                                                                        ..
Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EXOX_RHISN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             용
   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.lsb-slb.ch/announce/or send an email to license@isb-slb.ch).
                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                           Ranes-Goldberg M.G., Hori T., Mohan-Peterson S., Spits H.; "Identification of human pre-T/NK cell-associated genes."; J. Immunol. 151:5810-5821(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6068 MW; CD41EAFFD2161857 CRC64;
                                          5918153B2775AC4D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0000
                                                                         7 0000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
                                                                         Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                               16-CCT-2001 (Rel. 40, Created)
16-CCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-TNK cell associated protein 6H9A.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
30S ribosomal protein 527e.
                        SOMATOSTATIN-14.
                                                                                                                                                                                                                                57 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73 A.A.
               SOMATOSTATIN-34
    Cleavage on pair of basic residues; Hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-824-647-16 (1-2095) x 6H9A_HUMAN (1-57)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps:
                                                                                                                             Gaps:
                                                                                                                                                US-09-824-647-16 (1-2095) x SMS_PETMA (1-37)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2046 AGGGGTGTTTGTGTTTGGGT 2066
                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                     GCAGCAGCTGTAGCTGGCTCC 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ArgGlyValCysValLeuGly 38
                                                                                                                                                                             AlaAlaAlaValAlaGlySer 10
                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-94044805; PubMed-8228263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; L17330; AAA16782.1; -. SEQUENCE 57 AA; 6068 MW;
                37
37
37
4039 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.00
100.00%
100.00%
                                                                          546
7.00
100.00%
1.00.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                       24
26
37 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
                                                                                              Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                            NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
Pred. No.:
                                                                 Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RS27_METKA
                                                                                                                                                                                                                                  6H9A_HUMAN
Q13653;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32
                        PEPTIDE
DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q8TY87;
                PEPTIDE
                                                                                                                   Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 39
RS27_METKA
                                                                           ..
9
                                                                                                                                                                                                                        6H9A_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score:
                                                                                      Score:
                                                                            Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     625558
                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a
                                                                                                                                                                      å
                                                                                                                                                                                         셤
      81118
81118
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                               between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS Institute of Bioinformatics and the EMBL outstation -
Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
                                                                                              MEDLINE-90094217; PubMed-2152899; Gray J.K., Djordjevic M.A., Rolfe B.G.; Gray J.K., Djordjevic M.A., Rolfe B.G.; Two genes that regulate exopolysaccharide production in Rhizobium sp. strain NGR234: DNA Sequences and resultant phenotypes."; J. Bacteriol. 172:193-203(1990).
-1- FUNCTION: INHIBITION OF EXOPOLYSACCHARIDE SYNTHESIS (EPS) AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE010337; AAM01633.1; -. PROSITE; PS01168; RIBOSOMAL_S27E; 1. Thosomal protein; Zinc-finger; Metal-binding; Complete proteome. ZN_FING 728 SEQUENCE 73 AA; 8281 MW; FE715056D29C0E8B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rhizobium sp. (strain NGR234).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
01-JAN-2002 (Rel. 41, Last annotation update)
Exopolysaccharide production repressor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -1- PATHWAY: Exopolysaccharide biosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96. AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-824-647-16 (1-2095) x RS27_METKA (1-73)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1285 CAGCCACGATCTCGCTTCCTC 1265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NODULATION ABILITY (NOD).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    491
7.00
100.00%
100.00%
1.02%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
```

US-09-824-647-16 (1-2095) x SSIC_STRHY (1-111)

```
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-96176850; PubMed-8597568;
Terabe M., Kojima S., Taguchi S., Momose H., Miura K.-I.;
"New subtilisin-trypsin inhibitors produced by Streptomyces: primary
"Trew subtilisin-trypsin inhibitors produced by Streptomyces: primary
structures and their relationship to other proteinase inhibitors from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -1- SUBCELLULAR LOCATION: Secreted.
-1- SIMILARITY: BELONGS TO THE SERINE PROFEASE INHIBITORS SSI FAMILY.
HSSP; PO1006; 3SSI.
InterPro; IPR000691; Strep_subt_inhib.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biochim. Biophys. Acta 1292:233-240(1996).
-!- FUNCTION: STROM INHIBITORY ACTIVITY TOWARD SUBTILISIN BPN' AND
TO A LESSER EXTENT, TO TRYPSIN.
-!- SUBUNIT: HOMODIMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae; Actinomycetales; Streptomycineae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REACTIVE BOND (BY SIMILARITY). 608204D09C7D0376 CRC64;
                                                                                                                                                                                                                                          Exopolysaccharide synthesis; Nodulation; Transmembrane. TRANSMEM 6 26 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09R641;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Subtilisin inhibitor-like protein-12 (SIL-12) (SIL12).
                                                                                                                                                                                                                                                                                                  POTENTIAL. A66CAFC82A627D2D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                       96
0
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           111 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
Watches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BY SIMILARITY
BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-824-647-16 (1-2095) x EXOX_RHISN (1-96)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00720; SSI; 1.
PRINTS; PR00294; SSBTLAINHBTR.
ProDom; PD004028; Strep_subt_inhib; 1.
PROSITE; PS00999; SSI; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        317 GCTTCCACTGCAGTGCAGACG 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29 AlaSerThrAlaValGlnThr 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE, AND CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11696 MW;
                                                                                                                                                                                                                                                                                                                              10595 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptomyces hygroscopicus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Serine protease inhibitor.
                                                                                                                                                                                                           EMBL; X16704; CAA34675.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                            26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 111 AA;
                                                                                                                                                                                                                                                                                                                              96 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID-1912;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SSIC_STRHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID
                                                                                                                                                                                                                                                                                                     PRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SSIC_STRHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DDT TEN THE TEN TO THE TEN TO THE TEN 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
   SSSSSSEFFS
```

```
RADILE-20199016; PUNDED-10/31132;
RA MEDLINE-20199016; PUNDED-10/31132;
RA MEDLINE-20199016; PUNDED-10/31132;
RA MEDLINE-20199016; PUOL R. L. I. P. W., Hoskins R.A., Galle R.F., Sutton G.G., Wortman J.R., Taddell M.D., Zhang Q., Chen L.X., Sutton G.G., Wortman J.R., Taddell M.D., Zhang Q., Chen L.X., Sutton G.G., Wortman J.R., Taddell M.D., Zhang Q., Chen L.X., Sutton G.G., Wortman J.R., Sankers F. C., Change M., Pickiffer B.D., RA Brandon R.C., Baxter E.G., Helt G., Change M., Miklos G.L.G., RA Ballaw R.M., Basu A., An H.-J., Andrews-Pfennkoch C., Baldwin D., Ballaw R.M., Basu A., An H.-J., Andrews-Pfennkoch C., Baldwin D., Ballaw R.M., Basu A., Bouck J., Broxestein P., Botshakov S., Beros R.Y., Bencs P.V., Derman B.P., Bhandari D., Bolshakov S., Burtis R.C., Busam D.A., Bulter H., Cadieu E., Center A., Chang P., Burtis R.C., Denge S., Mays A.D., Dew I., Dietz S.M., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Doup L.E., Downey M., Dugan-Rocha S., Dunkov B.C., Dunn P., Duchin K.J., Evangelista C.C., Ferraz C., Ferriar S., Pleischmann W., Foslar C., Gabriellan A.E., Garg N.S., Gelbart W.M., Glasser R., Harrey D.M., Harvey D.M., Murphy B., Murphy L., McPherson D.L., Allang Y., Lin X., Markey B.M., Murphy B., Murphy L., Muzhy D.M., Nelson D.L., Ranger R.M., Round S.M., Woy M., Murphy B., Murphy L., Muzhy B.M., Walssenbach J., Wang X.M., Moodage T., Worley K.C., Wu D., Yang S., Zahu K., Sahuder R., Wang X.H., Zhong F.N., Zhong F.N., Zhong K., Wang S., Zhu X., Sahuh R., Shong R.M., Walssenbach J., Wang S., Zhu X., Zhong R.P., The Renner C. Of Drocesselland R.M., Walshand R.M., Walshand R.M., Walshand 
                                                                                                                                                                                                                                                                           LCP3 OR CG2043.

Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Mandibulàta; Pancrustacea; Hexapoda;

Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

NCBI_TaxID-7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              *Cuticle protein genes of Drosophila: structure, organization and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -i- FUNCTION: COMPONENT OF THE CUTICLE OF THE LARVA OF FRUIT FLY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Snyder M., Hunkapiller M., Yuen D., Silvert D., Fristrom J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The genome sequence of Drosophila melanogaster.";
                                                                                                                                 CLP3_DROME, STANDARD; PRT; 112 AA. P07188; O9V411; O1-APR-1988(Rel. 07, Created) O1-APR-1988(Rel. 07, Last sequence update) 15-JUN-2002; (Rel. 41, Last annotation update) Larval cutifie protein III precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
STRAIN-Oregon-R, and Canton-S; TISSUE-Larva;
MEDLINE-83103095; PubMed-6817923;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         evolution of four clustered genes.";
550 ACACCCACGGGCACCCACCCC 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-20196006; PubMed-10731132;
                          Science 287:2185-2195(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cell 29:1027-1040(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-Berkeley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Davidson N.
                                                                                       RESULT 42
CLP3_DROME
```

3

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseélsb-sib.ch).
                                between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
               This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-20504483; PubMed=11016950;
MEDLINE-20504483; PubMed=11016950;
MG W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
Shukla H.D., Lasky S.R., Ballga N.S.; Thorsson V., Sbrogna J.,
Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
Maddocks D.G., Jablonski P.E., Frebs M.P., Angevine C.N., Dale H.,
Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,
Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
Ebbardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;
"Genome sequence of Halobacterium species NRC-1.";
Proc. Natl. Acad. Sci. US.A. 97:12176-12181(2000).
                                                                                                                                                                                                                                                                                                                             LARVAL CUTICLE PROTEIN III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
                                                                                                                                                                                                                                                                                                                                                  PRO-RICH.
2C6AC731B77291A6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   113 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-824-647-16 (1-2095) x CLP3_DROME (1-112)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps:
                                                                                                                                                                                                                   ElyBase; FBgn0002534; Lcp3.
InterPro; IPR000618; Insect_cuticle.
Pfam; PF00379; Chitin_bind_4; 1.
PROSITE; PS00233; CUTICLE; 1.
Structural protein; Cuticle; Signal.
3GNNL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1130 CCTCCTCCGATACCTGCTGCC 1150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Halobacterium sp. (strain NRC-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91 ProProProlleProAlaAla 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Halobacteriaceae; Halobacterium.
NCBI_TaxID-64091;
                                                                                                                                                              EMBL; V00203; CAA23489.1; -. EMBL; AE003837; AAF59094.1; -.
                                                                                                                                                                                                                                                                                                                                                                    112 AA; 11857 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                         460
7.00
100.00%
100.00%
1.01%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VESICLE SYNTHESIS
                                                                                                                                                                                                  PIR; C25299; C25299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GVPI2 OR VNG6233G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plasmid pNRC200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein 2
                                                                                                                                                                                                                                                                                                                                                                                                        Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GVI2_HALN1
Q9HHT7;
                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match:
                                                                                                                                                                                                                                                                                                              SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No.:
                                                                                                                                                                                                                                                                                                                                   CHAIN
ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Huang 2., Depoortere I., De Clercq P., Peeters T.; "Sequence and characterization of cDNA encoding the motilin precursor from chicken, dog, cow and horse. Evidence of mosaic evolution in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene 240:217-226(1999).
-i- FUNCTION: PLAYS AN IMPORTANT ROLE IN THE REGULATION OF INTERDIGESTIVE GASTROINTESTINAL MOTILITY AND INDIRECTLY CAUSES RHYTHAIC CONTRACTION OF DUODENAL AND COLONIC SMOOTH MUSCLE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                     Bos taurus (Bovine).
Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                 30-MAY-2000 (Rel. 39) Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Motilin precursor [Contains: Motilin; Motilin associated peptide (MAP)].
                                                                                 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CRC64;
                proteome.
DEBFFF8033A0473E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hormone; Cleavage on pair of basic residues; Signal. SIGNAL 1 25 BY SIMILARITY. PEPTIDE 26 47 MOTILIN.
                                                                        1113
0
0
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOTILIN ASSOCIATED 017DDB70EEA5EE68
                                                                                     Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                             115 AA.
                                                                         Length:
                                                                                                                                                                             US-09-824-647-16 (1-2095) x GVI2_HALN1 (1-113)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@lsb-sib.ch)
                                                                                                                                                   Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Duodenal mucosa;
MEDLINE-20033565; PubMed-10564829;
                                                                                                                                                                                                             603
                                                                                                                                                                                                          ; Plasmid; Complete
113 AA; 12526 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF068196; AAC18864.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           115 AA; 13055 MW;
EMBL; AE005156; AAG20889.1;
Gas vesicle; Plasmid; Comple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      458
7.00
100.00%
100.00%
1.01%
                                                                           459
7.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                        Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID-9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 prepromotilin.'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Aliqument Scores:
                                                             Alignment Scores:
                                                                                                                                                                                                                                                                                                   MOTI_BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PEPTIDE
                                                                                                                                       Query Match:
                                                                            ..
9
                                                                                                                                                                                                                                                                                     MOTI_BOVIN
                                                                                            Score:
                                                                                                                                                                                                                                                                                                     ò
```

34

QQ

```
BOC842741F30326D CRC64;
                                                                                                                                                                                                                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
Indels:
           115 AA.
                                                                                                                                                                                                                                                                                                                                                                US-09-824-647-16 (1-2095) x YDG5_SCHPO (1-115)
                                                                                                                                                                                                                                                                                                                                                       Gaps:
       PRT;
                                                                                            MEDLINE-21848401; PubMed-11859360
                                                                                                                                                                                                                                                                                                     ll protein.
115 AA; 13477 MW;
                                                                                                                                                                                                                                                                                              EMBL; Z73100; CAA97362.1; -.
                                                                                                                                                                                                                                                                                                                                7.00
100.00%
100.00%
1.01%
                                                                                                                                                                                                                                         Nature 415:871-880(2002).
           STANDARD;
                                                                Schizosaccharomyces (CBI_TaxID=4896;
                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                     Alignment Scores:
                                                                                                                                                                                                                                                                                                     Hypothetical
          YDG5_SCHPO
010493:
                                                                                                                                                                                                                                                                                                          SEQUENCE
     TDG5_SCHPO
RESULT 45
```

```
Search completed: July 7, 2003, 16:02:08 Job time : 75 secs
            ò
                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Collins M., Connor R., Cronin A., Dataly P., Feltwell T., Fraser, A. Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., Hanloyd. S., Honbsy T., Howarth S., Hother E.J., Hunt S., Jagels K., James K., Jones L., Jones M., Leather S., McDonald S., McLean J., Money P., Moule S., Mungall K., Murphy L., Niblett D., Odell C., Older E.J., Sauders S., Seeger K., Sharp S., Selton J., Simmonds M., Squares R., Seeger K., Sharp S., Skelton J., Simmonds M., Squares R., Starter T., Whitehead S., McDoward J., Volckaert G., Aert R., Robben J., Grymonprez B., Meltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller Auer S., Borzym K., Langer I., Beck A., Tehrach H., Reinhardt R., Pohl T.M., Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M., A Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., Lucas M., Rochet M., Gallardin C., Tallada V.A., Garzon A., Thode G., Abaga R.R., Cruzado L., Jimenez J., Sanchez M., Gall Rey F., Enrich S., Ander S., Harst S.M., Porter S., Borzon A., Thode G., Angals. R., Porter S., Borland, T. M., Porter S., Bornelle B., Porter S., Bornelle B., Porter S., Bornelle B., Porter S., Rober S., Ro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as acts to make the modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Forsburg S.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lyne R., Stewart A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   am D., Bowman S.,
., Churcher C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Ben
Domingez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg
Cerrutti L., Lowe T., McComble W.R., Paulsen I., Potashkin J.,
Shpakovski G.Y., Ossery D., Barrell B.G., Nurse P.,
"The genome sequence of Schizosaccharomyces pombe.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Very hypothetical protein C26F1.05 in chromosome I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyn
Sgouros J., Peat N., Hayles J., Baker S., Basham D.
Brooks K., Brown D., Brown S., Chillingworth T., C
US-09-824-647-16 (1-2095) x MOTI_BOVIN (1-115)
                                                                                                                   1679 GCCACTGCTGTCCTGCTGGCT 1699
                                                                                                                                                                                         6 AlaThrAlaValLeuLeuAla 12
```

```
026036 trypanosoma (95036) and opposite of the control of the cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9rrk2 deinococcus
075608 homo sapien
077821 oryctolagus
P70470 rattus norv
P97823 m lphosphol
Q94888 drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ogatl6 zea mays (m
Ogpa28 xylella fas
O69819 streptomyce
O68521 myxococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q8qs62 chimpanzee
Q911t8 streptomyce
Q9bux4 homo sapien
Q9uqf9 homo sapien
O77820 oryctolagus
               Q9x402 methylosulf
Q8vuf4 azoarm
                                                                                                                    Q8y2x4 ralstonia s
P74015 synechocyst
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            streptomyce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9rz01 deinococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9at15 zea mays (m
Q39263 arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9c8d2 arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rattus norv
musculu
                                                                                                                                                                                                         26835 trypanosoma
Q98ke0 rhizobium
                                                                                                                                                                                                                                                                       trypanosoma
                                                                                                                                                                               drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-OVARIAN CARCINOMA;

ISOGAI T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
Nishikawa T., Nagai K., Sato H., Sugano S., Shiratori A., Sudo H.,
Nagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.
Takahashi M., Chiba Y., Ishida S., Wurakawa K., Ono Y., Takiguchi S.,
Watanabe S., Kimura K., Murakami K., Ishil S., Kawai Y., Saito K.,
Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
Ninoniya K., Iwayanagi T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2001 (TrEMBLrel: 16, Created)
1-MAR-2001 (TrEMBLrel: 16, Last sequence update)
01-UNA-2002 (TrEMBLrel: 21, Last annotation update)
00ARC;1001154 protein.
1-Mono saplens (Human).
Eukaryota; Metazoa; Chordita; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                    Q26763
Q26036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NEDO human cDNN sequencing project.";
ubmitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
MBL; AK023348; BAB14535.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     413 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q8QQM8
Q8QQM8
Q9PK90
Q8XX13
Q8QS62
Q9L1T8
Q9BUX4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9V8A8
Q9RZ01
Q9ATL6
Q9PA28
O69819
O68521
                                                                                                                                                                                                                                                                 026763
026036
0298134
0905G7
043202
007154
0915P6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9RRK2
Q75608
Q77821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P70470
P97823
                                                                                                                                                                                                         Q26835
Q98KE0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q916W2
Q916W1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9ATL5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q90QF9
077820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                             633
1191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09н851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 1.
09H8S1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    00000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCOCCOS DE TENTO DE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -WODEL-frame+_n2p.model -DEV-xlp
-Qr-Q002_1/R04PO_spool_1/R059824647/runat_07072003_154718_26035/app_guery.fasta_1.2247
-Qr-Q002_1/R05PO_spool_1/R059824647/runat_07072003_154718_26035/app_guery.fasta_1.2247
-DDS-SPREMBL_21 -OFWT-fastan -SUFFIX=std.rspt -WINMATCH=0.1 -LOOPEL=0.
-LOOPEXT=0 -UNITS-bits -START=1 -END=-1 -MATRIX=01190 -TRANS=human40.cdi
-LIST=45 -DGOALIGH=0.200 -THE_SCORES=0.0 -INTE_MIN=1 - ALIGH=45 -WODE=LOCAL
-USER-US09824647_CGCN_1 1_231_erunat_07072003_154718_26035 -NCPU=6 -ICPU=3
-NO_WMAP -LARGEQUERY -NRG_SCORES=0 -WART -DSPBLOCK=100 -LONGLOG
-FGAPOP=60 -VGAPORT=60 -DELOP=6 -DELEXT=7
-YGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9h8s1 homo sapien
                                                                                                                                                                                               7, 2003, 15:47:40 ; Search time 159.5 Seconds (without alignments) 5412.774 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                     1 cgcaggcagaccatgtggac......ataaagtttgtcactttctt 2095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1343044
                     GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

    protein search, using frame_plus_n2p model

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seqs, 206047115 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60.0
60.0
7.0
7.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            413 4 Q9H8S1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , Xgapext 6
, Ygapext 6
, Fgapext
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sp_unclassified:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60.0 , Ygapext
60.0 , Ygapext
6.0 , Fgapext
6.0 , Delext
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sp_fung1:*
sp_human:*
sp_invertebrate:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sp_vertebrate:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sp_mhc:*
sp_organelle:*
sp_phage:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sp_bacteriap:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq length: 0 seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sp_archea:*
sp_bacteria:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sp_plant:*
sp_rodent:*
sp_virus:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sp_archeap:*
                                                                                                                                                                                                                                                                                                                          US-09-824-647-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sp_rvirus:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sp_mammal:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Command line parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xgapop
Ygapop
Fgapop
Delop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              671580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22.3
                                                                                                                                                                                                     July
                                                                                                                                                                                                                                                                                                                                                                                                                                                 OLIGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         155
                                                                                                                                                                                                                                                                                                                                                            score:
                                                                                                                                                                                                                                                                                                                                                                                                                                              Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90
                                                                                                                                             OM nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Word size:
                                                                                                                                                                                                                                                                                                                                                                                     Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Minimum I
Maximum I
                                                                                                                                                                                                                                                                                                                                                         Perfect
                                                                                                                                                                                                     Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Result
                                                                                                                                                                                                                                                                                                                          Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Š
```

us-09-824-647-16.std.rspt

8888888

ð 셤 ò g ö 셤 ò 요 ò 윱

```
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             090WB4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus sp
                                                                                                                                                                                                                                                                                                          ..
2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score:
                                                                                                                                                                                                                                                                                                                     Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCTGTGTGCTGTGAGGACCACATACACTGCTGTCCCGCGGGGTTTACGTGTGACACGCAG 1005
                                                                                                                                                                                                                                                                                                                                                                                                  CTCAGCCTGCCAGACCCACAAGCCTTGAAGAGAGATGTCCCCTGTGATAATGTCAGCAGC 1125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGTCCCTCCTCCGATACCTGCTGCCAACTCACGTCGGGGAGTGGGGGCTGCTGTCCAATC 1185
                                                                                                                                                                                                            825
                                                                                                                                                                                                                                                         885
                                                                                                                                                                                                                                                                                111
                                                                                                                                                                                                                                                                                                                                                                                                                                                           211
                                                                                                                                                                                                                                                                                                       GATGGCTATACCTGCTGCCGTCTACAGTCGGGGCCTGGGGCTGCTGCCCTTTTACCCCAG 945
                                                                                                                                                                                                                                                                                                                   91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92 ThrLysLeuProAlaHisThrValGlyAspValLysCysAspMetGluValSerCysPro
                                                                                                                                                                                                                      826 ACTAAGCTGCCTGCGCACACAGTGGGCGATGTGAAATGTGACATGGGAGGTGAGCTGCCCCA
                                                                                                                                                                                                              GTGTGTGACCTGATCCAGAGTAAGTGCCTCTCCAAGGAGAACGCTACCACGGACCTCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Alzawa M., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCAGAGGCTGTCTGCTCGGACCACCAGCACTGCTGCCCCCAG 1230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2001 (TIEMBLrel. 17, Last sequence update)
01-JUN-2002 (TIEMBLrel. 21, Last annotation update)
Adult male kidney CDNA, RIKEN full-length enriched library, clone:0610012H06, full insert sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001118; Granulin.
InterPro; IPR001211; PhospholipaseA2.
Bam: PR00396; granulin; 4.
SWART; SW00277; GRAN; 4.
PROSITE; PS00799; GRANULINS; UNKNOWN.4.
SPROSITE; PS01198; PA2_HIS; UNKNOWN.1.
SEQUENCE 413 AA; 44132 WW; 0E3767A44BE314EC CRC64;
                                                                                                      413
155
0
0
0
                                                                                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             589 AA.
                                                                                                                                                               Gaps:
                                                                                                                                                                                       US-09-824-647-16 (1-2099) x Q9H8S1 (1-413)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -JUN-2001 (TrEMBLrel. 17, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=C57BL/6J; TISSUE=KIDNEY;
MEDLINE=21085660; PubMed=11217851;
                                                                                                    1,15e-145
155.00
100.00%
100.00%
22.33%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                             Percent Similarity:
Best Local Similarity:
                                                                                              Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                     946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    172
                                                                                                                                                                                                                                                                                                          988
                                                                                                                                                                                                                                                                                                                              112
                                                                                                                                                                                                                                                                                                                                                                            132
                                                                                                                                                                                                                                                                                                                                                                                                   1006
                                                                                                                                                                                                                                                                                                                                                                                                                         152
                                                                                                                                                                                                                                                                                                                                                                                                                                                1066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9D2V3
                                                                                                                                                     Query Match:
DB:
                                                                                                         Мо. :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score:
```

à

d ä g

. <u>a</u>

à

```
1396 GGGAGCTGGGCCTGCTGCTGCTGCTGCTGTGCTGCTGCGAGGATCGCCAGCACTGC 1455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           479
Ruehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schrill L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hoffmann M., Hume D.A., Kaniya M., Lee N.B., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerfä P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-Oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AEDLINE-93266526; PubMed-8496151;
Zhou J., Gao G., Crabb J.W., Serrero G.;
Zhou J., Gao G., Crabb J.W., Serrero G.;
Purification of an autocrine growth factor homologous with mouse epithelin precursor from a highly tumorigenic cell line.";
J. Biol. Chem. 268:10863-10869(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_raxID=10095;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WAY-2000 (TrEMBLrel. 13, Last annotation update)
PC cell-derived growth factor, PCDGF-EPITHELIN precursor homolog
                                                                                                                                                                                                                                                                                  Hayashizaki Y.;
*Punctional funotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                      EMEL; AKO1874; BAB31384.1; -
EMEL; AKO1874; BAB31384.1; -
MGI; 95832; Grn.
InterPro; IPR000118; Granulin.
InterPro; IPR0001211; PhospholipaseA2.
Pfam; PF00396; granulin; 7.
PROSITE; SM00277; GRAN, 7.
PROSITE; PS00799; GRANULINS; 7.
PROSITE; PS00118; PA2_HIS; UNKNOWN_1.
SEQUENCE 589 AA; 63405 MW; IDE8229C413CA292 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       589
32
0
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C349143EE4E942AF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-824-647-16 (1-2095) x Q9D2V3 (1-589)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.39e-22
32.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5473 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18.6
9.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fragments).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NON_TER
NON_CONS
NON_TER
SEQUENCE
```

m

```
RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B
                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EX COS E DE
                                                                                                                                                                                                                                                                                                                                                    De Marco P., Moradas-Ferreira P., Higgins T.P., McDonald I., Kenna B.M., Murrell J.C.;
Kenna B.M., Murrell J.C.;
"Molecular analysis of a novel methanesulfonic acid monooxygenase from the methylotroph Methylosulfonomonas methylovora.";
J. Bacteriol. 181:2244-2251(1999).
BERGIS, ARD26617.1;
NOW.TER 266 266
                                                                                                                                           09X402 PRELIMINARY; PRT; 266 AA.
09X402;
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
Putative ABC transporter membrane-associated protein (Fragment).
                                                                                                                                                                                                                                         Methylosulfonomonas methylovora.
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Methylosulfonomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; beta subdivision; Rhodocyclus group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mohr K., Herrmann H., Burchhardt G.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; A4128519; CAD21637.1; -
InterPro; IPR002085; Adh.zu_family.
InterPro; IPR0000345; CytC_heme_bind.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfan; PF00107; adh zinc; 1.
PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
SROUENCE 355 AA; 38211 MW; 5ELD930131F800A6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                      NON_TER 266 266
SEQUENCE 266 AA; 29281 MW; 2AFAEDC02B575010 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-WAR-2002 (TTEMBLrel. 20, Created)
01-WAR-2002 (TTEMBLrel. 20, Last sequence update)
01-JUN-2002 (TTEMBLrel. 21, Last annotation update)
6-hydroxycyclohex-1-ene-1-carboxyl-CoA dehydrogenase.
 00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                355 AA.
 Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1617 AGACAACCGACAGGGCTGGGCCTGCTG 1643
                                                               Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 ArgGlnProThrGlyLeuGlyLeuLeu 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-824-647-16 (1-2095) x Q9X402 (1-266)
                                      US-09-824-647-16 (1-2095) x Q9QWB4 (1-51)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                         MEDLINE-99194735; PubMed-10094704;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.00%
100.00%
1.30%
1.30%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                  NCBL_TaxID-50057;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=59406;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Azoarcus evansii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-KB740;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alignment Scores:
                                                                                                                                                                                                                                                                                                                            STRAIN-M2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Azoarcus
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q8VUF4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q8VUF4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..
Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B2DX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 5
                                                                                                                    RESULT
09X402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q8VUF4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred.
                                                                  à
                                                                                                                                                            ď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
```

```
STRAIN-GRIU000;
STRAIN-GRIU000;
STRAIN-GRIU000;
Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S., Arlat M., Billault A., Brottler P., Camus J.C., Cattolico L., Arlat M., Choisne N., Claudel-Frenard C., Cunnes S., Demange N., Gaspin C., Lavie M., Molsan A., Robert C., Saurin W., Schiex T., Siguier P., Thebault P., Whalen M., Wincker P., Levy M., Schiex T., Siguier P., Thebault P., Whalen M., Wincker P., Levy M., Schiex T., Genome sequence of the plant pathogen Ralstonia solanacearum."; Nature 415:497-502(2002).
                                                                                                    :Si
                                                                                                                                                                                                                                                                                                                                                                                                                                           Ralstonia solanacearum (Pseudomonas solanacearum).
Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          408 AA; 41634 MW; 2F9943B095187FC0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synechocystis sp. (strain PCC 6803).
Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
NCBL_TaxID=1148;
                  355.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 408
00
00
00
00
                                                                                                                                                                                                                                                                                                                                              01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UNY-2002 (TrEMBLrel. 21, Last annotation update)
Putative transporter transmembrane protein.
RSC0207 OR RS00639.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
                                                      Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                              408 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               633 AA
                    Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels:
                                                                                                                                                                                           741 GTGATCGGAGCAGCAGGTGGCGTTGGG 715
                                                                                                                                                                                                             173 ValileGlyAlaAlaGlyGlyValGly 181
                                                                                                                  Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AL646058; CAD13735.1; -
InterPro; IPR003662; sub_transporter.
Pfam; PF00083; sugar_tr; 1.
Complete proteome:
SEQUENCE 408 AA; 41634 MW: ?F00473E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sensory transduction histidine kinase
                                                                                                                                                   US-09-824-647-16 (1-2095) x Q8VUF4 (1-355)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-824-647-16 (1-2095) x Q8Y2X4 (1-408)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                              PRT;
                    15.3
9.00
100.00%
100.00%
1.31%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.00%
100.00%
1.31%
16
                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 \frac{15.1}{9.00}
                                                  Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBL_TaxID=305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alignment Scores:
Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ralstonia
                                                                                                                                                                                                                                                                                                          Q8Y2X4
Q8Y2X4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P74015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SLL1228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P74015
```

SOW SOW SERVICE STREET STREET

```
Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  098KEO;
                                                                                                                                                                                                                                                                  Query Match:
                                                                                                                                                                                                   Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                098KE0
                                                                                                                                                                                                                                                                                                                                                                                                                                           026835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    298KE0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score:
                                                                                                                                                                                                                     Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ð
                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cubadda T., Heitzler P., Ray R.P., Bourouis M., Ramain P., Gelbart W., Simpson P., Haenlin M.;
"u-shaped encodes a zinc finger protein that regulates the proneural genes achaete and scute during the formation of bristles in
                          Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura T., Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T., Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptea; Endopperglota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                        Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.";
DNA Res. 3:109-136(1996).
INDIARATY: THE N-TERMINAL REGION IS SIMILAR TO THAT OF OTHER REGULARORY COMPONENTS OF SENSORY TRANSDUCTION SYSTEMS.
ISTMILARITY: TO PROKARYOTE SENSORY TRANSDUCTION PROTEINS.
HESPI, D90911; BAA18086.1;
HSSP; P10957; IRNL.
                                                                                                         "Sequence analysis of the genome of the unicellular cyanobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kinase; Phosphorylation; Sensory transduction; Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2128D1E7D56F33C1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     633
0000
0000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 1191 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (U-shaped protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1322 CCCACCCCAGAGACATCGGCTGTGACC 1348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                401 ProThrProGluThrSerAlaValThr 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-824-647-16 (1-2095) x P74015 (1-633)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                   Interpro; IPR003594; ATPbind_ATPase.
Interpro; IPR004358; Bact_sens_pr_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-98037748; PubMed-9367989;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Response_reg; 1.
                                                                                                                                                                                                                                                                                Interpro; IPR003018; GAF.
Interpro; IPR004561; His_Kinh.
Interpro; IPR004359; HIS_Kin sig.
Interpro; IPR001789; Response_reg
SEQUENCE FROM N.A.
MEDLINE-97061201; PubMed-8905231;
                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00072; response_reg; 1. Pfam; PF00512; signal; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         633 AA; 69896 MW;
                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00344; BCTRLSENSOR.
ProDom; PD000039; Response_re
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; HATPase_c; 1.
                                                                                                                                                                                                                                                                                                                                               Pfam; PF01590; GAF; 1.
Pfam; PF02518; HATPase_c; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02,
05,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.00%
100.00%
1.30%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SKA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JAN-1998 (TrEMBLrel.
01-JAN-1998 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zinc-finger protein USH OSH OR CG2762.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14.4
9.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                SM00065; GAF; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SM00387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                             Tabata S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            018414;
                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             018414
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              018414
```

ð

```
SEQUENCE FROM N.A.
MEDILINE-86278091; PubMed-2942540;
MEDILINE-86278091; PubMed-2942540;
Brown K.H., Brentano S.T., Donelson J.E.;
"Mung bean nuclease cleaves preferentially at the boundaries of
"Mung bean nuclease glycoprotein gene transpositions in trypanosome DNA.";
J. Blol. Chem. 261:10352-10358(1986).
EMBL; M14022; AAA30308.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBL_TaxID=5691;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rhizobium loti (Mesorhizobium loti).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
(12Tat 2.4) variant surface glycoprotein TC gene (Fragment).
Trypanosoma brucei.
Genes Dev. 11:3083-3095(1997).

1-- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

R EMBL, Y12322; CAA72991.1; -

R EMBL, Y12922; CAA72991.1; -

R ETJYBASE; FBG100039563; ush.

R ITJYBASE; FR000985; ZINCTRINER.

R PRINTS; PR00098; ZINCTRINER.

R SMART; SM00355; ZnP_C2H2; 6.

R PROSITE; PS0157; ZINC_FINGER_C2H2_2; 3.

R PNN-binding; Nuclear protein; Zinc-finger.

R SEQUENCE 1191 AA; 124561 MW; C4C599C690C7096B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17 AA; 1783 MW; '4A20FBE55CF59E5B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein ms11520.
                                                                                                                                                                                                                                                                                                                    Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1632 GCCCTGTCGGTTGTCTCGGCAGCA 1609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-824-647-16 (1-2095) x 018414 (1-1191)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-824-647-16 (1-2095) x Q26835 (1-17)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel. 01, Created) (TrEMBLrel. 01, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.00%
100.00%
                                                                                                                                                                                                                                                                                                                    13.5
9.00
100.00%
100.00%
1.31%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           208
8.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                Alignment Scores:
```

```
01-NOV-1996 (TIEMBLrel. 01, Created)
01-NOV-1996 (TIEMBLrel. 01, Last sequence update)
01-DEC-2001 (TIEMBLrel. 19, Last annotation update)
variable surface antigen (Fragment).
Trypanosoma brucel.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
                                                                                                                                                                                                                                                                                  "DNA rearrangements of the variable surface antigen genes of the Trypanosomes.";
                                                                                                                                                                                                          SEQUENCE FROM N.A.
BEDLINES 4242548; PubMed-6737319;
Murphy W.J., Brentano S.T., Rice-Ficht A.C., Dorfman D.M.,
Donelson J.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                  68 AA; 7641 MW; 388437A80C8F5266 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-824-647-16 (1-2095) x Q9B134 (1-93)
                                                                                                                                                                                                                                                                                                                                                          J. Protozool, 31:65-73(1984).
EMBL; M31538; AAA30294.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Aliqument Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09B134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9B134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 М
М
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 13
                    DT REAR THE LEAD TO THE LEAD THE LEAD TO T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ð
                                                                                                                                                         Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S., Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Tamada M., Tabata S., Complete genome structure of the nitrogen-fixing symblotic bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBI_TaxID=5691;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Michels P.A.M., van der Ploeg L.H.T., Liu A.Y.C., Borst P.;
"The inactivation and reactivation of an expression-linked gene copy
for a variant surface glycoprotein in Trypanosoma brucei.";
EMBD. J. 3:1345-1351(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ol-mov-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Trypanosome brucei variable surface antigen 1.8 mRNA 3'-end
(Fragment).
                                                                                                                                                                                                                                                                                                                                DNA Res. 7:331-338(2000).
BMED; AP002997; BAB4884.1; -
Hypothelical protein; Complete proteome.
SEQUENCE 48 AA; 5437 MW; 37A2002130817620 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9CDD30CFA24461E8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  00000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1632 GCCCTGTCGGTTGTCTCGGCAGCA 1609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1310 CGCCGGCCAGCCATCTTCTCCAGT 1287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 ArgArgAlaGlyllePheSerSer 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-824-647-16 (1-2095) x Q26763 (1-59)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-824-647-16 (1-2095) x Q98KE0 (1-48)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                           STRAIN-MAFF303099;
MEDLINE-21082930; PubMed-11214968;
            Phyllobacteriaceae; Mesorhizobium NCBI_TaxID=381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE-84261425; Pubmed-6086319;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6642 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TrEMBLrel. 01,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.00%
100.00%
1.16%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                187
8.00
100.00%
100.00%
1.16%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                184
8.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lrypanosoma brucei.
                                                                                                                                                                                                                                                                                                              Mesorhizobium loti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59. AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity:
                                                                                       SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1996
01-NOV-1996
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Aliqument Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q26036
Q26036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               926763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ::
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        026763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   026036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ð
```

```
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Cyprinella.
NCBI_TaxID=28791;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=1, AND 2;
STRAIN=1, AND 2;
STRAIN=1, AND 2;
STRAIN=1, AND 2;
STOSE M.J., Willey E.O.;
"Phylogenetic relationships of the Hybopsis amblops species group (Teleostei: Cyprinidae).";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
-1- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
EMBL, AF216590; AAK34899.1;
InterPro; IPR001750; Oxidored_q1.
Fran: PF00361; Oxidored_q1.
Mitochondrion; NAD; Oxidoreductase; Ubiquinone.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10071 MW; A0C6713C0C0B3879 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              00000
                                                                                                                                                                                                                                                                                                                         01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUAR-2002 (TrEMBLrel. 20, Last annotation update)
NADH dehydrogenase subunit 2 (Fragment).
Cyprinella lutrensis (red shiner).
 8 80000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative:
Mismatches:
Indels:
                                   Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                       93 AA
Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
                                                                                                                                                                       1632 GCCCTGTCGGTTGTCTCGGCAGCA 1609
                                                                                                                                                                                           (1-68)
                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                  US-09-824-647-16 (1-2095) x Q26036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.00%
100.00%
1.15%
                                 Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 1.16%
                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                175
8.00
181
8.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
```

ద

```
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [3]
SEQUENCE FROM N.A.
                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
                                                                     construction.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                             Aliqument Scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                              red. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 16
                                                                                                                                                                                                                                                                                                                                                                                                   Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ð
STRAIN-CSTRL/63; TISSUB-TESTIS;

MEDLINE-2108560; PubMed=11217851;

A Rawal J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A Arakawa T., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Saito T., Okazaki Y., Gojobori T., Bono H., Rasukawa T., Saito R.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casvant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casvant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov B., Kochiwa H.,

Sakai K., Okido T., Pruno M., Aono H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Brownstein M.J., Bult C., Fletcher C., Fullia M., Gariboldi M.,

Rusonstein M.J., Bult C., Retcher C., Fullia M., Mombaerts P.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Nyasaki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

Nyasaki Y.,

Nyasak
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                 Mus musculus (Mouse).
Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AK015362; BAR29813.1; -.
MGD; MGI:1922144; 4930442H23Rik.
SEQUENCE 103 AA; 10763 MW; 7C7BC18D7E859890 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                             01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                104 AA
                                                                                                           103 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Probable lysophospholipase (Fragment).
CTGGGCCTGCTGCCAGTTGCCCCA 1424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-824-647-16 (1-2095) x Q9D5G7 (1-103)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-1998 (TrEMBLrel. 06, 01-JUN-1998 (TrEMBLrel. 06, 01-OCT-2001 (TrEMBLrel. 18,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.00%
100.00%
1.15%
11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 409:685-690(2001)
                                                                                                                                                                                                 4930442H23R1k protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                043202
                                                                                                             090567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 15
043202
                                                                       RESULT 14
Q9D5G7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ð
```

```
MEDLINE-93188700; PubMed-8446027;
Eiglmeler K., Honore N., Woods S.A., Caudron B., Cole S.T.;
"Use of an ordered cosmid library to deduce the genomic organization
of Mycobacterium leprae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycobacterium leprae.
Bacteria; Firmloutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1769;
MEDLINE-96207227; PubMed-8619474;
Andersson B., Wentland M.A., Ricafrente J.Y., Liu W., Gibbs R.A.;
"A 'double adaptor' method for improved shotgun library
                                                                                                                                                                                       Yu W., Andersson B., Worley K.C., Muzny D.M., Ding Y., Liu W., Ricafrente J.Y., Wentland M.A., Lennon G., Gibbs R.A.; "Large-scale concatenation cDNA sequencing."; Genome Res. 7:353-358(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
Oliver K., Harris D.;
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11 protein.
111 AA; 12241 MW; 13DD36663FDF0B8C CRC64;
                                                                                                                                                                                                                                                                                                                                                                      CE6C320EEA1011B3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                   40000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUL-1997 (TYEMBLIAEL: 04, Created)
01-JUL-1997 (TYEMBLIAEL: 04, Last sequence update)
01-NOV-1998 (TYEMBLIAEL: 08, Last annotation update)
Hypothetical 12.2 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1686 CTGTCCTGCTGCTTCCGCTGCGC 1709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-824-647-16 (1-2095) x 043202 (1-104)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LeuSerCysTrpLeuProLeuArg 23
                                                                                                                                                                                                                                                                                                  InterPro; IPR003140; PLP_Cesterase.
Pfam; PF02230; abhydrolase_2; 1.
NON TER 1 1
                                                                                                                                                          FISSUE-BRAIN;
MEDLINE-97264341; PubMed-9110174;
                                                                                 Anal. Biochem. 236:107-113(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mol. Microbiol. 7:197-206(1993).
EMBL; 296801; CAB09641.1; -.
                                                                                                                                                                                                                                                                                  EMBL; AF035293; AAB88180.1; -
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE 104 AA; 11403 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                            173
/8.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    172
8.00
100.00%
100.00%
1.16%
```

```
Plasmid 44:285-291(2000).
                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF01560;
                                           STRAIN-22243;
                                                                                                                                                                              Alignment Scores;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hepacivirus
                                                          Fauch A.;
Submitted
                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match:
                                                                                                                                                                                                                                                   Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                     Q916W2;
                                                                                                                                                                                                                                                                                                                                                                                                                    Q916W2
                                                                                                                                                                                             ..
Q
                                                                                                                                                                                                                                                                                                                                                                                          RESULT 19
                                                                                                                                                                                                           Score:
                                                                                                                                                                                                                                                                                                                                                                                                         Q916W2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ð
 SWADARAC
                                                                                                                                                                                                                                                                                                                            STRAIN-ATCC 15692 / PAO1;
MEDLINE-20437337; PubMed=10984043;
Stover C.K., Pham X. O.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
Stover C.K., Pham X. O.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.
Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
Reizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.;
"Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tauch A., Puhler A., Kalinowski J., Thierbach G.; "Tetz, a New Tetracycline Resistance Determinant Discovered in Gram-Positive Bacteria, Shows High Homology to Gram-Negative Regulated Efflux Systems.";
                                                                                                                                                                                                                                    Pseudomonas aeruginosa.
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Actinomycetales; Corynebacterineae; Corynebacteriaceae; Corynebacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            opportunistic pathogen.";
Nature 406:959-964(2000).
EMBL: AE004503; AAG04068.1; .
Hypothetical protein; Complete proteome.
SEQUENCE 143 AA; 15028 MW; 0235C65ECEDCF3DD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                          01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-0CT-2001 (TrEMBLrel. 18, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Corynebacterium glutamicum (Brevibacterium flavum).
Plasmid R-plasmid pAG1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             149 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1458 GCAGCAGTGCTGGCGATCCTCGCA 1435
                                         1392 CTGGCTCGGGCAGCAGGTTCCGCC 1369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-824-647-16 (1-2095) x Q915P6 (1-143)
             US-09-824-647-16 (1-2095) x 007154 (1-111)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16 AlaAlaValLeuAlaIIeLeuAla 23
                                                          PRT;
                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-20532766; PubMed-11078655;
                                                                                                                                                                                      01-OCT-2001 (TrEMBLrel. 18, Hypothetical protein PA0679.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  168
8.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.16%
16
                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID-1718;
                                                                                                                                                                                                                                                                                 KCBI_TaxID-287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-22243;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                    Pseudomonas
                                                                                                                              Q915P6
Q915P6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09X549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rag1D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 18
09X549
                                                                                                    RESULT 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score:
                                                                                                                                               ò
                                            ò
                                                                       요
```

```
Coat protein; Envelope protein; Glycoprotein; Nonstructural protein; Polyprotein; Transmembrane.

NON_TER 1 1 1

NON_TER 154 154
SEQUENCE 154 AA; 16728 MW; C4F5DA7B61F6C484 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2002 (TrEMBLrel. 20, Last annotation update)
Genome polyprotein (Contains: envelope glycoprotein E2 (GP68) (GP70)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (SEP-2001) to the EWBL/GenBank/DDBJ databases.
--- SIMILARITY: TO HEPATITIS C VIRUS ENVELOPE GLYCOPROTEIN E1.
EWBL; AF422337; AAL24649.1; --
InterPro; IPR002519; HCV_env.
InterPro; IPR002531; HCV_NS1.
                                       36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=ACL-92;
Lyra A.C., Fan X., Di Bisceglie A.M.;
"Evolution of hepatitis C viral quasispecies after liver
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases EMBL, AF121000; AAD25068.1; -InterPro; IRR03795; DUF192. Pfam; PF02643; DUF192; 1.
                                                                                          149 AA; 15897 MW; 398307CEEC67DA4D CRC64;
                                                                                                                                                     149
0
0
0
0
                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                            154 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels:
                                                                                                                                                                                                                                                     Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-824-647-16 (1-2095) x Q9X549 (1-149)
                                                                                                                                                                                                                                                                                                                            110 ACCCCGGAGGAGCCAGCTACAGCT 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-824-647-16 (1-2095) x Q916W2 (1-154)
                                                                                                                                                                                                                                                                                                                                                154 154
154 AA; 16728 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF01560; HCV_NS1; 1.
ProDom; PD186062; HCV_NS1; 1.
                                                                                                                                                                       8.00
100.00%
100.00%
1.15%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.00%
100.00%
1.15%
12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF01539; HCV_env; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           167
                                                                                                                                                       167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (NS1)] (Fragment).
Hepatitis C virus.
                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=11103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transplantation.
```

```
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-20150255, PubMed-10684935;
Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
White O., Hickey B.K., Peterson J., Utterback T., Berry K., Bass S.,
Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
Eisen J., Praser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-D/UW-3/CX;
MEDLINE-99000809; PubMed-9784136;
Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L.,
Mitchell W.P., Olinger L., Tatusov R.L., Shao Q., Koonin E.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genome sequence of an obligate intracellular pathogen of humans:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                proteome.
3CB88DD2D08B24BF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical protein TC0577.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
  80000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chlamydia muridarum.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
NCBI_FaxID-83560;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chlamydia trachomatis.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
                         Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                        171 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ź
  Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           178
                                                                                                              Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps:
                                                                                                                                                                                                                 1125 CIGICCCICCICCGAIACCIGCIG 1148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-824-647-16 (1-2095) x 084305 (1-171)
                                                                                                                                                                 US-09-824-647-16 (1-2095) x Q8QQM8 (1-154)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 LeuSerLeuLeuArgTyrLeuLeu 18
                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              al protein; Complete
171 AA; 19423 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Science 282:754-759(1998).
EMBL; AE001303; AAC67896.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                         084305;
01-NOV-1998 (TrEMBLIEL: 08, Cr
01-NOV-1998 (TrEMBLIEL: 08, La
01-MAR-2002 (TrEMBLIEL: 20, La
Hypothetical protein CT303.
CT303.
8.00
100.00%
100.00%
1.15%
12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            165
8.00
100.00%
1.10%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chlamydia trachomatis.
                Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=813;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Davis R.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match:
                                                                                                                                                                                                                                                                                                                                                                                  084305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09PK90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TC0577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No.:
                                                                                                                                                                                                                                                                                                                             RESULT 22
084305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 23
Q9PK90
        Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Probom; PD186062; HCV_NS1; 1.
Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
Polyprotein; Transmembrane.
NON_TER 1
                                                                                                           01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Genome polyprotein [Contains: envelope glycoprotein E2 (GP68) (GP70)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EI/E2 protein (Fragment).
Hepatitis C virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
                                                                                                                                                                                                                                             Hepatitis C'virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
-- SIMILARITY: TO HERPATTIS C VIRUS ENVELOPE GLYCOPROTEIN E1.
EMBL; AF422338; AAL24650.1; -
InterPro; IPR002519; HCV_env.
InterPro; IPR002531; HCV_env.
Pfam; PP01539; HCV_env; 1.
Pfam; PP01539; HCV_env; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lyra A.C., Fan X., Di Bisceglie A.M.; "Evolution of hepatitis C viral quasispecies after liver transplantation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                        .yra A.C., Fan X., Di Bisceglie A.M.;
Evolution of hepatitis C viral quasispecies after liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases EMBL; AF497310; AAM19566.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        154 AA; 16713 MW; 3592CC16C3BFEF15 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C4F5DA7B61E44F84 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       154
0000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                              154 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   154 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1196. TCTGCTGCTCGGACCACCAGCACT 1219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SerAlaAlaArgThrThrSerThr 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-824-647-16 (1-2095) x Q916W1 (1-154)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              154 154
154 AA; 16756 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8.00
100.00%
100.00%
1.15%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                            (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                             NCBI_TaxID-11103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID-11103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transplantation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-ACL-292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-ACL-93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hepacivirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0800M8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0800M8
                                                  Q916W1
                                                                                                                                                                                                                            (NS1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 21
Q8QQM8
     RESULT 20
                                 2916W1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DE PET REPRETATION OF LAND OF THE PRICE OF T
                                                           AND DESCRIPTION OF SERVICE OF SER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
```

```
Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S., Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L., Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schlex T., Weissenbach J., Boucher C.A., Wincker P., Levy M., Genome sequence of the plant pathogen Ralstonia solanacearum."; Martre 415.497-622(2002).
Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
                                                                                                                                                                                                                                                                                                                                                                                                                           Ralstonia solanacearum (Pseudomonas solanacearum).
Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
                                                                al protein; Complete proteome.
178 AA; 20384 MW; 5D11D1EA77B3DE39 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FE91790FB88B3649 CRC64;
                                                                                                                                                                                                                                                                                                                                                      01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Probable transmembrane protein.
RSC2305 OR RSO1247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               080562;
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
                                                                                                                                                  Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Š
                                                                                                                                                                                                                                                                                                                                188 AA
                                                                                                                        Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        190
                                                                                                                                                                                             Gaps:
                                                                                                                                                                                                                                            pneumoniae AR39.";
Nucleic Acids Res. 28:1397-1406(2000).
EMB. AE003236; AAF39412.1; --
TIGR; TC0577; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1454 GCTGCCCGGCTGCTACACCTGCA 1477
                                                                                                                                                                                                                  US-09-824-647-16 (1-2095) x Q9PK90 (1-178)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-824-647-16 (1-2095) x Q8XX13 (1-188)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AL646069; CAD16012.1; -.
InterPro; IPR000104; Antifreeze_1.
PRINTS; PR00308; ANTIFREEZEI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-21681879; PubMed-11823852;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     188 AA; '20087 MW;
                                                                                                                        164
8.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.00%
100.00%
1.15%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        163
                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                               Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complete proteome.
SEQUENCE 188 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-GMI1000;
                                                                  Hypothetical
                                                                                                         Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ralstonia.
                                                                               SEQUENCE
                                                                                                                                                                            Query Match:
                                                                                                                                                                                                                                                                                                                              08XX13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     080562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Мо.:
                                                                                                                       Pred. No.:
                                                                                                                                                                                                                                                                                                  RESULT 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 25
                                                                                                                                     Score:
                                                                                                                                                                                                                                                                                                                08XX13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       080562
δŏ
                                                                                                                                                                                                                                                                                                                                           ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 2 E E
```

```
STRAIN-A3(2) / M145;
Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kleser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kleser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
Warren T., Mietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Complete genome sequence of the model actinomycete Streptomyces
                                                                                                                                                                                                                                                       150
                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

Advison A.J., Akter P., Dolan A., Wright K.M., Addison C.,
Alcendor D.J., Hayward G.S., McGeoch D.J.;

"The human cytomegalovirus genome revisited.";

"The human cytomegalovirus genome revisited.";

"Submitted (FRB-2002) to the EMBL/GenBank/DBBJ databases.

EMBL, AF460884; AMMO0571.1;

SEQUENCE 190 AA; 21528 MW; E918F4FC02CEDD78 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C7ACFE12E7BE4B4C CRC64;
                                                                           chimpanzee cytomegalovirus.
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Betaherpesvirinae; Cytomegalovirus.
NCBL_TaxID-188763;
01-JUN-2002 (TIEMBLrel. 21, Last annotation update) Tegument protein UL26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-001-2000 (TrEMBLrel. 15, Created)
01-007-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical protein SC02957.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:\
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           192 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1212 GTGGTCCGAGCAGCAGACAGCCTC 1189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1088 GCTTGTGGGTCTGGCAGGCTGAGG 1065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           101 ValValArgAlaAlaAspSerLeu 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-824-647-16 (1-2095) x Q8QS62 (1-190)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-824-647-16 (1-2095) x Q9L1T8 (1-192)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA; 19652 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 417:141-147(2002).
EMBL; AL138851; CAB72203.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       163
8.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           163
8.00
100.00%
100.00%
1.16%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.16%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cal protein.
192 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           coelicolor A3(2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hopwood D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9L1T8
Q9L1T8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9L1T8
       DE RESERVATION OF THE RESERVATIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ð
```

```
01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TrEMBLrel. 20, Last annotation update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
02-scicum-independent phospholipase A2 isoform 1 (Fragment).
07-yctolagus cuhlculus (Rabbit).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheriax, Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Portilla D., Crew M.D., Grant D., Serrero G., Bates L.M., Dal G., Sasner M., Cheng J., Buonanno A.; "CDNA cloning and expression of a novel family of enzymes with calcium-independent phospholipase A2 and lysophospholipase activities.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Thermus/Deinococcus group; Deinococci; Deinococcales; Deinococcaceae; Deinococcus.
NCBI_TaxID=1299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           219 AA; 23602 MW; 3B6A4FEDC3BC912B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  219
8
0
0
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
80000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                  219 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      229 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Am. Soc. Nephrol. 9:1178-1186(1998).
EMBL; 097147; AAC63431.1; -.
HSSP; 05344; 1A00.
Interpro; IPR003140; PLP_Cesterase.
Interpro; IPR000379; Ser_estrs_site.
Pfam; PF02230; abhydrolase_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1686 CIGICCIGCIGGCTICCGCIGCGC 1709
                                                                              Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        131 LeuSerCysTrpLeuProLeuArg 138
                                                                                                                                                   1686 CTGTCCTGCTGCTTCCGCTGCGC 1709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-824-647-16 (1-2095) x 077820 (1-219)
                                                                                                             US-09-824-647-16 (1-2095) x Q9UQF9 (1-214)
                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-R1;
MEDLINE-20036896; PubMed-10567266;
                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=98308497; PubMed=9644627;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8.00.
100.00%
1.15%
                   100.00%
100.00%
1.15%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cytochrome C4, putative. DR2487.
                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
       Score:
Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-KIDNEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09RRK2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09RRK2
                                                              Query Match:
                                                                                                                                                                                                                                                                    077820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 30
                                                                                                                                                                                                                                     RESULT 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09RRK2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDILINE-20499367; PubMed-11042152; Zhao M., Zhao C.J., Fu G., Zhang Q.H., Ye M., Wu X.Y., Ren S.X., Zhao M., Zhao G.G., Zhang J.W., Shen Y., Fan H.Y., Lu G., Zhong M., Xu X.R., Han Z.G., Zhang J.W., Tao J., Huang Q.H., Zhou J., Hu G.X., Gu J., Chen S.J., Chen Z., Cloning and functional analysis of cDNAs with open reading frames for 300 previously undefined genes expressed in CD34+ hematopoietic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                             01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Similar to deoxythymidylate kinase (thymidylate kinase).
                                                                                                                                                                                                                                                                                                                                       Strausberg R.;
Strausberg R.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC001827; AAH01827.1;
HSSP; P00572; ITMK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63BCCC806F509CE8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           212 AA; 23819 MW; A52876625B3621B1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Lysophospholipase isoform.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         214 AA.
                                                                                          212 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam: PF02223; Thymidylate_kin; 1.
TIGREAMS; TIGR00041; DTWP_kinase; 1.
PROSITE; PS01331; THYMIDXIATE_KINASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-824-647-16 (1-2095) x Q9BUX4 (1-212)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pro; IPR000379; Ser_estrs_site.
PF02230; abhydrolase_2; 1.
NCE 214 AA; 22875 MW; 63BCC
                                                                                                                                                                                                                                                                                                                                                                                                                   nterPro; IPR000062; Thymidylate_kin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCAGCAGGCCACAGGGCAGAACTG 82
               156 AlaCysGlySerGlyArgLeuArg 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               issp; 053547; 1AUO.
nterpro; IPR003140; PLP_Cesterase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              stem/progenitor cells.";
Genome Res. 10:1546-1560(2000).
EMBL; AF077199; AAD26994.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        161
8.00
100.00%
100.00%
1.16%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                              PRELIMINARY;
                                                                                                                                                                                                             Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. TISSUE-MUSCLE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9UQF9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kinase
                                                                                                               Q9BUX4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No.:
                                                                                                09BUX4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 28
                                                          RESULT 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09UQF9
```

à g

SO OR SO OR

SO DR REPARENCE OF THE SO DR PERSON OF THE SERVICE OF THE SERVICE

```
1686 CTGTCCTGCTTCCGCTGCGC 1709
  [5]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                             Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                               077821;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match:
                                                                                                    EMBL;
                                                                                       EMBL;
                                                                                                                                                                                                                                                                                                                                                                                         RESULT 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D., Dodson R.J., Haft D.B., Gwinn M.L., Nelson W.C., Richardson D.L., Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C., Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D., Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Lysophospholipase (Acyl-protein thioesterase-1) (Lysophospholipase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Не К.,
                                                                                   "Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Devedjiev Y., Dauter Z., Kuznetsov S.R., Jones T.L., Derewen "Crystal Structure of the Human Acyl Protein Thioesterase I Single X-Ray Data Set to 1.5 A.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   s.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hu G.;
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Human lysophospholipase gene.";
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                               23653C80086FCB32 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
Shen Y., Guan Z., Gu J., Ye M., Zhou J., Zhang Q., Xu
Chen S., Mao M., Chen Z.;
                                                                                                                                                                                                                                                                                                                             Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         230 AA
                                                                                                                                                                                                                                                                                                    Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                     Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                 1370 GCGGAACCTGCTGCCGAGCCAGG 1393
                                                                                                                                                                                                                                                                                                                                                                                                                               133 AlaGluProAlaAlaArgAlaArg 140
                                                                                                                                                                                                                                                                                                                                                                                       US-09-824-647-16 (1-2095) x Q9RRK2 (1-229)
                                                                                                                                                            Interpro; IPR000345; Cytc_heme_bind.
Interpro; IPR003088; Cyt_CI.
Interpro; IPR002329; Cyt_CIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                 Pfam; PF00034; cytochrome_c; 2.
RNTWTS; PR00605; CYTCHROMECIC.
PRODOM; PD004020; CYT_CIC; 2.
PROSITE; PS00190; CYTOCHROME_C; 2.
                                                                                                                                                                                                                                                  Complete proteome.
SEQUENCE 229 AA; 23957 MW;
                                                                                                            Science 286:1571-1577(1999).
EMBL; AE002078; AAF12028.1; -
HSSP; 052369; LETP.
                                                                                                                                                                                                                                                                                                  160
8.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            structure 8:1137-1146(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
TISSUE-BONE MARROW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PubMed-11080636;
                                                                            Fraser C.M.;
                                                                                                                                                                                                                                                                                         Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                     Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       075608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LPL1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ð
```

```
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Calculum-independent phospholipase A2 isoform 2.
Oryctolagus cuniculus (Rabbit).
Cukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Portilla D., Crew M.D., Grant D., Serrero G., Bates L.M., Dai G., Sanner M., Cheng J., Buonanno A., 
SDNA cloning and expression of a novel family of enzymes with calcium-independent phospholipase A2 and lysophospholipase
                                                                             Si.
Strausberg R.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF081281; AAC31610.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PSO0339; AA_TRNA_LIGASE_II_2; UNKNOWN_1.
SROUENCE 230 AA; 24687 MW; 89AF2017AEFC9FAC CRC64;
                                                                                                                                                                       FEATH PROBLEM COSTENSE.
InterPro; IPR003140; Pir_Cesterase.
InterPro; IPR000379; Ser_estrs_site.
Pfam; PF02230; abhydrolase_2; 1.
SEQUENCE 230 AA; 24669 MW; 90C0522F765FlAC6 CRC64;
                                                                                                                                                                                                                                                                                               7
0
0
0
0
0
0
0
                                                                                                                                                                                                                                                                                                                 Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                230 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
                                                                                                                                                                                                                                                                                               Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels:
                                                                                                                                                                                                                                                                                                                                                                              Indels:
                                                                                                                                                                                                                                                                                                                                                                                                   Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J. Am. Soc. Nephrol. 9:1178-1186(1998).
EMBL; U97148; AAC63432.1; -.
HSSP; Q53547; IAUO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR002106; AALRNA_11gaseII.
InterPro; IPR003140; PLP_Cesterase.
InterPro; IRR000379; Ser_estrs_site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-824-647-16 (1-2095) x 077821 (1-230)
                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-824-647-16 (1-2095) x 075608 (1-230)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-98308497; PubMed-9644627;
                                                                             AAG10063.1; -...; AAH10397.1; -...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1998 (TrEMBLrel. 08, 01-NOV-1998 (TrEMBLrel. 08, 01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                               160
8.00
100,00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.00%
100.00%
1.15%
                                                           AAD26993.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             160
8.00
                                                                                                                                                            PMMA-2DPAGE; 075608; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9986;
                                                             AF291053;
                                                                                                                      BC008652;
                                                                                                     BC010397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity
                                                                                                                                      053547;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PISSUE-KIDNEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         activities."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Aliqument Scores:
                                                                                                                                                                                                                                                                               Allqument Scores:
                                                                                                                                                                                                                                          SEQUENCE
```

142

셤

P70470

RESULT 33

```
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1686 CTGTCCTGCTGCCTTCCGCTGCGC 1709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Interpro: IPR002106; AATRNA_ligaseII.
Interpro: IPR003140; PLP_Cesterase.
Interpro: IPR00379; Ser_estrs_site.
of_m. pr0.2240; abhvdrolase_2; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-824-647-16 (1-2095) x P97823 (1-230)
                                                                                      STRAIN-C57BL/6J; TISSUE-KIDNEY;
MEDLINE-21085660; PubMed-11217851;
                              E.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        U89352; AAB48627.1; -. AK002674; BAB22276.1; -. BC013536; AAH13536.1; -.
                            Deems R.A., Dennis
Chem. 0:0-0(0).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       160
8.00
100.00%
100.00%
1.15%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP; Q53547; 1AUO.
MGD; MGI:1344588; Lyplal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
[1]
SEQUENCE FROM N.A.
                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=KIDNEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bydrolase.
                                Wang A.,
J. Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SECUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09V8A8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9V8A8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CG5767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9V8A8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAX-1997 (TTEMBLE-1. 03, Last sequence update)
01-MAX-2002 (TTEMBLE-1. 20, Last annotation update)
LPHOSPHOLIPASE 1A (EC 3.1.1.5) (Lysophospholipase 1) (LECITHINASE B)
(LYSOLECTIFILINASE) (Phospholipase B) (Adult MALE kidney CDNA, RIKEN
FULL-length enriched LIBRARY, clone:0610025N20, FULL INSERT sequence)
                                                                                                                                                                                                                                                                                                          "Purification, cDNA cloning, and regulation of lysophospholipase from rat liver.";
                                                                                                                                                                   Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-98308497; PubMed-9644627;
Portilla D., Crew M.D., Grant D., Serrero G., Bates L.M., Dai G Sasner M., Cheng J., Buonanno A.;
"cDNA cloning and expression of a novel family of enzymes with calcium-independent phospholipase A2 and lysophospholipase activities.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PS00339; ĀA_TRNA_LIGASE_II_2; UNKNOWN_1.
230 AA; 24709 MW; AAFEBC4702EAAD74 CRC64;
                                                                                                         Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 230 AA
                                                                              230 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9:1178-1186(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1686 CTGTCCTGCTTCCGCTGCGC 1709
                                                                                                                                                                                                                                                              STRAIN-WISTAR; TISSUE-LIVER;
MEDLINE-96205961; PubMed-8631810;
Sugimoto H., Hayashi H., Yamashita S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR002106; AAtRNA_11gaseII.
InterPro; IPR003140; PLP_Cesterase.
InterPro; IPR003140; Ser_estrs_site.
Plam; PPC0230; abhydrolase_2; I.
PROSITE; PS00339; AA_TRNA_LIGASE_II_2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-824-647-16 (1-2095) x P70470 (1-230)
 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                          J. Biol. Chem. 271:7705-7711(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    U. Am. Soc. Nephrol. 9:1178-1
EMBL; D63865; BAA09935.1; -
EMBL; U97146; AAC63430.1; -
HSSP; Q53547; IAUO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-1997 (TrEMBLrel. 03,
                                                                                                         01-FEB-1997 (TrEMBLrel. 02, 01-FEB-1997 (TrEMBLrel. 02, 01-MAR-2002 (TrEMBLrel. 20, LYSOPHOSIPASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.00%
100.00%
1.15%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  160
8.00
                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Lysophospholipase 1).
                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=HYPOTHALAMUS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                                                   NCBI_TaxID-10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LYPLA1 OR PLA1A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alignment Scores:
```

SEQUENCE

.. 9

Pred.

Query Match: DB:

P97823

RESULT 34

ð 8

```
"Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
-1- CATALYTIC ACTIVITY: 2-LYSOPHOSPHATIDYLCHOLINE + H(2)0
GLYCEROPHOSPHOCHOLINE + A FATTY ACID ANION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      230 AA; 24687 MW; 89AF2017AEFC9FAC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-2000 (TTEMBLrel. 13, Created)
01-MAY-2000 (TTEMBLrel. 13, Last sequence update)
01-MAY-2000 (TTEMBLrel. 13, Last annotation update)
CG5767 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF02230; abhydrolase_2; 1.
PROSITE; PS00339; AA_TRNA_LIGASE_II_2; UNKNOWN_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              253 A.A.
```

```
Bacteria; Thermus/Deinococcus group; Deinococci; Deinococcales;
                  Deinococcaceae; Deinococcus.
NCBI_TaxID=1299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29ATL6
   RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Richters S. Ashburner M., Henderson S.N.,
Radion R.C., Rogers R.A., Zandell N.D., Zhang Q., Chen L.X.,
Button G.G., Wortman J.R., Yandell N.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell N.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Zandell N.D., Zhang Q., Chen L.X.,
RA Sutton R.C., Rogers Y.-H.C., Blazef R.G., Change M., Petelifer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Mikhos G.L.G.,
RA Beeson K.Y., Basud A., Baxendale J., Baytaktaroll L., Bealstey E.M.,
RA Beeson K.Y., Bence P.V., Berman B.P., Bhandari D., Bolshakov S.,
Burtis R.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
RA Burtis R.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
RA Burtis R.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
RA Burtis R.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischman R.,
ROGOR K., Gony F., Gorrell J.H.G., Gu Z., Gelbart W.M., Glasser K.,
RA Glodek A., Gony F., Gorrell J.H.G., Gu Z., Gelbart W.M., Glasser R.,
RA Butlin N., Kalush F., Karpen G. H., Kerlis S., Moshrefi A.,
Alalai M., Kalush F., Karpen G. H., Well M.-H., Ibeywam C.,
Alalai M., Kalush F., Karpen G. H., Well M.-H., Ibeywam C.,
Alakimel B.E., Kodira C.D., Kraft C., Kraft C., Kraft C., Kraft C., Kraft C., Moris S., Mulp D., Lai Z.,
Luu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.K.
Rand B.E., Wolson K.A., Nixon K., Nusskern D.R., Parl W., Reas M.,
Ralush W., Pittamos G.S., Pan S., Pollard J., Wang X.,
Rubor D.K., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
Rand S.W., Woodage T., Shon M., Zhang K., Sun E.,
Rand S., Welson K.A., Nixon K., Wang S., Yao Q.A.,
Rand S.W., Woodage T., Worley K.C., Wu D., Yang S., Zhon R., Shence S.,
Rand S., Welson R.A., Worley K., Sun S., Shun B.,
Rand S., Welson R.A., Worley K., Sun S., Shun S.,
Rand S., Welson S., Shun S., Shun S.,
Rand S., Welson S., Shun S., S
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25956 MW; 22A35668145C1946 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         253 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transcriptional regulator, ICLR family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1208 ACCACCAGCACTGCTGCCCCCAGC 1231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                191 ThrThrSerThrAlaAlaProSer 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-824-647-16 (1-2095) x Q9V8A8 (1-253)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                       STRAIN-BERKELEY;
MEDLINE-20196006; Pubmed-10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-MAK-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8.00
100.00%
100.00%
1.15%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AE003801; AAF57763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Deinococcus radiodurans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FBgn0034292:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity:
Query Match:
                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FlyBase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DRA0152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09RZ01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9RZ01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09RZ01
   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OS E BL LA BE
```

```
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIINE-21140306; PubMed-11244102;
Chaumont F., Barrieu F., Wojcik E., Chrispeels M.J., Jung R.;
"Aquaporins constitute a large and highly divergent protein family in
malze.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -i- SUBCELLUTAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
-i- SIMILARITY: BELONGS TO THE MIP/AQUAPORIN FAMILY (TC 1.A.8).
EMBL; AF326505; AAK26772.1; -.
HSSP; P29972; IFQY.
                                          MEDLINE-20036896; PubMed-10567266; White O., Elsen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D., Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L., Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C., Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.I.
                                                                                                                                                                                                                                                                            radiodurans R1.";
Science 286:1571-1577(1999).
-!- SIMILARITY: BELONGS TO THE ICLR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                      "Genome sequence of the radioresistant bacterium Deinococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26519 MW; DDD4C1AC3E7DB8D1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      253
8
0
0
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-070-2001 (TrEMBLrel. 17, Created)
01-070-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Tonoplast membrane integral protein ZmTIP4-1.
Zea mays (Maize).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA-binding; Transcription regulation; Complete SEQUENCE 253 AA; 27299 MW; DBB8F05ABE6F65A8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                255 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          135 ProHisAlaThrAlaSerGlyLys 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-824-647-16 (1-2095) x Q9RZ01 (1-253)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plant Physiol. 125:1206-1215(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ProDom; PD000295; MIP_family; 1. PROSITE; PS00221; MIP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000425; MIP_family.
Pfam; PF00230; MIP; 1.
                                                                                                                                                                                                                                                                                                                                                                             EMBL; AE001862; AAF12212.1; -..
TIGR; DRA0152; -..
Interprov; IFMO00285; HTH_ICIR.
Pfam; PF01514; ICIR; 1.
SWART; SM00346; HTH_ICIR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00783; MINTRINSICP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         158
8.00
100.00%
100.00%
1.16%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transmembrane; Transport
SEQUENCE 255 AA; 2651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
                                                                                                                                                                                                                              Fraser C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
                             STRAIN-R1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09ATL6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9ATL6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 37
```

us-09-824-647-16.std.rspt

Conservative:

```
SEQUENCE FROM N.A.
Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AL023496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGULATORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-A3(2);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hopwood D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
Pred. No.:
Score:
                                                                                                                                                                                                                                                                                                                             069819
                                                                                                                                                                                                                                                                               RESULT 39
                                                                                                                                                                                                                                                                                                         069819
                                                                                                                                                                                                                                                                                                                                                       A Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M., Alvarenga R., Alves L.M.C., Arruda J.E., Baia G.S., Baptista C.S., Barros, W.H., Bonaccorsi E.D., Bordin S., Bove J.M., Balones M.R.S., Bueno M.R.P., Camargo A.A., Carraro D.M., Carrer H., Bueno M.R.P., Cramargo A.A., Carrero D.M., Carrer G.M., Bueno M.R.P., Cristofani M., Dias.Net, E., Costa M.C.R., Costa-Neto C.M., R.A. Collauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M., R.A. Collanno L.L., Cristofani M., Dias.Net. E., Concena C., Bl-Dorry H., R. Ferreira A.J.S., Ferreira W., Coldman G.H., Goldman M.L., Kemper E.L., Kitajima J.P., Rrieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C., R.A. Lemos E.G.M., Lenos M.V.F., Lopes S.R., Marchado J.A., Marchado M.A., Madelira A.M.B.N., Madeira H.M.F., Marchado J.R., Marchado M.A., Magai M.A., Nascimento A.L.T.O., Netto L.E.S., Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S., Moon D.H., Nagai M.A., Mascimento A.L.T.O., Netto L.E.S., Marchado M.A., Madelira M.C., de Sa R.G., Santelli R.V., Sawasaki H.E., A de Silva A.R., de Souza A.J.M., de Souza A.J.M., de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H., Rago M.A., Zatz M., Meidanis J., Setubal J.C.; Siqueira M.J., de Souza A.B., Rago M.A., Zatz M., Meidanis J., Setubal J.C.; Statbal J.C.; Paran. R. The genome sequence of the plant pathogen Xylella fastidiosa."; Pergranal R. Paran. A. Par
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4F21E7001BA1265B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             256
                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                        Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                     256 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
                                   Length:
                                                                                                                                Indels:
                                                                                                                                                       Gaps:
                                                                                                                                                                                                                                                   GCAGCTGGTGTGCTGGTCACAGCC 1339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002043; U_DNA_glycsylse.
InterPro; IPR003249; U_glycosyl.
Pfam; PF03167; UDG; 1.
                                                                                                                                                                                                       US-09-824-647-16 (1-2095) x Q9ATL6 (1-255)
                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-20365717; PubMed-10910347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR005122; UDNA_glycos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ProDom; PD001589; U_glycosyl; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE004075; AAF85489.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     256 AA; 28187 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIGR00628; ung; 1.
                              158
8.00
100.00%
100.00%
1.16%
                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               158
8.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Uracil-DNA glycosylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xylella fastidiosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complete proteome. SEQUENCE 256 AA:
                                                                          Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID-2371;
       Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
Pred. No.:
Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-9A5C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TIGREAMS;
                                                                                                                                                                                                                                                                                                    72
                                                                                                                                                                                                                                                        1362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kylella
                                                                                                                           Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                               Q9PA28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       XF2692
                                                                                                                                                                                                                                                                                                                                                                                                     Q9PA28
                              Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP;
                                                                                                                                                                                                                                                                                                                                                    RESULT 38
                                                                                                                                                                                                                                                                                                                                                                                                        A COCCOS ON THE CONTRACT OF TH
                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                    g
```

```
SEQUENCE FROM N.A.

STRAIN-A3(2) / M445;

Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,

Bentley S.D., Chater K.F., Harris D.E., Quail M.A., Kieser H.,

Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,

Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,

Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,

Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,

Rabbinowitsch E., Rajandram M.A., Rutherford K., Rutter S.,

Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,

Marren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               coelicolor A3(2).";
Nature 417:141-147(2002).
-1- SIMILARITY: BELONGS TO THE ARAC/XYLS FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J., Kinashi H., Hopwood D.A.;
Kinashi H., Hopwood D.A.;
A set of ordered cosmids and a detailed genetic and physical map ithe 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Bacteria; Firmicutes; Actinobacteria; Actinomycetaceae; Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Complete genome sequence of the model actinomycete Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00041; HTH_ARAC_FAMILY_1; UNKNOWN_1.
PROSITE; PS01124; HTH_ARAC_FAMILY_2; 1.
NAN-binding; Hypothetical protein; Transcription regulation.
SEQUENCE 256 As; 27761 MW: 1971B47CBEB684C4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S.D., Barrell B.G., Rajandream M.A.;
to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oliver K., Harris D.;
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  256
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-00-1998 (TrEMBLrel. 07, Last sequence update) 01-00N-2002 (TrEMBLrel. 21, Last annotation update) Hypothetical protein SC06425.
      0000
                                 Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                           256 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
                                                                                                                                                                                                           1544 CTACGGGCCAGGAAGGTGGCAGGC 1521
                                                                                                                                                    US-09-824-647-16 (1-2095) x Q9PA28 (1-256)
                                                                                                                                                                                                                                             01-AUG-1998 (TrEMBLrel. 07, Created)
                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-A3(2);
MEDLINE-97000351; PubMed-8843436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000005; HTHAraC. Pfam; PF00165; HTH_AraC; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAA18912.1;
100.00%
100.00%
1.16%
16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00032; HTHARAC; SMART; SM00342; HTH_ARAC;
                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     158
8.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptomyces coelicolor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-A3(2);
Parkhill J., Bentley
Submitted (JAN-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
```

for

```
MEDLINE-21140306; PubMed-11244102;
Chaumont F., Barrieu F., Wojcik E., Chrispeels M.J., Jung R.;
"Aquaporins constitute a large and highly divergent protein family in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-824-647-16 (1-2095) x Q39263 (1-259)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                039263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               239263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            :.
⊗
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDNAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 42
          Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ward M.J., Lew H., Treuner-Lange A., Zusman D.R.;
"Regulation of motility behavior in Myxococcus xanthus may require an extracytoplasmic-function sigma factor.";
J. Bacteriol. 180:5668-567(1998).
EMBL: AF049107; AAC98489.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDILINE-96347136; PubMed-8736543;
Trudeau R.G., Ward M.J., Zusman D.R.;
Trudeau R.G., Ward M.J., Zusman D.R.;
"Identification and characterization of FrzZ, a novel response regulator necessary for swarming and fruiting-body formation in Wyrococcus xanthus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; delta subdivision; Myxobacteria; Myxococcales; Cystobacterineae; Myxococcaceae; Myxococcus.
NOBI_TaxID=34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 l protein.
257 AA; 28575 MW; 860E35015266C7EB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    257
0
0
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                    01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 28.6 kDa protein.
     0000
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tonoplast membrane integral protein 2mTIP4-2.
                                                                                                                                                                                                                                                                                                                             257 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             257 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels:
                                                                                Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1187 CAGAGGCTGTCTGCTCGGACC 1210
                                                                                                                                                                       US-09-824-647-16 (1-2095) x 068521 (1-257)
                                                                                                                         US-09-824-647-16 (1-2095) x 069819 (1-256)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66 GlnArgLeuSerAlaAlaArgThr 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-99009001; PubMed-9791117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Myxococcus xanthus.";
Mol. Microbiol. 20:645-655(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2002 (TrEMBLrel. 21,
100.00%
100.00%
1.15%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              158
8.00
100.00%
1100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Myxococcus xanthus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zea mays (Maize)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID-4577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-DZF1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-DZF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9ATL5;
                                                                                                                                                                                                                                                                                                                        068521
068521;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9ATL5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 41
                                                                                                                                                                                                                                                                            RESULT 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9ATL5
                                                                                                                                                                                                                                                                                                 SOUR TRANSPORT OF STREET O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ð
```

```
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                 SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pague B.W., Goodman H.M.;
Characterization of a family of Arabidopsis zinc finger protein
                   (BY
                                                                                                                                                                                                               465414DFCB7F7BE9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28644 MW; AE8F1B4A280067FD CRC64;
                                                                                                                                                                                                                                                                    257
8
0
0
0
Plant Physiol. 125:1206-1215(2001).
-- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN
--I- SIMILARITY: BELONGS TO THE MIP/AQUAPORIN FAMILY
EMBL; AF326506; AAK26773.1; --
HSSP; P29972; IROY.
InterPro: IPRO00425; MIP_family.
PF00230; MIP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TIEMBLrel. 01, Created)
(TIEMBLrel. 01, Last sequence update)
(TIEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                          Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 259 AA.
                                                                                                                                                                                                                                                                      Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                  Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00096; zf-C2H2; 1.
SMART; SM00355; ZnF_C2H2; 1.
PROSITE; PS00028; ZINC_FINGER_C2H2_1; 1.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zinc-finger
                                                                                                                                                                                                                                                                                                                                                                                                                                              1362 GCAGCTGGTGTGCTGGTCACAGCC 1339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-LANDSBERG ERECTA; TISSUE-ROOT;
MEDLINE-95322589; PubMed-7599312;
                                                                                                                                                                                                                                                                                                                                                                                                          US-09-824-647-16 (1-2095) x Q9ATL5 (1-257)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74 AlaAlaGlyValLeuValThrAla 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plant Mol. Biol. 28:267-279(1995).
EMBL, 139647; ABA87300.1; -.
TRANSFAC; TO9565; -.
INTERPIC: IPRO00822; Znf_C2H2.
                                                                                                                               PRINTS; PRO0783; MINTRINSICP.
PRODOM; PD000295; MIP_family;
PROSITE; PS00221; MIP, 1.
Transmembrane; Transport.
SEQUENCE 257 AA; 26603 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA-binding; Metal-binding;
                                                                                                                                                                                                                                                                                                        100.00%
100.00%
\1.16%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.00%
100.00%
1.16%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                      158
8.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zinc finger protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       259 AA;
                                                                                                                                                                                                                                                                                                                                Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                            Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1996 (
01-NOV-1996 (
01-MAR-2002 (
                                                                                                                                                                                                                                                    Aliqument Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
```

```
1219 AGTGCTGGTGGTCCGAGCAGCAGA 1196
                                                                                                                                                                                                                                                                                                            22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local S.
Query Match:
                                                                                                                                                                                                                               Query Match:
                                                                                                                                                                                                                                                                                                                                                        Q8RUU4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..
2
                                                                                                                                                                                   ..
80
.
                                                                                                                                                                                                                                                                                                                                  RESULT 44
                                                                                                                                                                                             Score:
                                                                                                                                                                                                                                                                                                                                              Q8RUU4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred.
                                                                                                                                                                                                                                                                                                                                                                             ð
                                                                                                                                                                                                                                                                                                            a
Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin Neumann G.,
Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
                                                                                                                                       Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shinn P., Chen H., Cheuk R., Kim C.J., Banh J., Bowser L., Carninci P., Chung M.K., Goldsmith A.D., Hayashizaki Y., Ishida J., Jones T., Ramiya.A., Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Mirrada M., Narusaka M., Nguyen M., Palm C.J., Pham P.K., Quach H.L., Sakano H., Sakurai T., Satou M., Seki M., Theologis A., Foriumi M., Tamada K., Yu G., Shinozaki K., Davis R.W. Theologis A., Ecker J.R.; Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Koesema E., Chen H., Cheuk R., Kim C.J., Meyers M.C., Shinn P., Banh J., Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y., Ishida J., Jang P.X., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M., Nguyen M., Ondera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A. Tang C.C.; Torlumi M., Yamada K., Yamamura Y., Yu G., Yu S.,
                                                                                           01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
C2H2-type zinc finger protein, putative (Atlg66140/F15E12_19).
F15E12.19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Arabidopsis cDNA clones.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
                                                                   260 AA
1269 TCCTCGCTGACACTGCCCCTCAGC 1246
           (TrEMBLrel. 17, Created)
                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 408:816-820(2000).
                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                         01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ecker J.R.;
                     55
                                                                                                                                                                                                                                                                                                                                                                                                                                                 thaliana
                                                                  09C8D2
                                           RESULT 43
                                                                  8
                     셤
```

```
STRAIN-CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1, BAC
clone:OSJNBB00026014.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1, BAC
clone:OSJNBa0042P21";
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
05JNBA0026J14.33 protein (OSJNBA0042P21.8 protein).
OSJNBA0026J14.33 OR OSJNBA0042P21.8.
OYZE SALIVE (Japonica cultivar-group).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                    : Si. :
Shinozaki K., Davis R.W., Theologis A., Ecker J.K.;

L Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.

R EMBL; AC026480; AA631296.1;

R EMBL; AX058087; AAL24195.1;

R EMBL; AX058087; AAL24195.1;

R EMBL; AX058087; AAL06967.1;

R FABL; AX058087; AALC242; 1;

R TATEPPC; IPR000962; Znf_C2H2.

R SMART; SM00355; Znf_C2H2.1;

R SWART; SN00355; Znf_CZH2.1;

R PROSITE; PS00028; ZlNC_FINGER_C2H2_1;

DR PROSITE; PS00028; ZlNC_FINGER_C3H2_2;

R DNA-binding;;Metal-binding; Zinc-finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AP004231; BAB89246.1; -.
EMBL; AP004614; BAB90800.1; -.
SEQUENCE 260 Aa; 26845 MW; 7C73972A6ECA4BEF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                Length:\\
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        260 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1269 TCCTCGCTGACACTGCCCCTCAGC 1246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-824-647-16 (1-2095) x Q8RUU4 (1-260)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-824-647-16 (1-2095) x Q9C8D2 (1-260)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SerSerLeuThrLeuProLeuSer 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2002 (TrEMBLrel. 21, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        158
8.00
100.00%
100.00%
1.16%
                                                                                                                                                                                                                                                                                                                                                                                                                                    100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.168
10
                                                                                                                                                                                                                                                                                                                                                                                         158
8.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=39947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Aliqument Scores:
                                                                                                                                                                                                                                                                                                                                                                    Aliqnment Scores:
```

iii.

115 SerAlaGlyGlyProSerSerArg 122

a

```
Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Ammmalla; Eutherla; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                             huang D.Z., Chou Y.-T., Yang Y.-C.; Structural and functional conservation of MRG family in system
                                                                                                                                                                                                                                                                                                                                    evolution.";
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF361476; AAK30621.1; -
SEQUENCE 269 AA; 28291 MW; 038DC4B21E4E21F1 CRC64;
                                                                     01-00N-2001 (TrEMBLrel. 17, Created)
01-00N-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Transcription factor MRG1.
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                       269 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-824-647-16 (1-2095) x Q99MA1 (1-269)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Search completed: July 7, 2003, 16:00:37 Job time: 186.5 secs
                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          157
8.00
100.00%
100.00%
1.16%
                                       PRELIMINARY;
                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-SPRAGUE-DAWLEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score:
Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                 CBI_TaxID-10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
RESULT 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ď
```

Sequence 113, App Sequence 6, Appli

Sequence Sequence

Patent No.

Sequence 113 Sequence 113

Sequence

Appli Appl

> Sequence Sequence

Title: Perfect score:

Sequence:

OM nucleic

Run on:

Scoring table:

Word size:

Searched:

```
GENERAL INCOMATION:
APPLICANT: Serrero, Ginette
TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REFERENCE: 2996.488/P001-A
CURRENT APPLICATION NUMBER: US/08/991,862
EARLIER APPLICATION NUMBER: 08/863,862
EARLIER FILING DATE: 1997-05-23
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: PEPTIDE
LOCATION: (1)..(1).
OCHER INFORMATION: Internal peptide of human GP88 used to develop
OTHER INFORMATION: neutralizing anti-human GP88 monoclonal antibody
                                                                                              Sequence 8
Sequence 9
Sequence 2
                                                                                                                                         Sequence
Sequence
Sequence
                                                                                                                                                                       Sequence (
                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                  Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1708 GCACGCAGGGGTACCAAGTGTTTGCGCAGGGGCCCCGCGC 1749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       440000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                  US-08-726-306A-161
US-08-602-999A-82
US-08-278-865<sup>3</sup>82
                              US-08-933-843-113
US-08-934-223-113
US-09-348-952A-5
                     US-08-934-224-113
US-08-933-843-113
                                                             US-09-413-492-113
US-09-053-611-6
                                                                                                                 US-09-099-543C-27
US-09-461-697-66
US-08-672-850-19
                                                                                                                                                                                                        JS-08-766-596A-40
                                                                                                                                                                                                                 US-08-445-745-120
US-09-120-365-82
           -09-231-797-113
                                                                                                                                                                                                                                                                                                                 -09-400-653A-11
                                                                                                                                                                                                                                                                                                                                     -09-302-305C-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-824-647-16 (1-2095) x US-08-991-862-7 (1-14)
                                                                                                                                                                                                                                     US-09-120-365-83
US-09-120-365-84
US-09-120-365-86
                                                                                                                                                                                            US-09-500-124-82
                                                                                                                                                                                                                                                                     us-09-515-039-82
                                                                                                                                                                                                                                                                                 JS-09-515-039-83
                                                                                                                                                                                   JS-09-183-841-4
                                                                                                                                                                                                                                                                                                                                                                                 ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps:
                                                                                    5470825-3
                                                                                                                                                                                                                                                                                                                                                                                                           US-08-991-862-7; Sequence 7, Application US/08991862; Patent No. 6309826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0:000321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14.00
100.00%
100.00%
2.02%
 თიიიიიიიე<u>ე</u>ე
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Human granulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity:
                                                                                  Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alignment Scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-991-862-7
                                LENGIH: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No.:
0 0 0 0 0 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        õ
                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Appli
Patent No. 5470825
Sequence 5, Appli
Sequence 39, Appli
Sequence 7, Appli
Sequence 113, Appli
                                                                                  (without alignments)
4251.105 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 7, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                      egcaggcagaccatgtggac.....ataaagtttgtcactttctt 2095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                     July 7, 2003, 16:00:43; Search time 29 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/laa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/laa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/laa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/laa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
       GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
                                                 using frame_plus_n2p model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-991-862-7
US-08-245-853-2
US-08-573-675-2
5470825-2
US-08-991-862-5
US-09-419-826-39
US-08-244-951A-7
US-08-244-951A-7
US-08-244-951A-7
US-08-244-25113
US-08-933-402-113
US-09-207-621-113
US-09-207-621-113
                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                        262574 seqs, 29422922 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
                                                                                                                                                                    > 60.0 , Xgapext 60.0
> 60.0 , Ygapext 60.0
> 6.0 , Fgapext 7.0
6.0 , Delext 7.0
                                                                                                                                                                                                                                                                                                                        Post-processing: Listing first 45 summaries
                                                                                                               US-09-824-647-16
694

    protein search,

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query
Match Length
                                                                                                                                                                                                                                                                                       Minimum DB seq length: 0
Maximum DB seq length: 15
                                                                                                                                                                                                                                                                                                                                             Command line parameters:
                                                                                                                                                         OLIGO
Xgapop
Ygapop
Fgapop
Delop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0,000,000,000,000
```

40000000

υo

6666666

Score

ş

Result

Database

Sequence 4, Sequence 17,

Sequence

Sequence

Sequence

Sequence

셤

```
US-09-824-647-16 (1-2095) x 5470825-2 (1-15)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match:
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: SCOTT, RANDY W.
APPLICANT: GLEICH, GERALD J.
APPLICANT: WILDE, CRAIG G.
TITLE OF INVENTION: BASOPHIL GRANULE PROTEINS
NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        865 GACATGGAGGTGAGCTGCCCAGATGGCTATACC 897
                                                                                                                                              APPLICANT: SCOTT, RANDY W.
APPLICANT: GLEICH, GERALD J.
APPLICANT: WILDE, CRAIG G.
TITLE OF INVERTION: BASOPHIL GRANULE PROTEINS
CORRESPONDENCE: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-824-647-16 (1-2095) x US-08-245-853-2 (1-15)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 24842-20059.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,813
FILING DATE: 11-SEP-1992
ATORNEY/GENT INFORMATION:
NAME: BOZICEVIC, KARL
REGISTRATION NUMBER: 28,807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/245,853
                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/08573675
Patent No. 5747283
GENERAL INFORMATION:
                                                                                                                                                                                                                                                             755 Page Mill Road
                                                                                             Sequence 2, Application US/08245853
Patent No. 5476839
                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 706141
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
FDNESS: single
                                                                                                                                                                                                                                                                                                     CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                         RY: USA
94304-1018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-573-675-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-245-853-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 3
                                                              RESULT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred.
```

```
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: SCOTT, RANDY W.;GLEICH, GERALD J.;
WILDE, CRAIG G.
TITLE OF INVENTION: BASOFHIL GRANULE PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-824-647-16 (1-2095) x US-08-573-675-2 (1-15)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
SSEE: Fish & Richardson
F: 2200 Sand Hill Road, Suite 100
Menlo Park
: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps:
                                                                                                                                                                                                                 CIASTELATION: 514
CIASTELATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,813
FILING DATE: 11.5EP-1992
ATORNEY AGGRY INFORMATION:
NAME: GREGG, VALETA
REGISTATION NUMBER: 35.127
REFERENCE/DOCKET NUMBER: 06514/0130
TELEPHONE: (415) 322-5070
TELEPHONE: (415) 824-0875
INFORMATION FOR SED ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/259,564 FILING DATE: 15-JUN-1994 PRIOR APPLICATION DATA: APPLICATION NUMBER: 551,263
                                                                                                                                                                  SOFTWARE: ASCIII
CURRENT APPLICATION DATA:
APPLICATION: NUMBER: US/08/573,675
APLICED DATE: 18-DEC-1995
CHASSIPHCATION: 514
                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 10-JUL-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11.00
100.00%
100.00%
1.59%
                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 8
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5470825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-573-675-2
                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO:2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5470825-2
```

Indels:

ð

Gaps:

us-09-824-647-16.lim.rai

```
Amino Acid
                                                                                                   Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                           Alignment Scores:
JS-09-419-826-39
                                                                                                                                                                                                                                                                                                                                                    US-08-244-951A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (14)
OTHER INFORMATION: Internal peptide of mouse GP88 used to raise the
OTHER INFORMATION: antisera against the GP88 used in the
OTHER INFORMATION: immunoaffinity step.
                                                                                                                                                                                               APPLICANT: Seriero, Ginette
TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REFERENCE: 29996. 488 READOIL-A
CURRENT APPLICATION NUMBER: US/08/991,862
CURRENT FILING DATE: 1998-08-17
EARLIER APPLICATION NUMBER: 08/863,862
EARLIER FILING DATE: 1997-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: PEPTIDE ANTIESTROGEN COMPOSITIONS AND METHODS TITLE OF INVENTION: FOR TREATING BREAST CANCER NUMBER OF SEQUENCES, 39 COMPOTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
Indels:
          865 GACATGGAGGTGAGCTGCCCAGATGGCTATACC 897
                                                     5 AspMetGluValSerCysProAspGlyTyrThr 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-824-647-16 (1-2095) x US-08-991-862-5 (1-14)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/419,826
FILING DATE: 14-OCT-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US98/07711
FILING DATE: 14-APR-1998
APPLICATION NUMBER: US 60/043,545
FILING DATE: 14-APR-1997
INFORMATION FOR SEQ ID NO: 39:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1714 AGGGGTACCAAGTGTTTGCGC 1734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 39, Application US/09419826
Patent No. 6306832
GENERAL INFORMATION:
APPLICANT:
                                                                                                                                     Sequence 5, Application US/08991862
Patent No. 6309826
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 ArgGlyThrLysCysLeuArg 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.00%
100.00%
1.01%
                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: mouse granulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-419-826-39
                                                                                                             US-08-991-862-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-991-862-5
                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 14
                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No.:
                                                                                            RESULT 5
            ò
                                                 ·
음
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
```

```
DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED PROTEIN TAU, HYBRIDOMAS SECRETING THESE ANTIBODIES, ANTIGEN RECOGNITION BY THESE MONOCLONAL ANTIBODIES AND THEIR APPLICATIONS
                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: VANDERMEEREN, MARC; MERCKEN, MARC;
APPLICANT: VANMECHELEN, EUGEEN; VAN DE VOORDE, ANDRE
                                           Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative:
                                                          Mismatches:
                                                                                                                                         US-09-824-647-16 (1-2095) x US-09-419-826-39 (1-8)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
  Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: MONOCLONEL ANTIBODIES TITLE OF INVENTION: DIRECTED AGAINST THE NTITLE OF INVENTION: ANTIBODIES, ANTIGEN RE NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                     Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/244,951A
FILING DATE: 19-JAN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: PCT/FEP93/03499
FILING DATE: 10-DEC-1993
FRICH APPLICATION DATA:
FILING DATE: 10-DEC-1993
APPLICATION NUMBER: EP/92/403403.6
FILING DATE: 14-DEC-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                               Sequence 7, Application US/08244951A Patent No. 5843779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BIERMAN & MUSERLIAN
                                                                                                                                                                                   1131 CTCCTCCGATACCTGCTG 1148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: CHARLES A. MUSERLIAN
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FELECOMMUNICATION INFORMATION TELEPHONE: (212) 661-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (212) 661-8000
TELEFAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                              1 LeuLeuArgTyrLeuLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6.43e+06
6.00
                                  100.00%
100.00%
0.86%
.23e+06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 600 THIRD AVENUE
CITY: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.00%
100.00%
0.87%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: Unknown TOPOLOGY: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS
                   8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 10016
COMPUTER READABLE FORM:
```

ò

```
US-09-824-647-16 (1-2095) x US-08-389-011-5 (1-9)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: EVANS, Herbert J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: DC
COUNTRY: USA
ZIP: 20007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-934-222-113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                         US-08-934-222-113
                                                                                                                                   RESULT 9
                                                                                                                                                                                                                                                                                                              DIRECTED AGAINST THE MICROTUBBLE-ASSOCIATED PROFEIN TAU, HYBRIDOMAS SECRETING THESE ANTIBODIES, ANTIGEN RECOGNITION BY THESE MONOCLONAL ANTIBODIES AND THEIR APPLICATIONS.
                                                                                                                                                                                                                                   PATENT NO. JOURNAL OF THE WARC; MERCKEN, MARC; GENERAL INFORMATION:
APPLICANT: VANDERMEEREN, ENGEEN: VAN DE VOORDE, ANDRE APPLICANT: VANMECHEEN, ENGELONAL ANTIBODIES
WITHER OF INVENTION: MONOCLONAL ANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CIASSIPLCATION 1943.

CIASSIPLCATION DATA:
APPLICATION NUMBER: 08/403,917
FILING DATE: 19-74N-1995.
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/403,916
FILING DATE: 19-74N-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/244,951
FILING DATE: 13-70N-1994
PRIOR APPLICATION NUMBER: 08/244,951
FILING DATE: 10-DEC-1993
PRIOR APPLICATION NUMBER: EP/92/403403.6
FILING DATE: 10-DEC-1993
PRIOR APPLICATION NUMBER: EP/92/403403.6
APPLICATION NUMBER: 19-92/403403.6
FILING DATE: 14-DEC-1993
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 19,683
                               US-09-824-647-16 (1-2095) x US-08-244-951A-7 (1-9)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/389,011
FILING DATE: 15-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 MUSERLIAN
                                                                                                                                                                                               Sequence 5, Application US/08389011
Patent No. 5861257
                                                                          465 GGGCAGCACCCCCAGGA 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (212) 661-8000
TELEFAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6.43e+06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6.00
100.00%
100.00%
0.87%
                                                                                                 1 GlyAlaAlaProProGly 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         600 THIRD AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: Amino Acid
STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
US-08-389-011-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 10016
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: BIERMAN
                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NEW YORK
: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: NEW YORK
STATE: NEW YOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                    US-08-389-011-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score:
                                                                                                                                                                     RESULT 8
```

```
Sequence 113, Application US/08934222
Sequence 113, Application US/08934222
Sequence 113, Application US/08934222
Patent NO. 5928896
GENERAL INFORMATION:
APPLICANT: EVANC, Herbert J.
APPLICANT: KINI, R. Manjunatha
TITLE OF INVENTION: Polypeptides That Include Conformation-
TITLE OF INVENTION: Site
TITLE OF INVENTION: Site
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSE: Foley & Lardner
STREET: Suite 500, 3000 K Street NW
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SISTEM: C-LUCYING WESTON #1.25
SOGTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,222
FILING DATE: 19-SEPT-1997
PRIOR APPLICATION NUMBER: 08/532,818
FILING DATE: 03-MAY-1996
PRIOR APPLICATION NUMBER: 0.5. 08/143,364
PRIOR APPLICATION NUMBER: U.S. 08/143,364
FILING DATE: 29-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/051,741
APPLICATION NUMBER: U.S. 08/051,741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-824-647-16 (1-2095) x US-08-934-222-113 (1-9)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: ISACSON, JOHN P.
REGISTRATION NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 040433/0148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: U.S. 08/051,741
FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-933-402-113
; Sequence 113, Application US/08933402
; Patent No. 5948887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    270 CCCAGAGGCCGTGGCATG 287
INFORMATION FOR SEQ ID NO: 113:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ProArgGlyArgGlyMet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6.00
100.00%
100.00%
0.86%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3.43e+06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
```

us-09-824-647-16.lim.rai

```
Sequence 113. Application US/08532818
Patent No. 5965698
GENERAL INFORMATION:
APPLICANT: EVANS, Herbert J.
APPLICANT: KINI, R. Manjunatha
TITLE OF INVENTION: Polypeptides That Include Conformation-
TITLE OF INVENTION: Site
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
                            SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
URRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-824-647-16 (1-2095) x US-09-207-621-113 (1-9)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
                                                       SULTWANE: PATECRILIN RELEASE $1.0, VETSI
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/207,621
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/532,818
FILING DATE: 33.4MY-1996
FILING DATE: 21.4MP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/143,364
FILING DATE: 29-007-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/143,364
FILING DATE: 29-007-1993
APPLICATION NUMBER: U.S. 08/051,741
FILING DATE: 23-APR-1993
ATTONNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels:
                                                                                                                                                                                                                                                                                                                                                                                          NAME: Isacson, John P.
REGISTATION'NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 040433/0148
INFORMATION FOR SEQ ID NO: 113:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Foley & Lardner
STREET: Suite 500, 3000 K Street NW
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    U.S. 08/143,364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/532,818
FILING DATE: 03-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/04294
FILING DATE: 21-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      270 CCCAGAGGCCGTGGCATG 287
           IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.43e+06
6.00
100.00%
100.00%
0.86%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERÌSTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY:
US-09-207-621-113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-532-818-113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: DC COUNTRY:
                                                  SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 12
  KINI, R. Manjunatha
FENTION: Polypeptides That Include Conformation-
FENTION: Constraining Groups Which Flank A Protein-Protein Interaction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 113, Application US/09207621
Patent No. 5552465
GENERAL INFORMATION: GENERAL SECONDARY OF THE FORMSTON TITLE OF INVENTION: POlypeptides That Include Conformation-TITLE OF INVENTION: Constraining Groups Which Flank A Proten-Protein Interaction NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/933,402
FILING DATE: 19-SEPT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/532,818
FILING DATE: 03-MAX-1996
PRIOR APPLICATION NUMBER: U.S. 08/143,364
FILING DATE: 29-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/143,741
APPLICATION NUMBER: U.S. 08/151,741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-824-647-16 (1-2095) x US-08-933-402-113 (1-9)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 040433/0148
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: ISACSON, JOHN P.
REGISTATION NUMBER: 33.751
REFERENCE ...
                                                                                                                             ADDRESSEE: Foley & Lardner
STREET: Suite 500, 3000 K Street NW
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      270 CCCAGAGGCCGTGGCATG 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ProArgGlyArgGlyMet 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Foley & Lardner
STREET: Suite 500, 3000 K (CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 20007
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6.43e+06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.00%
100.00%
0.86%
APPLICANT: KINI, R. Manj
TITLE OF INVENTION: Poly
TITLE OF INVENTION: CONS
TITLE OF INVENTION: SITE
NUMBER OF SEQUENCES: 155
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
SY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                  20007
                                                                                                                                                                                             8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-933-402-113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-207-621-113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                        STATE: D
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: D
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 11
```

```
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-231-797-113
                                                                                                                                                                                                                                                                                                        Percent Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: DC
COUNTRY: U
                                                                                                                                                                                                                                               Alignment Scores:
                                                                                                                                                                                                    US-08-403-917A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET:
                                                                                                                                                                                                                                                                    Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED PROTEIN TAU, HYBRIDOMAS SECRETING THESE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANTIBODIES, ANTIGEN RECOGNITION BY THESE MONOCLONAL ANTIBODIES AND THEIR APPLICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: VANDERMEEREN, MARC; MERCKEN, MARC;
APPLICANT: VANDECHELEN, EUGEEN;
APPLICANT: VAN DE VOORDE, ANDE
TITLE OF INVENTION: MONOCILONAL ANTIBODIES
TITLE OF INVENTION: DIRECTED AGAINST THE MICK
TITLE OF INVENTION: PROTEIN TAU, HYBRIDOMAS SE
TITLE OF INVENTION: ANTIBODIES, ANTIGEN RECOGN
TITLE OF INVENTION: MONOCIONAL ANTIBODIES AND
                                                                                                                                                                                                                                                                                                                                                                                  Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-824-647-16 (1-2095) x US-08-532-818-113 (1-9)
                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATE:
APPLICATION NUMBER: 08/244,951
FILING DATE: 13-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/03499
FILING DATE: 10-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/92/403403.6
ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSERLIAN
REGISTRATION NUMBER: 19,683
                                                                                                                                                                                                                                                                                                                                                                                                                        Indels:
                                                                                                                  REFERENCE/DOCKET NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 040433/0148
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/403,917A FILING DATE: 19-JAN-1995 PRIOR APPLICATION DATE: 08/256,167 FILING DATE: 27-JUN-1994
              FILING DATE: 29-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/051,741
FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5, Application US/08403917A Patent No. 6010913 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BIERMAN & MUSERLIAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               270 CCCAGAGGCCGTGGCATG 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ProArgGlyArgGlyMet 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           600 THIRD AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FLOPPY DISK
                                                                                                                                                                                                                                                                                                                                            6.43e+06
                                                                                                                                                                                                                                                                                                                                                                                100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                          0.86%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                        TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: NEW YORK
STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                US-08-532-818-113
                                                                                                                                                                                                                                                                                                                           Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 13
US-08-403-917A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
                                                                                                                                                                                                                                                                                                                                              Pred. No.:
```

```
US-00-231-797-113
US-00-231-797-113
Sequence 113, Application US/09231797
Sequence 113, Application US/09231797
Patent No. 6084066
GENERAL INFORMATION:
APPLICANT: EVANS, Herbert J.
APPLICANT: KINI, R. Manjunatha
TITLE OF INVENTION: Polypeptides That Include Conformation-
TITLE OF INVENTION: Constraining Groups Which Flank A Proten-Protein Interacti
TITLE OF INVENTION: Constraining Groups Which Flank A Proten-Protein Interacti
CORRESPONDENCE 153
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/231,797
                                                                                                                                                                                                                                                                                                                                    Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-824-647-16 (1-2095) x US-08-403-917A-5 (1-9)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: ISACSON, JOhn P.
RECISTRATION NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 040433/0148
INFORMATION FOR SEQ ID NO: 113:
                                                                                                                                                                                                                                                                                        Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION DATE: 21-APK-12...
FILING DATE: 21-APK-12...
APPLICATION NUMBER: U.S. 08/143,364
APPLICATION NUMBER: U.S. 08/143,364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/051,741
FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SSEE: Foley & Lardner
F: Suite 500, 3000 K Street NW
Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILLING DATE: 21-APR-1994
APPLICATION NUMBER: 08/532,818
FILLING DATE: 03-MAY-1996
APPLICATION NUMBER: PCT/US94/04294
FILLING DATE: 21-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           465 GGGCAGCACCCCAGGA 448
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 661-8000
TELEPAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5.43e+06
                                                                                                                                                                                                                                                                                                                                    100.00%
100.00%
0.87%
                                                                                                                                                                         STRANDEDNESS: Unknown TOPOLOGY: Unknown
                                                                                                                                                   Amino Acid
                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
```

```
Sequence 113, Application US/08933843
Patent No. 6111069
GENERAL INFORMATION:
APPLICANT: EVANS, Herbert J.
APPLICANT: KINI, R. Manjunatha
TITLE OF INVENTION: Polypeptides That Include Conformation-
TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interi-
TITLE OF INVENTION: 31
TITLE OF INVENTION: 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: EVANS, Herbert J.
APPLICANT: KINI, R. Manjunatha
ITILE OF INVENTION: Polypeptides That Include Conformation-
TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Intera
ITILE OF INVENTION: Site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-824-647-16 (1-2095) x US-08-933-843-113 (1-9)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: U.S. 08/051,741 FILING DATE: 23-APR-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/143,364
FILING DATE: 29-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/933,843
FILING DATE: 19-SEPT-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 113, Application US/08934223 Patent No. 6147189 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 08/532,818 FILING DATE: 03-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          270 CCCAGAGGCCGTGGCATG 287
                                                                                                                                                                                                                                                                                         ADDRESSEE: Foley & Lardner STREET: Suite 500, 3000 K : CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33,751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.ProArgGlyArgGlyMet 6
6.43e + 06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Isacson, John P. REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEC ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         998.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                         NS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                          20007
                                                                         JS-08-933-843-113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-933-843-113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-934-223-113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                  CITY:
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                ZIP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 17
                                                                                                                                                                                                                                                                                                     Sequence 113, Application US/08934224
Patent No. 610044
GENERAL INFORMATION:
APPLICANT: EYANS, Herbert J.
APPLICANT: EVANS, Herbert J.
TITLE OF INVENTION: Polypeptides That Include Conformation-
TITLE OF INVENTION: Constraining Groups Which Flank A Protein Interaction
TITLE OF INVENTION: Site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative:
Mismatches:
                                                     Conservative Mismatches:
                                                                                                                                               US-09-824-647-16 (1-2095) x US-09-231-797-113 (1-9)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-824-647-16 (1-2095) x US-08-934-224-113 (1-9)
            Length:
Matches:
                                                                                        Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/532,818
FILING DATE: 03.4M2T.1996
APPLICATION NUMBER: PCT/US94/04294
FILING DATE: 21.4PR-1994
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: 29-0CT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/143,364
FILING DATE: 23-4PR-1993
ATTORNEY AGENT INFORMATION:
NAME: ISAGSON, JOHN P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :: 040433/0148
113:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Foley & Lardner
Suite 500, 3000 K Street NW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/934,224
FILING DATE:
                                                                                                                                                                                  COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS AMC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               270 CCCAGAGGCCGTGGCATG 287
            43e+06
                                             100.00%
100.00%
0.86%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.00%
100.00%
0.86%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.43e+06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: ISACSON, JOhn P. RECISTRATION NUMBER: 33, REFERENCE/DOCKET NUMBER: INFORMATION FOR SEQ ID NO: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 20007
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
                                    Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-934-224-113
                                                                                                                                                                                                                                                                                   US-08-934-224-113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Aliqument Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match:
DB:
        Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No.:
                                                                                                                                                                                                                                                                  RESULT 15
                                                                                                                                                                                      ó
```

```
MEDIUM TYPE: FLOPPY DISK COMPUTER: IBM PC COMPATIBLE
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-413-492-113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-348-952A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      red. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: VANDENBERERN, MARC; MERCKEN, MARC;
APPLICANT: VANDECHELEN, EUGEEN;
APPLICANT: VAN DE VOORDE, ANDRE
TITLE OF INVENTION: MONOCLONAL ANTIBODIES
TITLE OF INVENTION: PROTEIN TAU, HYBRIDOMAS SECRÉTING THESE
TITLE OF INVENTION: ANTIBODIES, ANTIGEN RECCONITION BY THESE
TITLE OF INVENTION: ANTIBODIES, ANTIGEN RECCONITION BY THESE
TITLE OF INVENTION: ANDIOCLONAL ANTIBODIES AND THEIR APPLICATION
NUMBER OF SEQUENCES: 24
                                                                                                                                                                      COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PAPELICATION DATA:
APPLICATION NUMBER: US/08/934,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-824-647-16 (1-2095) x US-08-934-223-113 (1-9)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/532,818
FILING DATE: 03-MAY-1996
FILING DATE: 23-MAY-1996
FILING DATE: 21-APR-1994
FILING DATE: 21-APR-1994
FILING DATE: 29-OCT-1993
FILING DATE: 29-OCT-1993
FILING DATE: 39-OCT-1993
APPLICATION NUMBER: U.S. 08/143,364
APPLICATION NUMBER: U.S. 08/143,364
APPLICATION NUMBER: U.S. 08/051,741
FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: ISACSON, JOHN P.
REGISTRATION NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 040433/0148
INFORMATION FOR SEQ ID NO: 113:
                                  CORRESPONDENCE ADDRESS:
ADDRESSER: Foley & Lardner
STREET: Suite 500, 3000 K Street NW
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BIERMAN & MUSERLIAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5, Application US/09348952A
Patent No. 6232437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 270 CCCAGAGGCCGTGGCATG 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 600 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6.43e+06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.00%
100.00%
0.86%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 2. CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
GY: linear
                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity:
Query Match:
                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP; 10016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-934-223-113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 18
US-09-348-952A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                           20007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ð
```

```
Sequence 113, Application US/09413492

Patent No. 6258550

GENERAL INFORMATION:
APPLICANT: EVANS, Herbert J.
APPLICANT: EVANS, Herbert J.
APPLICANT: EVANS, Holypeptides That Include Conformation-
TITLE OF INVENTION: Constraining Groups Which Flank A Protein Interact
TITLE OF INVENTION: Site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-824-647-16 (1-2095) x US-09-348-952A-5 (1-9)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
              CURRENT APPLICATION DATA:
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/348,952A
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/403,917
FILING DATE: 19-JAN-1995
APPLICATION NUMBER: 08/256,167
FILING DATE: 27-JUN-1994
PRIOR APPLICATION NUMBER: 08/244,951
FILING DATE: 13-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/03499
FILING DATE: 10-DEC-1993
FILING DATE: 14-DEC-1993
FILING DATE: 14-DEC-1993
FILING DATE: 14-DEC-1993
APPLICATION NUMBER: EP/92/403403.6
FILING DATE: 14-DEC-1993
RAPE: CHARLES A. WUSERLIAN
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 19,003-1
TELECOMMUNICATION INFORMATION:
METERODATOR: 712,120,01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         465 GGGCAGCACCCCAGGA 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Suite 500, 3000 K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (212) 661-8000
TELEFAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6.43e+06
6.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Washington STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: Amino Acid
STRANDEDNESS: Unl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
Query Match:
```

```
E: PANITCH SCHWARZE JACOBS & NADEL, P.C. ONE COMMERCE SQUARE, 2005 MARKET STREET, 22ND FL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: MORAN, JOHN V.
APPLICANT: DOMBROSKI, BETH A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS OF USE OF
TITLE OF INVENTION: MAMMALIAN RETROTRANSPOSONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/847,844A
FILIKG DATE: 28-APP-1997
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
Mismatches:
                                                                                                               RESULT 21
5470825-3
; Patent No. 5470825
; APLICANT: SCOTT, RANDY W.; GLEICH, GERALD J.;
; WILDE, CRAIG G.
TITLE OF INVENTION: BASOPHIL GRANULE PROTEINS
; NUMBER OF SEQUENCES: 8
 US-09-824-647-16 (1-2095) x US-09-053-611-6 (1-9)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-824-647-16 (1-2095) x 5470825-3 (1-9)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 16-NOV-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/259,564
FILING DATE: 15-JUN-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/749,805
FILING DATE: 16-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-847-844A-80
; Sequence 80, Application US/08847844A
; Patent No. 6150160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: KAZAZIAN JR., HAIG H. APPLICANT: BOEKE, JEF D. APPLICANT: MORAN, JOHN V.
                                         1131 CTCCTCCGATACCTGCTG 1148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           637 CCGGACGCACGGTCCCGG 654
                                                                               1 LeuLeuArgTyrLeuLeu 6
                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 551,263
FILING DATE: 10-JUL-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ProAspAlaArgSerArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6.43e+06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.00%
100.00%
0.86%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: ONE COMMERCITY: PHILADELPHIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RY: U.S.A.
19103-7086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                          LENGIH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match:
                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                          5470825-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: No. 6410245throp, Jeffrey P.
APPLICANT: Hart, Charles P.
APPLICANT: Schatz, Peter J.
APPLICANT: Glaxo Group Limited
TITLE OF INVENTION: Compositions and Methods for Detecting Ligand Dependent
TITLE OF INVENTION: Nuclear Receptor and Coactivator Interactions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Description of Artificial Sequence:LCD (leucine OTHER INFORMATION: charged domain)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         00000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  00000
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-824-647-16 (1-2095) x US-09-413-492-113 (1-9)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: 2064
CURRENT APPLICATION NUMBER: US/09/053, 611
CURRENT FILING DATE: 1998-04-01
NUMBER OF SEQ ID NOS: 40
                                                                                                                                                                                 APPLICATION NUMBER: U.S. 08/143,364
FILING DATE: 29-0CT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/051,741
FILING DATE: 23-APR-1993
ATTORNEY AGENT: INFORMATION:
NAME: ISASSO, JOHN P.
                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/532,818
FILING DATE: 03-MAY-1996
APPLICATION NUMBER: PCT/US94/04294
FILING DATE: 21-APR-1994
PRIOR APPLICATION DATA:
                                 APPLICATION NUMBER: US/09/413,492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6, Application US/09053611
Patent No. 6410245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        270 CCCAGAGGCCGTGGCATG 287
                                                                                                                                                                                                                                                                                                NAME: Isacson, John P.
REGISTRATION NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 113:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 6
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.00%
100.00%
0.86%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.43e+06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6.00
100.00%
100.00%
0.86%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.43e+06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                      9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-413-492-113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-053-611-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-053-611-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score:
```

Cerottini, Jean-Charles

```
TITLE OF INVENTION: Isolated No. 6326200a - And Decapeptides Which Bind TITLE OF INVENTION: TO HLA Molecules, and the Use Thereof FILE REFERENCE: LUD 5483.2 CURRENT APPLICATION NUMBER: US/09/099,543C CURRENT FILING DATE: 1998-06-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-824-647-16 (1-2095) x US-09-099-543C-27 (1-10)
                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: DELIVATIVE Of SEQ ID NO:1
US-09-099-543C-27
                                                                                                 PRIOR APPLICATION NUMBER: US 09/061,388
PRIOR FILING DATE: 1998-04-16
PRIOR APPLICATION NUMBER: US 08/880,963
PRIOR FILING DATE: 1997-06-23
NUMBER OF SEQ ID NOS: 32
SEQ ID NO 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-461-697-66; Sequence 66, Application US/09461697; Patent No. 6277974
                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity
                                                                                                                                                                                                                                                                                                                                                          Aliqnment Scores:
                                                                                                                                                                                                                                                                                                                                                                             ₽
1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICARY: Baloh, Mobert H.

APPLICARY: Baloh, Robert H.

TITLE OF INVERFICON: Artenin, A No. 6284540el Neurotrophic Factor
TITLE OF INVERFICON: Artenin, A No. 6284540el Neurotrophic Factor
CURRENT APPLICATION NUMBER: US/09/220,528A
CURRENT FILING DATE: 1998-12-24
EARLIER APPLICATION NUMBER: 09/218,698
EARLIER FILING DATE: 1998-11-22
EARLIER FILING DATE: 1998-11-12
EARLIER FILING DATE: 1998-11-12
EARLIER FILING DATE: 1998-09-29
NUMBER OF SEQ ID NOS: 120
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                            Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-824-647-16 (1-2095) x US-09-220-528-91 (1-10)
                                                                                                                                                                                                                                                                                                                                                                                                      US-09-824-647-16 (1-2095) x US-08-847-844A-80 (1-10)
                                                                                                                                                                                                                                                                             Length:
Matches:
                     9596-2302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 27, Application US/09099543C Patent No. 6326200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 91, Application US/09220528A Patent No. 6284540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1325 ACCCCAGAGACATCGGCT 1342
                                                                                                                                                                                                                                                                                                                                                                                                                                              1164 GGAGTGGGGCTGCTGTCC 1181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 ThrProGluThrSerAla 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Milbrandt, Jeffrey D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 GlyValGlyLeuLeuSer 9
REGISTRATION NUMBER: 36,317
REFERENCE/DOCKET NUMBER: 95
TELECOMMUNICATION INFORMATION
TELEPRAN: 215-567-2991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5.37e+03
6.00
100.00%
100.00%
0.86%
                                                                                                                                                                                                                                                                               5.37e+03
6.00
                                                                                                                                                                                                                                                                                                              100.00%
100.00%
0.86%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Valmori, Danila
                                                                              TELEFAX: 215-567-2991
INFORMATION FOR SEQ ID NO:
SEQUENCE CHRACTERISTICS:
LENGTH: 10 amino acids
                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-099-543C-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
                                                                                                                                                                                                                            US-08-847-844A-80
                                                                                                                                                                                                                                                                Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-220-528-91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SULT 23
.09-220-528-91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 91
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
```

00000

Conservative: Mismatches:

Indels:

Length: Matches:

5.37e+03 100.00% 100.00%

```
DISORDERS, OR DISEASES INVOLVING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-824-647-16 (1-2095) x US-09-461-697-66 (1-11)
                                               APPLICANT: Barney, Shawn
APPLICANT: Barney, Shawn
APPLICANT: Thomas, Mary Beth
APPLICANT: Portbury, Stuart D.
APPLICANT: Portbury, Stuart D.
APPLICANT: Ratz, Lawrence C.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: COMPOSITIONS AND TREATING
CURRENT APPLICATION CLL DEATH
FILE REFRENCE: 10001-005-909
FILE REFRENCE: 10001-005-999
CURRENT RILING DATE: 1999-12-14
NUMBER OF SEQ ID NOS: 466
SEQ ID NO 66
SEQ ID NO 66
LENGTH: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches:
GENERAL INFORMATION:
APPLICANT: COGENT NEUROSCIENCE, Inc.
APPLICANT: Lo, Donald C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1311 GCGGCGGCCAGGCATCTT 1294
                                                                                                                                                                                                                                                                                                                                                                                                                                                5.28e+03
6.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 AlaAlaGlyArgHisLeu
                                                                                                                                                                                                                                                                                                                                                                              GRGANISM: Homo sapiens US-09-461-697-66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match:
```

```
WEDUTATION TYPE: Diskette, 3.50 inch, 1.44 Mb storage COMPUTER: IN PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: MOOTOPERfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/726,306A
FILING DATE: 02-Oct-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/009,832
FILING DATE: 01-30-1995
PROOR APPLICATION DATA:
APPLICATION NUMBER: US 60/009,832
FILING DATE: 01-30-1996
ATTORNEY/AGENT: INFORMATION:
NAME: Williams, Ph.D., Rathleen M.
NAME: Williams, Ph.D., Rathleen M.
REGISTRATION NUMBER: 34,380
REFERENCE/DOCKET NUMBER: 96,048-A (3255/00784)
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        James B.
S. SH3 BINDING PEPTIDES AND METHODS OF I. ISOLATING AND USING SAMES: 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-824-647-16 (1-2095) x US-08-726-306A-161 (1-13)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US/08/602,999A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 82, Application US/08602999A
Patent No. 6184205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OUILITAM, Lawrence A.: DER, Channing J.: FOWIKES, Dana M.: RIDER, James E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1663 AGACGCCCTGGGCGTAGG 1646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 ArgArgProGlyArgArg 9
                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (617) 345-9111
INFORMATION FOR SEQ ID NO: 16
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPARKS, Andrew B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KAY, Brian K.
THORN, Judith M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.15e+03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.00%
100.00%
0.87%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: New York STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ercent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-726-306A-161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -08-602-999A-82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ŏ
                                                                                                                                        STREET: Flehr, Hohbach, Test, Albritton & Herbert STREET: Embarcadero Center, Suite 3400 CITY: San Francisco STATE: California COUNTRY: United 1
                                                                                                                                                                                                                                                                                                                            COMPUTER READDBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,850
FILING DATE: 24-JUL-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: van Leeuwen, Frederik Willem
APPLICANT: Burbach, Johannes Peter Henri
APPLICANT: Grosveld, Franklin G.
TITLE OF INVENTION: DIAGNOSIS METHOD AND REAGENTS
NUMBER OF SEQUENCES: 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-824-647-16 (1-2095) x US-08-672-850-19 (1-12)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REPERENCE/DOCKET NUMBER: A.63610
TELECOMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3349
INFORMATION FOR SEQ ID NO: 19:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff, Ltd.
STREET: 1 Financial Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 161, Application US/08726306A
Patent No. 5958684
GENERAL INFORMATION:
                                  oequence 19, Application US/08672850
Patent No. 6140117
                                                                               GENERAL INFORMATION:
APPLICANT: Milbrandt, Jeffrey
APPLICANT: Arakl, Toshiyuki
TITLE OF INVENTION: NINJURIN
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1946 GGCCTTAGATTGAGGCCC 1929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 GlyLeuArgLeuArgPro 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: S11va, Robin M.
REGISTRATION NUMBER: 38,304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5.21e+03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS: LENGTH: 12 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Boston
                                                                                                                                                                                                                                                                                                                 94111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-726-306A-161
                         US-08-672-850-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
```

US-08-672-850-19

Query Match:

STATE: M. COUNTRY:

```
unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
Query Match:
amino acid
                                                                                                                                                 Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-500-124-82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
APPLICANT:
                   TOPOLOGY:
                                                                                           Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT
                                                                                                                                                                                     Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No.:
                                                                                                                  Pred. No.:
                                                                                                                                    Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: SIC SH3 BINDING PEPTIDES AND METHODS OF TITLE OF INVENTION: ISOLATING AND USING SAME NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT.
P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1755 S. Jefferson Davis Highway, Suite 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/278,865
                                                                                                                                                                                                                                                                                                                                                                                                      Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-824-647-16 (1-2095) x US-08-602-999A-82 (1-13)
                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Villacorta, Gilberto M.
REGISTRATION NUMBER: 34,038
REFRENCE/POCKET NUMBER: 4880-007-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 82, Application US/08278865
Patent No. 6303574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: KAY, BRIAN K.
APPLICANT: SPARKS, ANDREW B.
APPLICANT: THORN, JUDITH M.
APPLICANT: QUILLIAM, LAWRENCE A.
APPLICANT: DER, CHANNING J.
                                                                                                                                         | TELEPHONE: (212) 790-9090
| TELEFAX: (212) 869-9741/8864
| TELEX: 66141 PENNIE
| INFORMATION FOR SEQ ID NO: 82:
| SEQUENCE CHARACTERISTICS:
| LENGTH: 13 amino acids
| TYPE: amino acid
| TOPOLOGY: unknown
| MOLECULE TYPE: peptide
| US-08-602-999A-82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1513 AGACCACTTCCTTCGC 1496
                                CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mistock, S. Lesie
REGISTRATION NUMBER: 18,872
REFERENCE/POCKET NUMBER: 1101
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .15e+03
                                                                                                                                                                                                                                                                                                                                                                                                    100.00%
100.00%
0.87%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 13 amino acids
                 FILING DATE: 16-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                virginia
: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Arlington
                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                      Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                           red. No.:
                                                                                                                                                                                                                                                                                                                                                                                                Score:
```

```
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:No. 6423680el sequence
US-09-183-841-4
                                                                                                                                                                                                                                               Sequence 4, Application US/09183841

Patent No. 6423680

GENERAL INFORMATION:
APPLICANT: Hospital for Sick Children
TITLE OF INVENTION:
FILE REFERENCE: vana20010

CURRENT APPLICATION NUMBER: US/09/183,841

CURRENT FILING DATE: 1998-10-30

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 4

LENGTH: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0000
                                                        0000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative:
Mismatches:
Indels:
                                                                                   Conservative:
Mismatches:
                                                                                                                                                          US-09-824-647-16 (I-2095) x US-08-278-865-82 (1-13)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-824-647-16 (1-2095) x US-09-183-841-4 (1-13)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
                                                                          Matches:
                                                                                                                   indels:
                                                        Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: SH3 BINDING PE
TITLE OF INVENTION: ISOLATING AND
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 82, Application US/09500124 Patent No. 6432920 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OUILLIAM, Lawrence A. DER, Channing J. POWLKES, Dana M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    680 AGCTGCCCAGTGGGAAGT 697
                                                                                                                                                                                         1513 AGACCACTTCCTTCTCGC 1496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KAY, Brian K.
THORN, Judith M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.15e+03
6.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 SerCysProValGlySer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RIDER, James E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.00%
100.00%
0.86%
                                                                                                                                                                                                       4 ArgProLeuProSerArg
                                                           5.15e+03
                                                                                     100.00%
100.00%
0.87%
MOLECULE TYPE: peptide US-08-278-865-82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPARKS,
```

```
APPLICANT: Pierschbacher, Michael D.
APPLICANT: Cheng, Soan
APPLICANT: Craig, William S.
APPLICANT: Tschopp, Juerg F.
TITLE OF INVENTION: Methods and Composition for Treating
TITLE OF INVENTION: Thrombosis
NUMBER OF SEQUENCES: 168
                                                                                                                                                                                                                                                                                                                                                                                                                           0000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Campbell and Flores
4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-824-647-16 (1-2095) x US-08-766-596A-40 (1-13)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels:
                                                                                                           NAME: YUN, Allen C.
REGISTRATION UNBER: 37,971
REFERENCE/DOCKET NUMBER: SOTO-JARA-1A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEPHONE: 202-737-3528
INFORMATION FÖR SEQ ID NO: 40:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 08/050,73614
FILING DATE: 14-APR-1993
               FILING DATE: 10-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/478,326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/171,068
FILING DATE: 20-DEC-1993
APPLICATION NUMBER: US 08/079,441
FILING DATE: 18-JUN-1993
us 08/630,645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/445,745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 120, Application US/08445745
Patent No. 5672585
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-APR-1996
                                                                     FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                         1.15e+03
                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 168
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell an
STREET: 4370 La Jolla
CITY: San Diego
STATE: California
                                                                                                                                                                                                                                                                                                          single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 14-APR-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: Si
                                                                                                                                                                                                                                                                                                                           .inear
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                 US-08-766-596A-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -08-445-745-120
                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BAUMANN, MAIC
FRANCIONE, Blas
VENTION: PEPTIDES AND PHARMACEUTICAL
FENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
VENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
FENTION: DEPOSITS
                                                                 OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3: BROWDY AND NEIMARK
419 Seventh Street, N.W., Suite 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-824-647-16 (1-2095) x US-09-500-124-82 (1-13)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/766,596A
                                                                                                                           APPLICATION NUMBER: US/09/500,124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No. 6462171
GENERAL INFORMATION:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/602,999
FILING DATE: 16-FEB-1996
ATTORNEI/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1513 AGACCACTTCCTTCGC 1496
                                                                                                                                                                                                                                                                                                                                   (212) 790-9090
(212) 869-9741/8864
                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                              NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 11
                                                                                                                                                                                                                                                                                                                  PELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                           TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 82:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 ArgProLeuProSerArg
   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.15e+03
                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 13 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 69
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 20004
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: FRANKIONE
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE:
                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JS-08-766-596A-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-500-124-82
                                                                                                                                                                                                                                                                                                                                                       TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE:
                                                                                                                                                                                                                                                            NAME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        red.
```

```
US-09-824-647-16 (1-2095) x US-09-120-365-84 (1-14)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-824-647-16 (1-2095) x US-09-120-365-83 (1-14)
                                                               APPLICANT: Natori, Shunji
APPLICANT: Natori, Shunji
TITLE OF INVENTION: NEW PROTEASE
FILE REFERENCE: 32290-144749
CURRENT APPLICATION NUMBER: US/09/120,365
CURRENT FILING DATE: 1998-07-22
EARLIER APPLICATION NUMBER: UP 9-333 474
EARLIER FILING DATE: 1997-11-18
NUMBER OF SEQ ID NOS: 101.
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Natori, Shunji
TITLE OPT: Natori, Shunji
FILE REFERENCE: 32290-144749
CURRENT APPLICATION NUMBER: US/09/120,365
CURRENT FILING DATE: 1998-07-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 86, Application US/09120365
Patent No. 6103514
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 84, Application US/09120365
Patent No. 6103514
Sequence 83, Application US/09120365
Patent No. 6103514
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1270 AGCGAGATCGTGGCTGGA 1287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1270 AGCGAGATCGTGGCTGGA 1287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Natori, Shunji
TITLE OF INVENTION: NEW PROTEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 SerGlulleValAlaGly 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 SerGluileValAlaGly 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EARLIER APPLICATION NUMBER: JP 9
EARLIER FILING DATE: 1997-11-18
NUMBER OF SEQ ID NOS: 101
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.09e+03
6.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.00%
100.00%
0.86%
                                                                                                                                                                                                                                                                                                                                                                                                                                                100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3,868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: bovine
                                                                                                                                                                                                                                                                                               TYPE: PRT CRGANISM: rattus US-09-120-365-83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-120-365-86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-120-365-84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-120-365-84
                                                                                                                                                                                                                                                                                                                                                                                          Alignment Scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
                                                                                                                                                                                                                                                              SEQ ID NO 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                        Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-824-647-16 (1-2095) x US-09-120-365-82 (1-14)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-824-647-16 (1-2095) x US-08-445-745-120 (1-14)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: NEW PROTEASE
FILE REFERENCE: 32290-144749
FULE REPERENCE: 32290-144749
CURRENT APPLICATION NUMBER: US/09/120,365
CURRENT FILING DATE: 1998-07-22
REALIER APPLICATION NUMBER: JP 9-333 474
RALIER FILING DATE: 1997-11-18
NUMBER OF SEQ ID NOS: 101
SOFTWARE: PATENTIN Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: /note= "Xaa = (orn)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps:
                 APPLICATION NUMBER: US 07/681,119
FILING DATE: 05-APR-1991
PRIOR APPLICATION DATE: ...
APPLICATION NUMBER: US 07/506,444
FILING DATE: 06-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFRENCE/DOCKET NUMBER: P-LA 9829
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 82, Application US/09120365
Patent No. 6103514
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1270 AGCGAGATCGTGGCTGGA 1287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            653 CGGGACCGTGCGTCCGGA 636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 SerGlulleValAlaGly 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 ArgAspArgAlaSerGly 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5.09e+03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5.09e+03
6.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.00%
100.00%
0.87%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.86%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: circular
                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: Peptide LOCATION: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                               amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: murine
```

US-09-120-365-82

RESULT 34

g

Conservative: Mismatches:

Indels:

US-08-445-745-120 Alignment Scores:

Query Match:

Score:

LOCATION:

Matches:

Length:

400000

Conservative: Mismatches: Indels:

RESULT 35 US-09-120-365-83

ò g

Alignment Scores:

US-09-120-365-82

SEQ ID NO 82 LENGTH: 14

Length: Matches:

```
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                             US-09-824-647-16 (1-2095) x US-09-120-365-86 (1-14)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-824-647-16 (1-2095) x US-09-515-039-82 (1-14)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches:
                                                                                                                                                                                                                                                                                                                          Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
                                                                                                                                                                                                                                                                                                                                       Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels:
FILE REFERENCE: 32290-144749
CURRENT APPLICATION NUMBER: US/09/120,365
CURRENT FILING DATE: 1998-07-22
EARLIER APPLICATION NUMBER: 1P 9-333 474
EARLIER FILING DATE: 1997-11-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 32290-144749
CURRENT APPLICATION NUMBER: US/09/515,039
CURRENT FILING DATE: 2000-03-06
EARLIER FILING DATE: 1997-11-18
NUMBER OF SEQ ID NOS: 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/515,039
CURRENT FILING DATE: 2000-03-06
EARLIER APPLICATION NUMBER: UP 9-333 474
EARLIER FILING DATE: 1997-11-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 83, Application US/09515039
Patent No. 6214599
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 82, Application US/09515039
Patent No. 6214599
                                                                                                                                                                                                                                                                                                                                                                                                                                  1270 AGCGAGATCGTGGCTGGA 1287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1270 AGCGAGATCGTGGCTGGA 1287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Natori, Shunji
TITLE OF INVENTION: NEW PROTEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 SerGlulleValAlaGly 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Natori, Shunji
TITLE OF INVENTION: NEW PROTEASE
FILE REFERENCE: 32290-144749
                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 SerGluIleValAlaGly 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.09e+03
                                                                                                                                                                                                                                                                5.09e+03
                                                                                                                                                                                                                                                                                                 100.00%
100.00%
0.86%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.00%
100.00%
0.86%
                                                                                          NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver.
SEQ ID NO 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Ver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: chicken
US-09-120-365-86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; .ORGANISM: murine US-09-515-039-82
                                                                                                                                                                                                                                               Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-515-039-82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-515-039-83
                                                                                                                                                      LENGTH: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
                                                                                                                                                                                                                                                                                                                                       Query Match:
                                                                                                                                                                                                                                                              Pred No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   red. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ŏ
```

```
0000
                                                                                                                                                       Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative:
                                                                                                                                                                                                                                         US-09-824-647-16 (1-2095) x US-09-515-039-83 (1-14)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-824-647-16 (1-2095) x US-09-515-039-84 (1-14)
                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                     Length:
Matches:
                                                                                                                                                                                          Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels:
                                                                                                                                                                                                          Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Natori, Shunji
TITLE OF INVENTION: NEW PROTEASE
FILE REFERENCE: 32290-144749
CURRENT APPLICATION NUMBER: US/09/515,039
CURRENT FILING DATE: 2000-03-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/515,039 CURRENT FILING DATE: 2000-03-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9-333 474
                                                                                                                                                                                                                                                                                                                                                                             Sequence 84, Application US/09515039
Patent No. 6214599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 86, Application US/09515039 Patent No. 6214599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1270 AGCGAGATCGTGGCTGGA 1287
                                                                                                                                                                                                                                                                           1270 AGCGAGATCGTGGCTGGA 1287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Natori, Shunji
TITLE OF INVENTION: NEW PROTEASE
FILE REPERENCE: 32290-144749
                                                                                                                                                                                                                                                                                             6 SerGlulleValAlaGly 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 SerGluIleValAlaGly 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EARLIER APPLICATION NUMBER: JP 9 EARLIER FILING DATE: 1997-11-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EARLIER APPLICATION NUMBER: JP
EARLIER FILING DATE: 1997-11-18
                                                                                                                     5.09e+03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.00
100.00%
100.00%
0.86%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5.09e+03
                                                                                                                                  6.00
100.00%
100.00%
0.86%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 101
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 84
LENGTH: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 101
SOFTWARE: Patentin Ver. ?
                                                                                                                                                  Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: bovine US-09-515-039-84
                                             ; ORGANISM: rattus
US-09-515-039-83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
                                                                                                     Alignment Scores
                                                                                                                                                                                                                                                                                                                                                                  US-09-515-039-84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 41
US-09-515-039-86
                  LENGTH: 14
SEQ ID NO 83
                                  TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
                                                                                                                                                                                        Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH:
                                                                                                                                         Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score:
```

```
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                Alignment Scores: ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-248-061B-9
                                                                                                                                                    Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Zwijsen, Renate
TITLE OF INVENTION: Interaction Between Cyclin D1 and Steroid Receptor
TITLE OF INVENTION: Co-Activators and Uses Thereof in Assays
FILE REPERENCE: 4238/80713
CURRENT APPLICATION NUMBER: US/09/302,305C
CURRENT FILING DATE: 1999-04-30
PRIOR APPLICATION NUMBER: PC7/GB99/00440
                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Kim, Secong-Tae
APPLICANT: Kim, Secong-Tae
APPLICANT: Lim, Dae-Sik
APPLICANT: St. Jude Children's Research Hospital
TITLE OF INVENTION: ATM Kinase Modulation for Screening and Therapies
FILE REFERENCE: 2427/IF142
CURRENT APPLICATION NUMBER: US/09/400,653A
CURRENT FILING DATE: 1999-09-21
PRIOR FILING DATE: 1999-02-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-824-647-16 (1-2095) x US-09-400-653A-11 (1-14)
                                                                                                      Conservative:
Mismatches:
                                                                                                                                                                                          US-09-824-647-16 (1-2095) x US-09-515-039-86 (1-14)
                                                                      Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels:
                                                                                                                                         Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NOS: 49 FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps:
                                                                                                                                                                                                                                                                                                             5-09-400-653A-11
Sequence 11, Application US/09400653A
Patent No. 6348311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/09302305C Patent No. 6350572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1270 AGCGAGATCGTGGCTGGA 1287
                                                                                                                                                                                                                                             6 SerGlulleValAlaGly 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5.09e+03
6.00
                                                                      5.09e+03
6.00
100.00%
100.00%
0.86%
                                                                                                                                                                                                                                                                                                                                                                                     Kastan, Michael
Canman, Christine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.00%
100.00%
0.87%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Bernards, Rene
APPLICANT: Zwijsen, Renat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 11
LENGTH: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                       Percent Similarity:
Best Local Similarity:
Query Match:
          ; ORGANISM: chicken US-09-515-039-86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-400-653A-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-302-305C-4
                                                           Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 1/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..
Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 43
                                                                                                                                                                                                                                                                                                      RESULT
                                                                                                score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                   ð
```

```
APPLICANT: Kastan, M. APPLICANT: Caman, C. APPLICANT: Caman, C. APPLICANT: Caman, C. APPLICANT: Lim, S-T. APPLICANT: Lim, D-S. APPLICANT: Lim, D-S. T. Jude Children's Research Hospital TITLE OF INVENTION: ATM Kinase Modulation for Screening and Therapies FILE REFERENCE: 2427/0F142
CURRENT APPLICATION NUMBER: US/09/248,061B
CURRENT FILING DATE: 1999-02-10
NUMBER OF SEQ ID NOS: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and Steroid Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Bernards, Rene
APPLICANT: Bernards, Rene
TITLE OF INVENTION: Interaction Between Cyclin D1 and Steroid Recipitation of Inventions interaction Between Cyclin D1 and Steroid Recipitation of Inventions Co-activators and Uses Thereof in Assays
FILE OF INVENT 428/480713
CURRENT FILING DATE: 1999-04-30
CURRENT FILING DATE: 1999-04-30
PRIOR FILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 17
LENGTH: 14
                                                                                               and it
CTHER INFORMATION: Description of Artificial Sequence:Peptide OTHER INFORMATION: containing an LXXLL motif found in steroid oTHER INFORMATION: receptor coactivators
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-824-647-16 (1-2095) x US-09-302-305C-17 (1-14)
                                                                                                                                                                     Conservative:
                                                                                                                                                                                                                                                                US-09-824-647-16 (1-2095) x US-09-302-305C-4 (1-14)
                                                                                                                                                                                           Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
                                                                                                                                   Length:
Matches:
                                                                                                                                                                                                             Indels:
                                                                                                                                                                                                                                                                                                                                                                                                US-09-302-305C-17
; Sequence 17, Application US/09302305C
; Patent No. 6350572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 9, Application US/09248061B Patent No. 6387640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1131 CTCCTCCGATACCTGCTG 1148
                                                                                                                                                                                                                                                                                                            1131 CTCCTCCGATACCTGCTG 1148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 LeuLeuArgTyrLeuLeu 10
                                                                                                                                                                                                                                                                                                                              5 LeuLeuArgTyrLeuLeu 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.09e+03
6.00
100.00%
100.00%
0.86%
                                                                                                                                 5.09e+03
6.00
100.00%
100.00%
0.86%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Homo sapiens US-09-302-305C-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Kastan,
                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
```

```
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 9
; IENGTH: 14
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-248-061B-9
Alignment Scores:
Fred. No.:
Score:
Fred. No.:
Frecht Similarity:
Forcent Similar
```

Search completed: July 7, 2003, 16:09:34 Job time: 33 secs

US-09-824-647-16 (1-2095) x US-09-248-061B-9 (1-14)

Sequence 732, App Sequence 11, Appl Sequence 2, Appl 1 Sequence 8, Appl 1 Sequence 8, Appl 1 Sequence 3, Appl 1 Sequence 3, Appl 1 Sequence 5, Appl 1 Sequence 5, Appl 1 Sequence 3, Appl 1

Sequence Sequence Sequence S Sequence Sequence

Sequence

Sequence Sequence

Sequence

Sequence

Sequence 8, Sequence 8, Sequence 7, Sequence 2, Sequence 2,

Sequence S

Sequence

Sequence

score:

Title: Perfect

Sequence:

nucleic

Run on:

Scoring table:

Word size: Searched:

```
GENERAL INCORNATION:
APPLICANT: Serrero, Ginette
TITLE DE INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
TITLE DE INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REFERENCE: 29996.488/P0011-A
CURRENT APPLICATION NUMBER: US/08/991,862
CURRENT FILING DATE: 1998-08-17
EARLIER APPLICATION NUMBER: 08/863,862
EARLIER FILING DATE: 1997-05-23
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 17
LENGTH: 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches:
Conservative:
Mismatches:
Indels:
                PCT-US91-02321-6
US-08-991-862-6
US-07-668-648-8
US-08-429-998-8
US-08-431-333-8
PCT-US91-02321-8
                                                                                                                                                                                                              5470825-2
US-09-060-756-732
US-08-584-031-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-724-394A-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-372-422A-26
US-09-372-422A-26
US-09-282-305-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -09-060-756-727
                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-216-001-3
US-09-216-386-3
US-09-216-386-5
US-08-878-862-3
US-09-213-394-3
                                                                                                                                                                                                                                                                                                     JS-08-106-507-10
                                                                                                                                                                                                                                                                                                                                              PCT-US93-10034-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-282-305-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-805-118-1
US-09-391-958-1
                                                                                                                                                                     US-08-245-853-2
US-08-573-675-2
                                                                                                                                                                                                                                                                                                                                                                                            US-09-022-940-3
US-09-022-940-5
                                                                                                                                                  -08-991-862-7
                                                                                                                                                                                                                                                                                US-08-106-507-2
                                                                                                                                                                                                                                                                                                                            US-08-446-922-8
                                                                                                                                                                                                                                                                                                                                                                        US-08-844-120-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 17, Application US/08991862
Patent No. 6309826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           593.00
100.00%
100.00%
85.45%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Human GP88 CDNA
US-08-991-862-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -08-991-862-17
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No.:
00000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -WODEL-frame+_n2p.model -DEV-xlp
-Q-Cogn2_1702PC_2ppol_VG098024647runat_07072003_154719_26078/app_query.fasta_1.2247
-Q-Cogn2_1702PC_2ppol_VG098024647runat_07072003_154719_26078/app_query.fasta_1.2247
-Q-Cogn2_1702PC_2ppol_VG098024647refastan -SNFFIX-setd.rai -MINMATCH-0.1 -LOOPCL-0
-LOOPEXT-0 -UNITS-bits -START-1 -END--1 -MATRIX-oligo -TRANS-human40.cdi
-LIST-45 -DCALIGN-020 -THEAPSTIZE-500 -MATRIX-NO00000000
-USFR-US09824647_CGCN_1 1_33_erunat_07072003_154719_26078 -NCPU-6 -ICPU-3
-NO_MARP -LARGEQUERY NEG_SCORES-0 -WAIT -DSPBLOCK-100 -LONGLOG
-NGARN_TIMEOUT-120 -WARN_TIMEOUT-30 -THERADS-1 -XGAPOP-66 -XGAPEXT-60 -KGAPOP-6
-FGAPORT-7 -YGAPOP-60 -YGAPEXT-60 -DELOP-6 -DELEXT-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Appli
                                                                                                                                                                         (without alignments)
5136.752 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                   ......ataaagtttgtcactttctt 2095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 17, Sequence 4, Sequence 4, Sequence 4, Sequence 2, Sequence 2, Sequence 2, Sequence 2, Sequence 6, Seque
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Description
                                                                                                                                                     ; Search time 24 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cgn2_6/ptodata/1/laa/5A_COMB.pep:*
/cgn2_6/ptodata/1/laa/5B_COMB.pep:*
/cgn2_6/ptodata/1/laa/6A_COMB.pep:*
/cgn2_6/ptodata/1/laa/6B_COMB.pep:*
/cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
                    GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                       - protein search, using frame_plus_n2p model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-991-862-17
US-07-668-648-4
US-08-429-998-4
US-08-431-333-4
PCT-US91-02321-4
US-07-668-648-2
US-08-429-998-2
US-08-429-998-6
US-08-431-333-2
US-08-431-333-2
US-08-431-333-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               seqs, 29422922 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                   60.0
60.0
7.0
7.0
                                                                                                                                                  July 7, 2003, 15:47:40
                                                                                                                                                                                                                                                                                                                                                 , Xgapext 6
, Ygapext 6
, Fgapext
, Delext
                                                                                                                                                                                                                                                                                   cgcaggcagaccatgtggac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Issued_Patents_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                       US-09-824-647-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                 60.0
60.0
6.0
6.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Command line parameters:
                                                                                                                                                                                                                                                                                                                       OLIGO
Xgapop (
Ygapop (
Fgapop
Delop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         262574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query
Match
```

CCAGATGTCAGTTCTGCCCTGTGGCCTGCTGCTGCACCCCGGAGGAGCCACTACAGC 132

US-09-824-647-16 (1-2095) x US-08-991-862-17 (1-593)

13

ò 셤 ò

4444 406 32 32 32 32 32 32 32 32 32

Score

Result Š

Database

73

Sequence

593 00.00 0

20 72

QQ	21 ProAspGlyGlnPheCysProValAlaCysCysLeuAspProGlyGlyAlaSerTyrSer 40		1213 CAGCACTGCTGCCCC
ox O	133 TGCTGCCGTCCTTCTGGACAAATGGCCCACAACACTGAGCAGGCATCTGGGTGGCCCC 192 	G 8	
o d	193 TGCCAGGTTGATGCCCACTGCTGTGCCACTCCTGCATCTTTACGGTCTCAGGACT 252 	₹ 6 ¢	
oy G	253 TCCAGTTGCTGCCCTTCCCAGAGGCCGTGGCATGCGGGATGGCCATCACTGCTGCTCCCA 312 	ko da	
ço Go	313 CGGGGCTTCCACTGCAGTGCAGACGGGGATCCTGCTTCCAAAGATCAGGTAACAACTCC 372 	λο α . ·	
В да	373 GTGGGTGCCAGTGCCCTGATAGTCAGTTCGAATGCCCGGACTTCTCCACGTGCTGT 432 	ž 8 .	
\$ g	433 GTTARGGTCGARGGCTCCTGGGGGTGCTCCCAGGCCTTCCTGCTGTGAAGAC 492 	Š	501
\$ 6	493 AGGGTGCACTGCTGCCCACGGTGCCTTCTGCGACCTGGTTCACACCCGCTGCATCACA 552 	25 A 6	
Oy	553 CCCACGGGCACCCCCCGGCAAAGAAGCTCCCTGCCCAGAGGACTAACAGGGCAGTG 612 	e e e	1603 COMMUNICATION 11603 C
Oy qq	613 GCCTTGTCCAGCTCGGTCATGTCCCGACGCACGGTCCCGGTGCCCTGATGGTTCTACC 672 	ž a	1093 GCIGGCIICCGCIGCG
ठ व <u>ु</u>	673 TGCTGTGGCTGCCGAGGAAGTATGGCTGCTGCCCAATGCCCAACGCCACCTGCTGC 732 	qa q	1753 GACGCCCCTTTGAGGG
	733 TCCGATCACCTGCACTGCCCCCAAGACACTGTGTGTGACCTGATCCAGAGTAAGTGC 792 	KESULT US-07- ; Sequ	2 668-648-4 ence 4, A nt No. 54
oy da	793 CTCTCCAAGGAGACGCTACCACGGACCTCCTCACTAAGCTGCGCACACACGGGG 852 	A A P E	GENEKAL INFORMATION: MOHAMM APPLICANT: Sloyab, MOHAMM APPLICANT: Plowman, Gree TITLE OF INVENTION: EPIT
oy G	853 GATGTGAAATGTGACAFGGGGGGGGGGGGGGGGGGGGTATACCTGCTGCCGTCTACAG 912 	4 Z O	NUMBER OF INVENTION: MODULABLE OF SEQUENCES: 12 CORRESPONDENCE ADDRESS: ADDRESSEE: Pennie & Ed
& 8 _.	913 TCGGGGCCTGGGGCTGCTTTTTACCCAGCTGTGTGTGTGT		ST: LISS AVENUE: New York S: New York PRY: USA
ራ 8	973 TGCTGTCCCGCGGGGTTTACGTGTGACACGCAGAAGGGTACCTGTGAACAGGGGCCCCAC 1032 		ORM: PPY COM
<i>\$</i> 6	1033 CAGGTGCCCTGGATGGAGAAGGCCCCAGCTCACCTGCCAGCAGAACCCTG 1092 		COERRATING SISTEM: PC-L SOFTWARE: Patentin Rel CURRENT APPLICATION DATA: APPLICATION NUMBER: US
\$ g	1093 AAGAGAGATGTCCCCTGTGATAATGTCAGCTGCTCCCTCC	· 4	FILING DAIE: 19910019 CLASSIFICATION: 514 ATTORNEY/AGENT INFORMATIC NAME: Misrock, S. Lesl
Oy Op	1153 CTCACGTCTGGGGAGTGGGCTGTCCAATCCCAGAGGCTGTCTGCTGCTCGGACCAC 1212 	E	REGISTRATION NUMBER: 1 REFERENCE/DOCKET NUMBER TELECOMMUNICATION INFORM TELEPHONE: (212)790-90

TTCTGCCATGATAACCAGACCTGCTGCCGAGACAACCGACAGGGC 1632 TACGCCCAGGGCCTCTGTTGTGCTGATCGCGCCACTGCTGCTCT 1692 TECTCCCAGTTGCCCCATGCTGTGTGCCGGGGAGGATCGCCAGCAC 1452 ACCTTCCTGGCCCGTAGCCCTACGTGGGTGTGAAGGACGTGGAG 1572 CAGCACACCAGCTGCCCGGTGGGCGGAACCTGCTGCCCGAGCCAG 1392 500 GGOFY D. THELINS: NOVEL CYSTEINE-RICH GROWTH DULATING PROTEINS elease #1.0, Version #1.25 eslie 18,872 BER: 5624-161-999 RMATION: Edmonds of the Americas n: 15/07/668,648 DOS/MS-DOS 707668648 atible :NOI

1032

1092

360

ð 셤 à g

ð

g

ö 셤 ď.

8

g

ð

음 ð ö

us-09-824-647-16.std.rai

```
1093 AAGAGAGATGTCCCCTGTGATAATGTCAGCAGCTGTCCCTCCTCCGGTACCTGCTGCCAA 1152
                                                                                                                                                                                                                                                                                                                  CTCACGTCTGGGGGAGTGGGGCTGCTGTCCAATCCCAGAGGCTGTTGTGTGGTCGGACCAC 1212
                                                                                                                                                            LeuSerLysGluAsnAlaThrThrAspLeuLeuThrLysLeuProAlaHisThrValGly 280
                                                                                                                                                                                                    1033 CAGGTGCCCTGGATGGAGAAGGCCCCAGCTCACCTCAGCCTGCCAGACCCACAAGCCTTG
                                                                                                                                                                                                                    AspValLysCysAspMetGluValSerCysProAspGlyTyrThrCysCysArgLeuGln
                                                                                                                                             TGCTGTCCCGCGGGGTTTACGTGTGACACGCAGAAGGGTACCTGTGAACAGGGGCCCCCAC
                                                                                                                                                                                                                                                                                                                                  GATGTGAAATGTGCATGGAGGTGAGCTCCCAGATGGCTATACCTGCTGCTGCTACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CYSTEINE-RICH GROWTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/08429998
Patent No. 2885961
GENERAL INFORMATION:
APPLICANT: Shoyab, Mohammed
APPLICANT: PLOWMEN, GENEGOLY D.
TITLE OF INVENTION: EPITHELINS: NOVEL CY
TITLE OF INVENTION: MODULATING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5624-161-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Vel
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/429,998
FILING DATE: 27-APR-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 07/668,648
FILING DATE: 13-MAR-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                        1213 CAGCACTGCTCCCCCAG 1230
                                                                                                                                                                                                                                                                                                                                                                                        401 GlnHisCysCysProGln 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18,872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 56
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (212)790-9090
(212) 869-9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 593 amino aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: protein US-08-429-998-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-429-998-4
     261
                                                                                                                                                                                                                                                                                                                  1153
                                                           281
                                                                                                                                             973
                                                                                                                                                                                                                                                                                      361
                                                                                                                                                                                                                                                                                                                                              381
                                 853
                                                                                                                a
                                 ò
                                                          d
                                                                                      δ
                                                                                                                                             ò
                                                                                                                                                                         셤
                                                                                                                                                                                                    à
                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                            å
                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                               132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           240
                                                                                                                                                                                                                                                                                                                                                                                     192
                                                                                                                                                                                                                                                                                                                                                                                                                                           252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      852
                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                         40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80
                                                                                                                                                                                                                                                                                                20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCAGATGGTCAGTTCTGCCCTGTGCCTGCTGGACCCCGGAGGAGCCAGCTACAGC
                                                                                                                                                                                                                                                                                                                                         133 IGCTGCCGTCCCCTTCTGGACAAATGGCCCACAACACTGAGCAGGCATCTGGGTGGCCCC
                                                                                                                                                                                                                                                                                                                                                                                                 TGCCAGGTTGATGCCCACTGCTCTGCCGGCCACTCCTGCATCTTTACCGTCTCAGGGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCCAGTTGCTGCCCCTTCCCAGAGGCCGTGGCATGCGGGGGATGGCCATCACTGCTGCCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTGGGTGCCATCCAGTGCCCTGATAGTCAGTTCGAATGCCCGGACTTCTCCACGTGCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTTATGGTCGATGCTCCTGGGGGTGCTGCCCCATGCCCCAGGCTTCCTGCTGTGAAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGGGTGCACGCTGCGTGCCTTCTGCGACCTGGTTCACACCCGCTGCATCACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCCACGGGCACCCACCCCTGGCAAAGAAGCTCCCTGCCCAGAGGACTAACAGGGCAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCCTTGTCCAGCTCGGTCATGTGTCCGGACGCACGGTCCCGGTGCCCTGATGGTTCTACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGCTGTGAGCTGCCCAGTGGGAAGTATGCCTGCCCAATGCCCAACGCCACCTGCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCCGATCACCTGCACTGCCCCCCAAGACACTGTGTGTGACCTGATCCAGAGTAAGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATGTGGACCCTGGTGAGCTGGCTTAACAGCAGGGCTGGTGGCTGGAACGCGGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          593
0 0
0 0
0 0
                                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                       US-09-824-647-16 (1-2095) x US-07-668-648-4 (1-593)
                                                                                                                                                                                                    Indels:
                                                                                                                                                      406.00
100.00%
100.00%
58.50%
TELEFAX: (212) 869-9741
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 593 amino acids
TYPE: AMINO ACID
                                                                                   MOLECULE TYPE: protein
                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
                                                                                                                          Alignment Scores:
Pred. No.:
                                                                    TOPOLOGY:
                                                                                                 US-07-668-648-4
                                                                                                                                                                                                                                                                     13
                                                                                                                                                                                                                                                                                                                            73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               253
                                                                                                                                                                                                                                                                                                                                                                                                                                        193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           793
                                                                                                                                                                                               Query Match:
DB: .
```

energia estimaticam e come es en el exception (Messian Conference) e casa estimaticamente en el estimaticamente el estimaticamente en el estimaticamente en el estimaticamente el estimaticamente el estimaticamente el estimaticamente el estimat

Db 301 Se	973 321 1033	1003		Oy 1153 CT	Db 381 Le	401	RESULT 4	US-08-431-333-4 ; Sequence 4, Ap ; Patent No. 596 ; CHNEDAL INFOR	APPLICANT:	TITLE OF IN		STREET:	; STATE: N ; COUNTRY:	86	COMPUTER:	; SOFTWARE:	; APPLICATI ; FILING DA	CLASSIFIC PRIOR APPLI	ATTORNEY/AG	E 6	TELEPHONE		SEQUENCE CE	TOPOLOGY	US-08-431-333-4	Alignment Scores	Score: Percent Similari	Query Match:
	Alignment Scores: Pred. No.: Score: Score: 100.004 Percent Similarity: 100.008 Best Local Similarity: 2 8.504 Gaps: 100.005 Indels: 100.006 Indels: Ind	US-09-824-647-16 (1-2095) x US-08-429-998-4 (1-593)	13 ATGTGGACCTGGTGAGCTGGGTGGCCTTAACAGCAGGGCTGGTGGCTGGAACGGGTGC 72	CCAGATGATCAGTTCTGCCTGTGGCCTGCTGGACCCCGGAGGAGCCAGCTACAGC				193 TGCCAGGTTGATGCCCACTGCTGGGGCCACTCTGCATCTTTACCGTCTCAGGGACT 252	253 FCCAGTFGCTGCCCCTTCCCAGAGGCCGTGGCATGCGGGGATGGCCATCACTGCTGCTGCCCA 312	81 SerSysCysProPheProGlualaValAlaCysGlyAspGlyHisHisCysCysPro 100	313 CGGGCTTCCACTGCAGTGCAGACGGCGATCCTCCAAAGATCAGGTAACAACTCC 372	GTGGGTGCCATCCAGTGCCCTGATAGTCAGTTCGAATGCCCGGACTTCTCCACGTGCTGT	ValGlyAlaIleGlnCysProAspSerGlnPheGluCysProAspPheSerThrCysCys	433 GTTATGGTCGATGGTCCTGGGGGTGCTGCCCCAGGCTTCCTGCTGTGAAGAC 492	141 ValMetValAspGlySerTrpGlyCysCysProMetProGlnAlaSerCysCysGluAsp 160	AGGGGCACTGCTGCGCACGCTCTCTGCGACCTGGTTCACACCCGCTGCATCACA		553 CCCACGGCACCCCCCCCCGCAAAGAAGCTCCCTGCCCAGAGGACTAACAGGGCAGTG 612 	613 GCCTTGTCCAGCTCGGTCATGTGTCCGGACGCACGGTCCCGGTGCCCTGATGGTTCTACC 672	201 AlaLeuSerSerSerValMetCysProAspAlaArgSerArgCysProAspGlySerThr 220	673 IGCIGIGAGCIGCCCAGIGGGAAGTAIGGCIGCCCCAAIGCCCAAGGCCACCIGCIGC 732		TCCGATCACCTGCACTGCTGCCCCCCAAGACACTGTGTGTG	SerAspHisLeuHisCysCysProGinAspThrValCysAspLeulieGinSerLysCys	793 CTCTCCAAGGAAACGCTACCACGGACTCCTCACTAAGCTGCTGCACACACTGGC 852 		AspvallysCysAspMetGluValSerCysProAspGlyTyTThrCysCysArgLeuGln	913 TCGGGGGCCTGGGGCTGCTGTTTACCCAGGCTGTGTGTGT
	Alignr Pred. Score Percer Best I Query DB:	0-SD	ço g	è	6	ολ	qa ·	ð 8	Qy	q	δy da	8 8	ය සි	δ	q	δo .	셤	\$ 6 6	δλ	. dg	δ	අ	ò.	වු	ð á	3 8	2 8	ογ

	-					
320 1032 340	1092 360	115 2 380	1212			
301 SerGlyAlaTrpClyCysCysProPheThrGlnAlaValCysCysGluAspHis1leHis 3 973 TGCTGTCCGGGGGTTTACGTGTGACACGCAGAAGGGTACCTGTGAACAGGGGCCCCAC 1 1111111111111111111111111111111	1033 CAGGTGCCTGGATGGAGAAGGCCCCAGCTCACCTCAGCCTGCCAGACCCACAAGCCTTG 1	1093 AAGAGAGATGTCCCTGTGATAATGTCAGCAGCTGTCCCTCCGATACCTGCTGCCAA 1 	1153 CTCACGTCTGGGGAGTGGGGCTGCTCAATCCCAGAGGCTGTCTGCTGCTCGGACCACCACCACCACCACGAGGCTGTTTTTTTT	1213 CAGCACTGCCCCCAG 1230 	RESULT 4 18-608-431-333-4 18-608-431-333-4 18-608-431-333-4 18-608-431-333-4 18-608-431-333-4 18-608-431-333-4 18-608-431-333-4 18-608-431-333-4 18-608-431-333-4 18-608-608-608-608-608-608-608-608-608-60	20 4 5 H H
90 A9	Q Q	Q P	Q Q	o d	US CONTRACTOR CONTRACT	Pre-

1212

```
341 GlnValProTrpMetGluLysAlaProAlaHisLeuSerLeuProAspProGlnAlaLeu 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     133 TGCTGCCGTCCCCTTCTGGACAAATGGCCCACACACTGAGCAGGCATCTGGGTGGCCCC 192
                     ATGTGGACCCTGGTGACCTGGTGGCCTTAACAGCAGGGCTGGTGGCTGGAACGCGGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCAGATGGTCAGTTCTGCCCTGTGCCTGCTGCCTGGACCCCGGAGGAGCCAGCTACAGC
                                                                                                                                                                                                              Plowman, Gregory D. FINTED REPLIES BY GROWTH FINION: EPITHELINS: NOVEL CYSTEINE-RICH GROWTH FUNION: MODULATING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          593
0
0
0
0
0
                                                                                                                                                                                                                                                                                                                                                                         SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-824-647-16 (1-2095) x PCT-US91-02321-4 (1-593)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
                                                                                                                                                                                                                                                                    3: Bristol-Myers Squibb Company 3005 First Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: ON0071A-PC TELECOMMUNICATION INFORMATION: TELEPHONE: (206)728-4800
                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/02321
FILING DATE: 19910403
                                                                                                                                                                            Sequence 4, Application PC/TUS9102321
GENERAL INFORMATION:
                                                                                                            1213 CAGCACTGCTGCCCCCAG 1230
                                                                                                                      401 GinHisCysCysProGln 406
                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Poor, Brian W. REGISTRATION NUMBER: 32,928
                                                                                                                                                                                                    Shoyab, Mohammed
                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    406.00
100.00%
100.00%
58.50%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (206)448-4775
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                   12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein
                                                                                                                                                                                                                        TITLE OF INVENTION: EP
TITLE OF INVENTION: MO
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                            ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                           CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM SOFTWARE: Paten
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE:
                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                   PCT-US91-02321-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores
                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                   APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                 STREET:
                      1093
                                          361
                                                                1153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score:
                      ò
                                          셤
                                                                ö
                                                                                     셤
                                                                                                            å
                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGCTGTCCCGCGGGGTTTACGTGTGACACGCAGAAGGGTACCTGTGAACAGGGGCCCCAC 1032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAGGTGCCTGGATGGAGAGCCCCAGCTCACCTCAGCCTGCCAGACCCACAAGCCTTG 1092
                                                                                                                                                                                                                                                                                                                                                                                                                                          612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             192
                                                                                                                                                                                                                        492
                                                                                                                                                                                                                                                                                                                                                           672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCAGATGGTCAGTTCTGCCCTGTGGCCTGCTGGACCCCGGAGGAGCCAGCTACAGC 132
                                                                                                                                                                  252
                                                                                                                                                                                                             312
                                                                                                                                                                                                                                                           372
                                                                                                                                                                                                                                                                      432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GATGTGAAATGTGACATGGAGGTGAGCTGCCCAGATGGCTATACCTGCTGCCGTCTACAG 912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               340
                             ATGTGGACCCTGGTGAGCTGGGTGGCCTTAACAGCAGGCTGGTGGCTGGACGCGGTGC 72
                                                                                                40
                                                                                                                              80
                                                                                                                                                                          21 ProAspGlyGlnPheCysProValAlaCySCysLeuAspProGlyGlyAlaSerTyrSer
                                                                                                                    TGCTGCCGTCCCCTTCTGGACAAATGGCCCACACACTGAGCAGGCATCTGGGTGGCCCC
                                                                                                                                                               TGCCAGGTTGATGCCCACTGCTCTGCCGGCCACTCCTGCATCTTACCGTCTCAGGGACT
                                                                                                                                                                                                            TCCAGTTGCTGCCCCTTCCCAGAGGCCGTGGCATGCGGGGATGGCCATCACTGCTGCCCA
                                                                                                                                                                                                                                                         CGGGGCTTCCACTGCAGTGCAGACGGGCGATCCTGCTTCCAAAGATCAGGTAACAACTCC
                                                                                                                                                                                                                                                                                                    GTGGGTGCCATCCAGTGCCCTGATAGTCAGTTCGAATGCCCGGACTTCTCCACGTGCTGT
                                                                                                                                                                                                                                                                                                                                                GTTATGGTCGATGGCTCCTGGGGGTGCTGCCCCATGCCCCAGGCTTCCTGCTGTGAAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                       CCCACGGGCACCCACCCCTGGCAAAGAAGCTCCCTGCCCAGAGGACTAACAGGGCAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCCTTGTCCAGCTCGGTCATGTGTCCGGACGCACGGTCCCGGTGCCCTGATGGTTCTACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               673 IGCTGTGAGCTGCCCAGTGGGAAGTATGGCTGCCCAATGCCCAACGCCACCTGCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-431-333-4 (1-593)
         ×
       US-09-824-647-16 (1-2095)
                                                                                                                   133
                                                                                                                                                                                                           253
                                                                        73
                                                                                                                                        £.1
                                                                                                                                                               193
                                                                                                                                                                                      61
                                                                                                                                                                                                                                 81
                                                                                                                                                                                                                                                       313
                                                                                                                                                                                                                                                                             101
                                                                                                                                                                                                                                                                                                   373
                                                                                                                                                                                                                                                                                                                                                433
                                                                                                                                                                                                                                                                                                                                                                                                                                       553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                321
                             ö
                                               셤
                                                                       à
                                                                                            셤
                                                                                                                   ò
                                                                                                                                       셤
                                                                                                                                                               ð
                                                                                                                                                                                                          å
                                                                                                                                                                                                                               a
                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                         q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               음
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
```

132

40

72 20

P

ð

5 6

à

```
101 GlnHisCysCysProGln 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                  COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-07-668-648-6
                                                                                                                                                                                                                                                                                                                      LENGTH:
                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                        US-07-668-648-2
                          US-07-668-648-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             480
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match:
                                                                                                                                                                                                                                                                                                                                                                                   Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
                  RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAGGTGCCCTGGATGGAGAAGGCCCCAGCTCACCTCAGCCTGCCAGACCCACAAGCCTTG 1092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAGAGAGATGTCCCCTGTGATAATGTCAGCAGCTGTCCCTCCTCCGATACCTGCTGCCAA 1152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TECTGTCCCGCGGGGTTTACGTGTGACACGCAGAAGGGTACCTGTGAACAGGGGCCCCCAC 1032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        492
                                                                                                                                                                                   160
                                                                                                                                                                                                                     180
                                                                                                                                                                                                                                      612
                                                                                                                                                                                                                                                      200
                                                                                                                                                                                                                                                                       672
                                                                                                                                                                                                                                                                                GATGTGAAATGTGACATGGAGGTGAGCTGCCCAGATGGCTATACCTGCTGCCGTCTACAG 912
                                                                                                                                                                                                                                                                                                                                                                                                                     432
                                                                                                                                                                                                    AGGGTGCACTGCTCCCCACGGTGCCTTCTGCGACCTGGTTCACACCCGCTGCATCACA 552
                                                                      372
                            252
                                                             TCCAGITGCTGCCCCTTCCCAGAGGCCGTGGCATGCGGGGATGGCCATCACTGCTGCCCA 312
                                     CGGGGCTTCCACTGCAGTGCAGACGGGCGATCCTGCTTCCAAAGATCAGGTAACAACTCC
                                                                                                                                 GTGGGTGCCATCCAGTGCCCTGATAGTCAGTTCGAATGCCCGGACTTCTCCACGTGCTGT
                                                                                                                                                                  GTTATEGTCGATGGCTCCTGGGGGTGCTGCCCCATGCCCCAGGCTTCCTGCTGTGAAGAC
                                                                                                                                                                            CCCACGGGCACCCACCCCTGGCAAAGAAGCTCCCTGCCCAGAGGACTAACAGGGCAGTG
                                                                                                                                                                                                                                                GCCITGICCAGCTCGGTCATGICTCCGGACGCACGGTCCCGGIGCCCTGATGGITCTACC
  TGCCAGGTTGATGCCCACTGCTGCCGGCCACTCCTGCATCTTTACCGTCTCAGGGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAGCACTGCTGCCCCCAG 1230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1213
                                                                                                                                                                                                                                                                                                                                                                                              261
                                                                                                                                                                                                                                                                                                                                                                                                                               281
                                                                                                                                                                                                                                                                                                                                                                                                                                                913
                                                                                                                                                                                                                                                                                                                                                                                                                                                               301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      381
                                                                                                                                                                                                                                                                                                                                                                                                               853
                                                                                                                                                                                                                                                                                          201
                                                                                                                                                                                                                                                                                                           673
                                                                                                                                                                                                                                                                                                                            221
                                                                                                                                                                                                                                                                                                                                            733
                                                                                                                                                                                                                                                                                                                                                            241
                                                                                                                                                                                                                                                                                                                                                                             793
                                                                                                                                                                                                        493
                                                                                                                                                                                                                        191
                                                                                                                                                                                                                                         553
                                                                                                                                                                                                                                                         181
                                                                                                                                                                                                                                                                          613
                                                                                                                                    373
                                                                                                                                                                     433
                41
                               193
                                                                253
                                                                                 81
                                                                                                  313
```

셤

g

õ

9 & 90 19 & 90

ò

g

셤

Oy Db 음

à

à

 윱

à

ò

```
APPLICANT: Shorab, Mohammed
APPLICANT: Showan, Gregory D.
TITLE OF INVENTION: EPITHELINS: NOVEL CYSTEINE-RICH GROWTH
TITLE OF INVENTION: MODULATING PROFEINS
NUMBER OF SEQUENCES: 12
Sequence 2, Application US/07668648
Sequence 2, Application US/07668648
Patent No. 5416192
GENERAL INFORMATION:
APPLICANT: Shoyab, Mohammed
APPLICANT: Plowman, Gregory D.
TITLE OF INVENTION: EPITHELINS: NOVEL CYSTEINE-RICH GROWTH
TITLE OF INVENTION: MODULATING PROTEINS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   288
000
000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1456 TGCCCGGCTGGCTACACCTGCAACGTGAAGGCTCGA 1491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-824-647-16 (1-2095) x US-07-668-648-2 (1-589)
                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 5624-161-999
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps:
                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/668,648
FILING DATE: 19910819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6, Application US/07668648 Patent No. 5416192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pennie & Edmonds
                                                                                                                                                                                                                                                                                                                            IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.12e-20
32.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (212)790-9090
TELEFAX: (212) 869-9741
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            589 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                               STREET: 1155 Ave
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               vercent Similarity
                                                                                                                                                                                                                                                                      ZIP: 10036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
```

```
Sequence 6, Application US/08429998
Patent No. 5885961
GENERAL INFORMATION:
APPLICANT: Ployab, Mohammed
APPLICANT: Ployab, Mohammed
TITLE OF INVENTION: EPITHELINS: NOVEL CYSTEINE-RICH GROWTH
TITLE OF INVENTION: MODULATING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1456 TGCCCGGCTGGCTACACCTGCAACGTGAAGGCTCGA 1491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                480 CysProAlaGlyTyrThrCysAsnValLysAlaArg 491
                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-824-647-16 (1-2095) x US-08-429-998-2 (1-589)
                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                               Length:
                                                                                                                             REFERENCE/DOCKET NUMBER: 5624-161-999 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Pennie & Edmonds
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/668,648
FILING DATE: 13-MAR-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/429, 998
FILING DATE: 27-APR-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIF: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PELECOMMUNICATION INFORMATION
                         APPLICATION NUMBER: US 07
FILING DATE: 13-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Mistock, S. Leslie
REGISTRATION NUMBER: 18, E
                                                                                                                                                                 TELEPHONE: (212)790-9090
TELEFAX: (212) 869-9741
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                   100.008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Misrock, S. Leslie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 18, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (212)790-9090
                                                                                                                                                                                                                                                   LENGTH: 589 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (212) 869-9741
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein US-08-429-998-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: EP TITLE OF INVENTION: MO NUMBER OF SEQUENCES: 1 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity: Best Local Similarity: Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: New York STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                        Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JS-08-429-998-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
                                                                                                                                                                                                                                                                                                                                                                                               Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1396 GGGAGCTGGGCCTGCTGCTGCTGTGTGTGTGTGTGCGAGGATCGCCAGCACTGC 1455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Shoyab, Mohammed
APPLICANT: Plowman, Gregory D.
TITLE OF INVENTION: EPITHELINS: NOVEL CYSTEINE-RICH GROWTH
TITLE OF INVENTION: MODULATING PROTEINS
                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: TBM FC Compatible
OPERATING SYSTEM: FC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 19910019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1456 TGCCCGCCTGCTACACCTGCAACGTGAAGGCTCGA 1491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 480 CysProAlaGlyTyrThrCysAsnValLySAlaArg 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-824-647-16 (1-2095) x US-07-668-648-6 (1-589)
STREET: 1155 Avenue of the Americas
CITY: New York
CATRE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: Pennie & Edmonds
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/429,998
FILLING DATE: 27-APR-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/08429998
Patent No. 5885961
                                                                                                                                                                                                                                                                                                     NAME: Misrock, S. Lesiie
REGISTRATION UNUBER: 18,872
REFERENCE/DOCKET NUMBER: 5624
TELECOMMUNICATION INFORMATION:
TELEPAN: (212) 869-9741
INPORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                              TTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.00%
100.00%
4.61%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 589 amino acids TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , MOLECULE TYPE: protein US-07-668-648-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New York
: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                              COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-429-998-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
```

000

```
Gregory D. EPITHELINS: NOVEL CYSTEINE-RICH GROWTH MODULATING PROTEINS
                                                                                                1396 GGGAGCTGGCTGCTGCCAGTTGCCCCATGCTGTGTGCTGCGAGGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1456 TGCCCGGCTGGCTACACCTGCAACGTGAAGGCTCGA 1491
                                                                                                                                                             1456 TGCÇCGGCTGGCTACACCTGCAACGTGAAGGCTCGA 1491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                            Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-824-647-16 (1-2095) x US-08-431-333-6 (1-589)
                                                              US-09-824-647-16 (1-2095) x US-08-431-333-2 (1-589)
 Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                           E: Pennie & Edmonds
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/431,333
FILING DATE: 27-APR-1995
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/668,648
FILING DATE: 13-MAR-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                           Sequence 6, Application US/08431333
Patent No. 5965723
GENERAL INFORMATION: ApplicaNT: Shoyab, Mohammed
APPLICANT: Plowman, Gregory D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.12e-20
32.00
100.00%
1.00.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (212)790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (212) 869-9741
Best Local Similarity: 100.00%
Query Match: 4.61%
DB: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein
                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie 6 F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: New York STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-431-333-6
                                                                                                                                                                                                                                                     US-08-431-333-6
                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           red. No.:
                                                                                                                                                                                                                                     RESULT 11
                                                                                                                                                                                                    셤
                                                                                                        ŏ
                                                                                                                                                                                                                                                                                      1396 GGGAGCTGGCCTGCTGCCAGTTGCCCCATGCTGTGTGCTGCGAGGATCGCCAGCACTGC 1455
                                                                                                                                                                                                                                                                                                           Jetucher No. 5965/2.
GENERAL INFORMATION:
APPLICANT: Shoyab, Mohammed
APPLICANT: Plowman, Gregory D.
APPLICANT: PLOWMAN: EPPTHELINS: NOVEL CYSTEINE-RICH GROWTH
TITLE OF INVERTION: MODULATING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             589
32
0
                                                                                                                                                                                                                                                                                                                                                          1456 TGCCCGGCTGGCTACACCTGCAACGTGAAGGCTCGA 1491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                           480 CysproAlaGlyTyrThrCysAsnValLysAlaArg 491
                                                                                                                                            Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                          US-09-824-647-16 (1-2095) x US-08-429-998-6 (1-589)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/668,648
FILING DATE: 13-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 5624-161-999
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                            Indels:
                                                                                                                                                                                                                               Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Pennie & Edmonds
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/431,333
FILING DATE: 27-APR-1995
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08431333 Patent No. 5965723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.12e-20
32.00
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (212)790-9090
TELEFAX: (212) 869-9741
INFORMATION FOR SEQ ID NO: 2
        TYPE: amino acids
TYPE: amino acids
Olfococy: 14-
                                                                                                                                               ..12e-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                            100.00%
100.00%
4.61%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    589 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: protein
                SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTIC
                                                                                 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
                                                                               , MOLECULE TYPE:
US-08-429-998-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-431-333-2
                                                                                                                                   Alignment Scores
                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-431-333-2
                                                                                                                                                                                                                 Query Match
                                                                                                                                                   ..
Q
                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 10
                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                 ð
                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                 ð
```

용

```
460 GlySèrTrpAlaCysCysGlnLeuProHisalaValCysCysGluAspArgGlnHisCys 479
                                                                                                                                                                                                                                                                                                                                                1396 GGGAGCTGGCCTGCCAGTTGCCCCATGCTGTGTGCTGCGAGGATCGCCAGCACTGC
                                                                                                                                    Sec.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6, Application PC/TUS9102321
GENERAL INFORMATION:
APPLICANT: Sloyab, Mohammed
APPLICANT: Plowman, Gregory D
TITLE OF INVENTION: EPITHELINS: NOVEL CYSTEINE-RICH GROWTH
TITLE OF INVENTION: MODULATING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                        1456 TGCCCGGCTGGCTACACCTGCAACGTGAAGGCTCGA 1491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/02321
FILING DATE: 19910403
VFROBMEY: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                               480 CysProAlaGlyTyrThrCysAsnValLysAlaArg 491
                                                                                                                                                                                                                                                                                                    US-09-824-647-16 (1-2095) x PCT-US91-02321-2 (1-589)
                                                                                                                                                                                                                 Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative:
Mismatches:
                                                                                                                                                                                                                                      Mismatches:
                                                                                                                                                                                 Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Squibb Company
                                                                                                                                                                                                                                                        Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels:
                                                                                                                                                                                                                                                                             Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY AGENT INFORMATION:
NAME: POOL, Brian W.
REGISTRATION NUMBER: 32,928
REFERENCE/DOCKET NUMBER: 0N0071A-PC
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Bristol-Myers 3005 First Avenue
                                                                                                                                                                               1.12e-20
32.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.12e-20
32.00
                                                                                                                                                                                                               100.00%
100.00%
4.61%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (206)728-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.00%
100.00%
4.61%
                                                : 589 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       589 amino acids
AMINO ACID
             INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEC ID NO:
                                SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS
                                                                                                    ; MOLECULE TYPE: protein PCT-US91-02321-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS: ADDRESSE: Bristol-M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Plowman, (
TITLE OF INVENTION: 1
TITLE OF INVENTION: 1
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Seattle
STATE: Washington
                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98121
                                                                                    TOPOLOGY:
                                                                                                                                                             Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CT-US91-02321-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PCT-US91-02321-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPAX:
                                                LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET:
                                                                                                                                                                                                                                                      Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match:
OB:
                                                                                                                                                                               No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1396 GGGAGCTGGGCCTGCTGCCAGTTGCCCCATGTGTGTGCTGCGAGGATCGCCAGCACTGC 1455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Serrero, Ginette
TITLE OF INFORMATION:
TITLE OF INFORMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REPERENCE: 29996.48PP001-8
CURRENT APPLICATION NUMBER: 0S/08/991,862
CURRENT FILIAG DATE: 1998-08-17
EARLIER APPLICATION NUMBER: 08/863,862
EARLIER PILIAG DATE: 1997-05-23
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Shoyab, Mohammed
APPLICANT: Plowman, Gregory D.
TITLE OF INVENTION: EPITHELINS: NOVEL CYSTEINE-RICH GROWTH
TITLE OF INVENTION: MODULATING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                        589
32
0
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1456 TGCCCGGCTGGCTACACCTGCAACGTGAAGGCTCGA 1491
480 CysProAlaGlyTyrThrCysAsnValLysAlaArg 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 480 CysProAlaGlyTyrThrCysAsnValLySAlaArg 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-824-647-16 (1-2095) x US-08-991-862-2 (1-589)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Bristol-Myers Squibb Company 3005 First Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: PCT/US91/02321
FILING DATE: 19910403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PCT-0391.02321-2; Sequence 2, Application PC/TUS9102321; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Mouse epithelin/granulin
US-08-991-862-2
                                                                                              Sequence 2, Application US/08991862
Patent No. 6309826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 514
ATORNEY/AGENT INFORMATION:
NAME: POOT, BEIAN W.
REGISTRATION NUMBER: 32,928
REFERENCE/POSKET UNMBER: ONOO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)728-4801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.12e-20
32.00
100.00$
100.00$
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (206)448-4775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Bristol-M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Plownan, G
TITLE OF INVENTION: E
TITLE OF INVENTION: M
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 19
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98121
                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
                                                                                                                                                                                                                                                                                                                     SEQ ID NO 2
LENGIH: 589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    red. No.:
```

RESULT 13

a

us-09-824-647-16.std.rai

```
TOPOLOGY: linea
                                                                                                                                                                                                                                                                                          Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JS-08-429-998-8
                                                                                                                                                                                                                                                                                                                                                                             Query Match:
                                                                                                                                                                                                                                                                                                           No.:
                                                                                                                                                                                                                                                                                                                               Score:
                                                                                                                                                                                                                                                                                                           Pred.
                           1396 GGGAGCTGGCCTGCTGCCAGTTGCCCCATGCTGTGCTGCGAGGATCGCCAGCACTGC 1455
                                                 1048 GAGAAGGCCCCAGCTCACCTCAGCCTGCCAGACCCACAAGCCTTGAAGAGAGATGTC 1104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Serreco, Ginette
APPLICANT: Serreco, Ginette
TITLE OF INVENTION: 88 KDA TUMORICENIC GROWTH FACTOR AND ANTAGONISTS
FILE REFERENCE: 29996.488/P001-A
FULR REPERENCE: 29996.488/P001-A
CURRENT APPLICATION NUMBER: 08/08/3,862
EARLIER APPLICATION NUMBER: 08/08/3,862
EARLIER FILING DATE: 1997-05-23
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (1)..(19) OTHER INFORMATION: Internal peptide of human GP88 used to develop OTHER INFORMATION: neutralizing anti-human GP88 monoclonal antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EPITHELINS: NOVEL CYSTEINE-RICH GROWTH MODULATING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA.
                                                                                                     1456 TGCCCGGCTGCTACACCTGCAACGTGAAGGCTCGA 1491
                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
Indels:
US-09-824-647-16 (1-2095) x PCT-US91-02321-6 (1-589)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-824-647-16 (1-2095) x US-08-991-862-6 (1-19)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC COMPATIBLE OPERATING SISTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 8, Application US/07668648
Patent No. 5416192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Shoyab, Mohammed
APPLICANT: Plowman, Gregory D.
                                                                                                                                                                                                          Sequence 6, Application US/08991862
Patent No. 6309826
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19.00
100.00%
100.00%
2.74%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 10036
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Human granulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-07-668-648-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-991-862-6
                                                                                                                                                                                                      us-08-991-862-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 16
                                                                                                                                                                                     RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              å
                                                                              셤
                                                                                                                 ö
```

```
APPLICANT: Shoyab, Mohammed AppLICANT: Shoyab, Mohammed ApPLICANT: Plowman, Gregory D. TITLE OF INVENTION: EPTTHELINS: NOVEL CYSTEINE-RICH GROWTH TITLE OF INVENTION: MODULATING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          892 TATACCTGCTGCCGTCTACAGTCGGGGGCCTGGGGCTGCTGCCTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SUGTREMY APPLICATION DATA:
APPLICATION NUMBER: US/08/429,998
                                                                                                                                                                                                                                                                                                                                                                                                      Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-824-647-16 (1-2095) x US-07-668-648-8 (1-179)
                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
                                                                            ALONGE, MASTOCK, S. Lealie

RAME: MISTOCK, S. Lealie

REGISTRATION NUMBER: 18 872

REGISTRATION INFORMATION:

TELECHONE: (212)790-9090

TELEPRANE: (212) 869-9741

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/668,648
FILING DATE: 13-MAR-1991
ATTORNET/AGENT INFORMATION:
NAME: MISTOCK, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 5624-161-99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 27-APR-1995
CLASSIEICATION: 514
IOR ADDITOR
APPLICATION NUMBER: US/07/668,648
FILING DATE: 19910819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 8, Application US/08429998 Patent No. S885961 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (212) 869-9741
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 179 amino acids amino acid
                                                                                                                                                                                                                                                                                                                                                                                                            100.00%
100.00%
2.31%
                                                          ATTORNET/AGENT INFORMATION: NAME: Misrock, S. Leslie
                                                                                                                                                                                                                                    . 179 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: protein US-07-668-648-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: New York STATE: New York
                                                                                                                                                                                                                                                                                linear
                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity: Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10036
```

```
66 TyrThrCysCysArgLeuGlnSerGlyAlaTrpGlyCysCysProPhe 81
                                                                                                                                                                                                                        892 TATACCTGCTGCCGTCTACAGTCGGGGCCTGGGGGCTGCTGCCCTTTT 939
                                                                                                                                                                                                                                            NOVEL CYSTEINE-RICH GROWTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                    Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-824-647-16 (1-2095) x US-08-431-333-8 (1-179)
                                                                                                                                                                                        US-09-824-647-16 (1-2095) x US-08-429-998-8 (1-179)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
                                                                                                                                         Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels:
                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Shoyab, Monammer APPLICANT: Shoyab, Monamen, Gregory D. APPLICANT: Plowman, Gregory D. TITLE OF INVENTION: EPITHELINS: NOVEL CYTILE OF INVENTION: MODULATING PROFEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Pennie & Edmonds
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TION NUMBER: US 07/668,648
DATE: 13-MAR-1991
AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/431,333
FILING DATE: 27-APR-1995
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                             Sequence 8, Application US/08431333 Patent No. 5965723 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misrock, S. Leslie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                00.00%
                                                                                    16.00
100.00%
100.00%
2.31%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (212)790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 179 amino acids amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (212) 869-9741 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sest Local Similarity:
                                                                                                                      Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New York
; MOLECULE TYPE:
US-08-429-998-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
                                                                                                    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                   Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: Ne
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JS-08-431-333-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match:
                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No.:
                                                                       ..
Q
                                                                                                                                                                                                                                                                                              RESULT 18
                                                                                                                                                                                                                            Š
```

```
APPLICANT: Serrero, Ginette
TITLE OF INVENTION: 88 KBA THORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REFERENCE: 29996.488/P001-A
CURRENT APPLICATION NUMBER: US/08/991,862
                                                                    Gregory D. EPITHELINS: NOVEL CYSTEINE-RICH GROWTH MODULATING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66 TyrThrCysCysArgLeuGlnSerGlyAlaTrpGlyCysCysProPhe 81
                                                                                                                                                                                                                                                                                                                                                                                                      Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-824-647-16 (1-2095) x PCT-US91-02321-8 (1-179)
                                                                                                                            TOTAL SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF STREET: 3005 First Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/02321
FILING DATE: 19910403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EARLIER APPLICATION NUMBER: 08/863,862
Sequence 8, Application PC/TUS9102321
GENERAL INFORMATION:
APPLICANT: Shoyab, Mohammed
APPLICANT: Plowman, Gregory D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7, Application US/08991862 Patent No. 6309826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 514
ATTORNEY AGENT INFORMATION:
NAME: POOL, Brian W.
REGISTRATION NUMBER: 32,928
                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EARLIER FILING DATE: 1997-05-23
NUMBER OF SEQ ID NOS: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT FILING DATE: 1998-08-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.00%
100.00%
2.31%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein PCT-US91-02321-8
                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Ver.
                                                                                                                                                                                                                                                Washington
                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                      TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AMINO ACID
                                                                                                                                                                                                                         CITY: Seattle
STATE: Washingt
COUNTRY: USA
ZIP: 98121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -08-991-862-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 7
```

```
Conservative:
Mismatches:
                                                                                                                                                                                                                                              APPLICANT: SCOTT, RANDY W.
APPLICANT: GLEICH, GERALD J.
APPLICANT: WILDE, CRAIG G.
TITLE OF INVENTION: BASOPHIL GRANULE PROTEINS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: F4sh & Richardson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  865 GACATGGAGGTGAGCTGCCCAGATGGCTATACC 897
                                                                          865 GACAIGGAGGIGAGCIGCCCAGAIGGCIAIACC 897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No. 5470825

APPLICANT: SCOTT, RANDY W.; GLEICH, GERALD J.;
WILLDE, CRAIG G.

TITLE OF INVENTION: BASOPHIL GRANULE PROTEINS
NUMBER OF SEQUENCES: 8
                                                                                                5 ASPMETGIUVALSErCysProAspGlyTyrThr 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JS-09-824-647-16 (1-2095) x US-08-573-675-2 (1-15)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 AspMetGluValSerCysProAspGlyTyrThr 15
                                     US-09-824-647-16 (1-2095) x US-08-245-853-2 (1-15)
                                                                                                                                                                                                                                                                                                                                        STREET: 2200:Sand Hill Road, Suite 100 CITY: Menlo Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 06514/013002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 322-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING ASCIII
SOFTWARE: ASCIII
CURRENARE: ASCIII
APPLICATION DATA:
RILING DATE: 18-DEC-1995
FILING DATE: 18-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,813
FILING DATE: 11-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: GREGG, VALETA
REGISTRATION NUMBER: 35.127
                                                                                                                                                                      US-08-573-675-2 , Sequence 2, Application US/08573675 ; Patent No. 5747283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (415) 854-0875
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 94025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-573-675-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3470825-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              score:
                                     NAME/KEY: PEPTIDE
LOCATION: (1). (14).
OTHER INFORMATION: Internal peptide of human GP88 used to develop
OTHER INFORMATION: neutralizing anti-human GP88 monoclonal antibody
                                                                                                                                                                                                                                                                                                                                                       1708 GCACGCAGGGTACCAAGTGTTTGCGCAGGGAGGCCCCGCGC 1749
                                                                                                                                                                                                                                                                                                                                                                           1 AlaArgArgGlyThrLysCysLeuArgArgGluAlaProArg 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                 Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: SCOTT, RANDY W.
APPLICANT: GLEICH, GERALD J.
APPLICANT: WILDE, CRAIG G.
TITLE OF INVENTION: BASOPHIL GRANULE PROTEINS
WOMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative:
Mismatches:
                                                                                                                                                                                                                                    Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                US-09-824-647-16 (1-2095) x US-08-991-862-7 (1-14)
                                                                                                                                                                            Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 28,807
REFERENCE/DOCKET NUMBER: 24842-20059.20
FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,813
FILING DATE: 11-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: BOZICEVIC, KARL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/245,853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: MORRISON & FOERSTER
755 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/08245853
Patent No. 5476839
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                      0.000321
14.00
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.159 · 11.00 · 100.00% 100.00% 1.59%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15 amino acids
                                                                                                                                                                                                                                                      .02%
ORGANISM: Human granulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
                                                                                                                                                                                                                                    Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score:
Percent Similarity:
Best Local Similarity
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                             ercent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
                                                                                                                                                          Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-245-853-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-245-853-2
                                                                                                               us-08-991-862-7
                                                                                                                                                                                                                                                      Query Match:
                                                                                                                                                                          red. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 21
                                                                                                                                                                                                                                                                                                                                                       ŏ
                                                                                                                                                                                                                                                                                                                                                                                              셤
```

Hi.

```
193
0
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/106,507
                                                                                                                                                                                                                                                US-09-824-647-16 (1-2095) x US-08-584-031-11 (1-151)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative:
                                                                                                                                                        Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-824-647-16 (1-2095) x US-08-106-507-2 (1-193)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches:
Indels:
                                                                                                                                                                           Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
                                                                                                                     Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps:
                                                                                                                                                                                                           Gaps:
                                                                                                                                                                                                                                                                                  1734 CAGGGAGGCCCCGCGCTGGGACGC 1757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/941,648
FILING DATE: 08-SEP-1992
ATTORNEY/AGENT: INFORMATION:
NAME: WIGHT, CHRISTOPHER L.
                                                                                                                                                                                                                                                                                                    32 GlnGlyGlyProAlaLeuGlyArg 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: CD27 LIGAND NUMBER OF SEQUENCES: 10 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                        og US/08106507
                                                                                                                                                                                                                                                                                                                                                                                                                                                               GOODWIN, RAYMOND G.
GIRI, JUDITH G.
ARMITAGE, RICHARD J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: WIGHT, CHRISTOPHER L
REGISTRATION NUMBER: 31,68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.00%
100.00%
1.15%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                KMANN, M. P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORM?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 193 amino aci
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: protein US-08-106-507-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO
                                 TYPE: PRT
ORGANISM: Homo sapiens
US-08-584-031-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity:
                                                                                                                                                       Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: WA COUNTRY: US ZIP: 98101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                      Alignment Scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT
SEQ ID NO 11
                                                                                                                                                                                              Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                               Patent No
GENERAL
                                                                                                                         ..
0
                                                                                                                                                                                                                                                                                                                                                                                            equence
                                                                                                                                                                                                                                                                                                                                                         RESULT 26
                                                                                                                                             Score:
                                                                                                                                                                                                                                                                                    ð
                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Cole, Stewart

APPLICANT: Bulbiteser-Brosch, Roland
APPLICANT: Bulbiteser-Brosch, Roland
APPLICANT: Billault, Alain
APPLICANT: Billault, Alain
TITLE OF INVENTION: METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INV
TITLE OF INVENTION: LIBRARY APPLICATION TO THE DETECTION OF MYC;
FILE REPERRORE: 3495-0169
CURRENT APPLICATION NUMBER: US/09/060,756
CURRENT FILING DATE: 1998-04-16
NUMBER OF SEQ ID NOS: 743
SOFTWARE: PALENTIN Ver. 2.0
SEQ ID NO 732
                                                                                                                                                                                              Length:
Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-824-647-16 (1-2095) x US-09-060-756-732 (1-29
                                                                                                                                                                                                                                                                                                                                                         865 GACATGGAGGTGAGCTGCCCAGATGGCTATACC 897
                                                                                                                                                                                                                                                                                                                                                                           5 AspMetGluValSerCysProAspGlyTyrThr 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches:
Indels:
                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                   Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/08/584,031A CURRENT FILING DATE: 1996-01-09
                                                                                                                                                                                                                                                                                     Gaps:
                                                                                                                                                                                                                                                                                                                     US-09-824-647-16 (1-2095) x 5470825-2 (1-15)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1231 GCTGGGGCAGCAGTGCTGGTGGT 1208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 AlaglyGlySerSerAlaGlyGly 13
 ...ек: US/08/259, 564
35-JUN-1994
N Dam:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      dS/08584031A
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 732, Application US/09060756 Patent No. 6183957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: APO-2 LIGAND FILE REFERENCE: 11669.22US03
                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 551,263
FILING DATE: 10-JUL-1990
SEQ ID NO:2:
                                                                                                                                                                                                                               100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Mycobacterium sp. US-09-060-756-732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Ver. 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                   ..598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 11, Application
Patent No. 6030945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 17
                  APPLICATION NUMBER
FILING DATE: 15-JUI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No. 6030945 CGENERAL INFORMATION: CAPPLICANT: Ashkenazi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
                                                                                                                                                                           Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                us-09-060-756-732
                                                                                                                         LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-584-031-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 29
TYPE: PRT
                                                                                                                                                                                                                                                                   Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match:
                                                                                                                                                                                                 :.
Q
                                                                                                                                    5470825-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ð
```

```
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8, Application US/08446922
Patent No. 5716805
GENERAL INFORMATION:
APPLICANT: Spriggs, Melanie
APPLICANT: Stinivasan, Subhashini
TITLE OF INVENTION: Methods of Preparing Soluble, Oligomeric
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/106,507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-824-647-16 (1-2095) x US-08-106-507-10 (1-216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION UNDRER: US 07/941,648
FILING DATE: 08 SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: WIGHT, CHRISTOPHER L.
REFERENCE/DOCKET NUMBER: 2809-A
TELECHONE: 206-587-0430
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99 GlnGlyGlyProAlaLeuGlyArg 106
                                         76 GlnGlyGlyProAlaLeuGlyArg 83
                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: BECKNANN, M. P.
APPLICANT: GOODWIN, RAYMOND G.
APPLICANT: GIST, JUDITH G.
APPLICANT: ARMITAGE, RICHARD J.
ITTLE OF INVENTION: CD27 LIGAND
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                         SEE: IMMUNEX CORPORATION: 51 UNIVERSITY STREET SEATTLE
                                                                                                                                          Sequence 10, Application US/08106507 Patent No. 5573924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.00%
100.00%
1.15%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             216 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: protein US-08-106-507-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  98101
                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                  RESULT 27
US-08-106-507-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-446-922-8
                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                  STREET:
                                                                                                                                                                                                                                                                                                                                                                                                            STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     red. No.:
```

```
PCT-US93-10034-8
: Sequence 8, Application PC/TUS9310034
; GENERAL INFORMATION:
: APPLICANT: Spriggs, Melanie
: APPLICANT: Srintvasan, Subhashini
: TITLE OF INVENTION: Methods of Preparing Soluble, Oligomeric
: TITLE OF INVENTION: Proteins
: NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 98101

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                             MEDIUM TYPE: Floppy disk COMPUTER: Apple MacIntosh OPERATING SYSTEM: Apple Operating System 7.1 SOFTWARE: MICROSOft Word for Apple, Version CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-824-647-16 (1-2095) x US-08-446-922-8 (1-216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels:
                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/107,353
FILING DATE: 08-13-93
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1734 CAGGGAGGCCCCGCGCTGGGACGC 1757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99 GlnGlyGlyProAlaLeuGlyArg 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PCT/US93/10034
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 34,693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION TELEPHONE: (206)587-0430
                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.00%
100.00%
1.15%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 216 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (206)233-064
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
Query Match:
                                  CITY: SC. STATE: WA COUNTRY: USA
                                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-446-922-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE:
```

```
0000
0000
0000
                                      Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-824-647-16 (1-2095) x US-09-022-940-3 (1-230)
                                                                                                                                    US-09-824-647-16 (1-2095) x US-08-844-120-3 (1-230)
                                                          Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Shah, Purvi
APPLICANT: Murry, Lynn E.
TITLE OF INVENTION: HUMAN LYSOPHOSPHOLIPASE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Incyte Pharmaceuticals, Inc.
                                                                                              Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1686 CTGTCCTGCTGGCTTCCGCTGCGC 1709
                                                                                                                                                                        1686 CTGTCCTGCTGCTTCCGCTGCGC 1709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             142 LeuSerCysTrpLeuProLeuArg 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/022,940 FILING DATE: Filed Herewith PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                     Sequence 3, Application US/09022940
Patent No. 5965423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Billings, Lucy J. REGISTRATION NUMBER: 36 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 3174 Porter Dr
Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 650-845-416:
INFORMATION FOR SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
                                      Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-022-940-5
```

```
onservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-824-647-16 (1-2095) x US-09-216-001-3 (1-230)
                                            SOFTWARE: FASTEM:. DOS
SOFTWARE: FASTEED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/216,001
FILLING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Hilman, Jennifer L.
APPLICANT: Shah, Purvi
APPLICANT: Murry, Lynn E.
APPLICANT: HUNTY, LYNN E.
NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: DOS
STUTWARE: PESASEDO for Windows Version 2.0
CUCRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/216,386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ndels:
                                                                                                                                                                                                                                                            NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0329 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1686 CTGTCCTGCTGCTTCCGCTGCGC 1709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   142 LeuSerCysTrpLeuProLeuArg 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/022,940
                                                                                                                                                              CLASSIFICATION:
RICHARDA APPLICATION DATA:
APPLICATION, NUMBER: 08/878,862
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/09216386 Patent No. 6093561 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM Compatible
                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3: Incyte Phar
3174 Porter Dr
                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
LENGTH: 230 amino aci
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM MEDIUM TYPE: Disket
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: singl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LIBRARY: GenBank
CLONE: 1552244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IMMEDIATE SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ercent Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -09-216-386-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET:
                                                                                                                                                                                                                                                                                                                                                                                             TELEX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
**APPLICANT: #111man, Jennifer L.

**APPLICANT: Shah, Purvi B.

**APPLICANT: Murry, Lynn E.

**TITLE OF INVENTION: HUMAN LYSOPHOSPHOLIPASE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:

**ADDRESSEE: Incyte Pharmaceuticals, Inc.

**STREET: 3174 Porter Dr.

CITY: Palo Alto

**STATE: CA

COUNTE: CA

COUNTE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: COILEY, Neil C.
APPLICANT: MULTY, Lynn E.
TITLE OF INVENTION: NEW HUMAN LYSOPHOSPHOLIPASE
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-824-647-16 (1-2095) x US-09-022-940-5 (1-230)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1686 CIGICCIGCIGCTICCGCIGCGC 1709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         142 LeuSerCysTrpLeuProLeuArg 149
                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/022,940 FILING DATE: Filed Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Application US/09216001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Billings, Lucy J.
REGISTRATION UDMBER: 36,74
REFERENCE,POCKET NUMBER: PELECOMMUNICATION INFORMATION
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hillman, Jennifer
                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shah, Purvi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear
US-09-022-940-5 .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE:
```

ð

```
Pred. No.:
                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-824-647-16 (1-2095) x US-09-216-386-3 (1-230)
                                                                                                                                                                                                                                                                                                                                                             Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Hillman, Jennifer L.
APPLICANT: Shah, Purvi
APPLICANT: Murry, Lynn E.
TITLE OF INVENTION: HUMAN LYSOPHOSPHOLIPASE
NOMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                    Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1686 CTGTCCTGCTGCTTCCGCTGCGC 1709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/216,386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/022,940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           se 5, Application US/09216386
No. 6093561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Billings, Lucy J. 18 REGISTRATION NUMBER: 36,749 REFERENCE/DOCKET NUMBER: PF. TELECOMMUNICATION INFORMATION:
                                                                   ELECOMMUNICATION INFORMATION TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                         TELEPAX: 650-843. TELEPAX: 650-843. INPORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 230 anino acid TVPE: amino acid TVPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 3174 Porter Dr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94304
                                                                                                                                                                                                                                                                                   Alignment Scores:
                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                          US-09-216-386-3
                                                                                                                                                                                                                                                                                                                         Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
```

Alignment Scores

```
.0000
0000
                                                                                                                                                                                                                                                                                                                                       APPLICANT: Corley, Neil C.
APPLICANT: Murry, Lynn E.
TITLE OF INVENTION: NEW HUMAN LYSOPHOSPHOLIPASE
NUMBER OF SEQUENCES: 4
                                 Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                 US-09-824-647-16 (1-2095) x US-09-216-386-5 (1-230)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-824-647-16 (1-2095) x US-08-878-862-3 (1-230)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NSTEM: DOS
FastSEQ for Windows Version 2.0
 Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                             Incyte Pharmaceuticals, Inc
                                                                                    Gaps:
                                                                                                                                                   1686 CIGICCIGCIGGCIICCGCIGCGC 1709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1686 CIGICCIGCIGCTICCGCIGCGC 1709
                                                                                                                                                                    142 LeuSerCysTrpLeuProLeuArg 149
                                                                                                                                                                                                                                                   Sequence 3, Application US/08878862 Patent No. 6143544
                                                                                                                                                                                                                                                                                                         APPLICANT: Hillman, Jennifer L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION TELEPHONE: 415-855-0555 TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                            3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3: Diskette
IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 230 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Billings, Lucy J
REGISTRATION NUMBER: 3
REFERENCE/DOCKET NUMBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               URRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM MEDIUM TYPE: Disket
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Palo Alto
                                   Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1552244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alignment Scores:
                                                                                                                                                                                                                                       -08-878-862-3
                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: F
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ô
```

RESULT 37

```
PRIOR APPLICATION NUMBER: 60/080,563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
                                                                                                                                                                                                        Aliqument Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-282-305-14
                                                                                                                               TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match:
DB:
                                                                                                                                                                                                                         No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      red. No.:
                                                                                                                                                                                                                                                 Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Rudolf Jung
APPLICANT: Francois Barrieu
TITLE OF INVENTION: Maize Aquaporins and Uses Thereof
FILE REFERENCE: 0919
                                                                                                                                              APPLICANT: Hillman, Jennifer L.
APPLICANT: Shah, Purvi
APPLICANT: Shah, Purvi
APPLICANT: Murry, Lynn E.
ATTLE OF INVENTION: NOVEL HUMAN LYSOPHOSIPASE
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-824-647-16 (1-2095) x US-09-213-394-3 (1-230)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT, APPLICATION NUMBER: US/09/372,422A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1686 CTGTCCTGCTGGCTTCCGCTGCGC 1709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/844,120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/213,394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 28, Application US/09372422A
Patent No. 6313375
GENERAL INFORMATION:
                                                                                        Sequence 3, Application US/09213394
Patent No. 6319701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET UNBER: PF-TELECOMMUNICATION: TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                            STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                               IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51.8
8.00
100.00%
100.00%
1.15%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   230 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM:
                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDAGE. Gene-
LIBRARY: Gene-
552244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                       94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JS-09-372-422A-28
                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JS-09-213-394-3
                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match:
```

RESULT 38

core:

```
APPLICANT: Baldwin, Donald A.
APPLICANT: Briggs, Steven P.
APPLICANT: Crane, Virginia C.
TITLE OF INVENTION: Maize Histone Deacetylases And Their Uses FILE REFERENCE: 5718-44,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-372-422A-26
Sequence 26, Application US/09372422A
Sequence 26, Application US/09372422A
GENERAL INFORMATION:
APPLICANT: Rudolf Jung
APPLICANT: Francois Barrieu
TITLE OF INVENTION:
TITLE OF INVENTION:
APPLICANT: Adaption and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-824-647-16 (1-2095) x US-09-372-422A-26 (1-272)
                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-824-647-16 (1-2095) x US-09-372-422A-28 (1-257)
                                                                                                                                                                                                                                                                                            Matches:
                                                                                                                                                                                                                                                                         Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/372,422A CURRENT FILMS DAFE: 1999-08-11 PRICATION NUMBER: US 60/098,692 PRIOR FILING DATE: 1998-08-31
PRIOR APPLICATION NUMBER: US 60/098,692
PRIOR FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 49
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 28
LENGTH: 257
TAPE: APPLICATION NUMBER: LENGTH: 257
TAPE: APPLICATION NUMBER: LENGTH: 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 49
SOFWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 26
LENGTH: 272
                                                                                                                                                                                                                                                                                                                                                                               Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/282,305
CURRENT FILING DATE: 1999-03-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1362 GCAGCTGGTGTGCTGGTCACAGCC 1339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1362 GCAGCTGGTGTGCTGGTCACAGCC 1339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72 AlaAlaGlyValLeuValThrAla 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 14, Application US/09282305
Patent No. 6287843
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50.4
8.00
100.00%
                                                                                                                                                                                                                                                                                                                100.00%
100.00%
1.16%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: 0919
                                                                                                                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Zea mays US-09-372-422A-26
                                                                                                                                                                                     ; ORGANISM: Zea mays
US-09-372-422A-28
```

```
SODIUM-DEPENDENT
                                                                                                                                                                                                                                                                                                                                                                   US-09-824-647-16 (1-2095) x US-09-060-756-727 (1-318)
                                                                                                                                                                                                                                                          Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Lal, Preetl
APPLICANT: Bandman, Olga
TITLE OF INVENTION: NOVEL HUMAN SODIUM-DEPEN
TITLE OF INVENTION: PHOSPHATE CO-TRANSPORTER
                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
                                                                                                                                                                                                                                          Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                        Indels:
                                                                                                                                                                                                                                                                                                                              Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/605,118
FILING DATE: Filed Herewith
CLASSIFICATION 1435
PRIOR APPLICATION TOWNER:
APPLICATION NUMBER:
APPLICATION WOMBER:
APPLICATION WOMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0221 US
TELECOMENULCATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                             1231 GCTGGGGCAGCAGTGCTGGTGGT 1208
                                                                                                                                                                                                                                                                                                                                                                                                                                                66 AlaglyglyşerSerAlaGlyGly 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/08805118 Patent No. 5985604
  CURRENT FILING DATE: 1998-04-16
NUMBER OF SEQ ID NOS: 743
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 727
LENGTH: 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: anino acids
TYPE: anino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                           ; TYPE: PRT
; ORGANISM: Mycobacterium sp.
US-09-060-756-727
                                                                                                                                                                                                                                                                                                        .168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47.4
8.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NEORMATION FOR SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BRAITUT02
                                                                                                                                                                                                                                                                                  Best Local Similarity:
                                                                                                                                                                                                                                                            Percent Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
Pred. No.:
Score:
                                                                                                                                                                                              Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JS-08-805-118-1
                                                                                                                                                                                                                                                                                                      Query Match:
                                                                                                                                                                                                                       Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST FROM TITLE OF INVENTION: THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA TITLE OF INVENTION: LIBRARY APPLICATION TO THE DETECTION OF MYCOBACTERIA FILE REFERENCE: 3495-0169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Baldwin, Donald A.
APPLICANT: Briggs, Steven P.
APPLICANT: Crane, Virginia C.
TITLE OF INVENTION: Maize Histone Deacetylases And Their Uses
                                                                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                   US-09-824-647-16 (1-2095) x US-09-282-305-14 (1-302)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-824-647-16 (1-2095) x US-09-282-305-12 (1-305)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: 5718-44,
CURRENT APPLICATION NUMBER: US/09/282,305
CURRENT FILING DATE: 1999-03-31
PRIOR APPLICATION NUMBER: 60/080,563
PRIOR FILING DATE: 1998-04-03
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
SERIOR DATE: 1305
                                                                                                                                                                                                                                                                                                        Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/060,756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1822 AGGCTGCAGAGTCTTCAGTACTG 1799
                                                                                                                                                                                                                                                                                                                                                                                                           1822 AGGGCTGCAGAGTCTTCAGTACTG 1799
                                                                                                                                                                                                                                                                                                                                                                                                                                   209 ArgalaAlaGluSerSerValLeu 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    209 ArgAlaAlaGluSerSerValLeu 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 727, Application US/09060756 Patent No. 6183957 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Cole, Stewart
APPLICANT: Buchirlesar-Brosch, Roland
APPLICANT: Gordon, Stephen
APPLICANT: Billault, Alain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 12, Application US/09282305 Patent No. 6287843
PRIOR FILING DATE: 1998-04-03
NUMBER OF SEQ ID NOS: 18
                                                                                                                                                                                                                                                        100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                00.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         168
                                                                                                                                                                                                                                                                                                   1.16%
                                                                                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Zea mays
US-09-282-305-12
                                                                                                           ; TYPE: PRT
; ORGANISM: Zea mays
US-09-282-305-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-060-756-727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
                                                                                                                                                                                            Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JS-09-282-305-12
                                                               SEQ ID NO 14
LENGTH: 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
                                                                                                                                                                                                                                                                                               Query Match:
DB:
                                                SOFTWARE:
                                                                                                                                                                                                                    So.
```

us-09-824-647-16.std.rai

Tue Jul

```
GENERAL NO. 0.5000.
GENERAL INFORMATION:
APPLICANT: LAI, Preeti
APPLICANT: Bandman, Olga
TITLE OF INVENTION: NOVEL HUMAN SODIUM-DEPENDENT
TITLE OF INVENTION: PHOSPHATE CO-TRANSPORTER
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative:
Mismatches:
Indels:
                                                                                              US-09-824-647-16 (1-2095) x US-08-805-118-1 (1-401)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-824-647-16 (1-2095) x US-09-391-958-1 (1-401)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Incyte Pharmaceuticals, Inc
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY CARENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0221 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               380 CCATCCAGTGCCCTGATAGTCAGT 403
                                                                                                                                      380 CCATCCAGTGCCCTGATAGTCAGT 403
                                                                                                                                                          281 ProSerSerAlaLeuIleValSer 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 281 ProSerSerAlaLeuIleValSer 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/805,118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/391,958
                                                                                                                                                                                                                                                       Sequence 1, Application US/09391958 Patent No. 6326207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION TELEPHONE: 415-855-0555 TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.00%
100.00%
1.15%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 401 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 3174 POR
Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ΩS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ర
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match:
                                         Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
```

RESULT 45

```
APPLICANT: FOLCE, OFFICE M.
APPLICANT: Tauer, Peter M.
APPLICANT: Tauer, Peter M.
APPLICANT: Thomas, Minston
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Megabase Transcript Map: No. 5872237el
NUMBER OF SEQÜENCES: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                              ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-824-647-16 (1-2095) x US-08-724-394A-11 (1-480)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 017957-000100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/724,394A FILING DATE: 01-02T-1996 CLASSIFICATION: 536 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           380 CCATCCAGTGCCCTGATAGTCAGT 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    360 ProSerSerAlaLeuIleValSer 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search completed: July 7, 2003, 15:49:11
Job time: 57 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: Region
LOCATION: 1..480
OTHER INFORMATION: /note= "NPT4"
Sequence 11, Application US/08724394A
Patent No. 587237
GENERAL INFORMATION:
APPLICANT: Feder, John N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.00%
100.00%
1.15%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 480 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA,
2IP: 94111-3834
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JS-08-724-394A-11
```

Porphyromona ging Mouse GP88 autocri Human API-108 tryp PDGF inhibitor (PG Human TSH receptor Chlamydial VDI epi Oestrogen receptor Peptide sensor TUK

AAW85479 ABB52180 AAM97797 AAR67120 AAR73224 AAR66383

Melan A/MART epito Coactivator leucin Human cancer antig

LXXLL signature mo Vascular endotheli Melanoma-specific

E.Coli 50s ribosom

Peptide sensor TUK HLA Class I motif Cancer testis tumo

Human cancer antig Human cancer antig

AAY42208 AAY06031 AAY06039 AAY06035

AAY13578

AAY10533

AAB85642 AAB85641

AAU09998 AAU73544 AAR82184

AAW42528

Human GP88 autocri BGP N-terminal fra Basophil granule p N-terminal amino a

N-terminal amino

Description

SUMMARIES

Query Match Length

```
υç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -MODEL-frame-Large model -DEV-xlp
-Q-Cgn2_1/USPTO_spool/US09824647/runat_07072003_154758_26607/app_query.fasta_1.2247
-Q-Cgn2_1/USPTO_spool/US09824647/runat_07072003_154758_26607/app_query.fasta_1.2247
-DB-A_Geneseq_101002 - GFWT-stastan -SUFFTX=1.in.rag -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS-blts -START=1 -END=-1 -MATRIX-ol190 -TRAS-human40.cd1
-LIST=45 -DOCALIGN=200 -THR_SCORE-quality -THR_MINH=1 -ALIGN=45 -MODE-LOCAL
-USRT=47 -DOCALIGN=200 -THR_SCORE-quality -THR_MINH=1 -ALIGN=45 -MODE-LOCAL
-USRT=050924647 -GCGN_1_1.149_erunat_07072003_154758_26607 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NGG_SCORES-0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELOP=7
                                                                                                                               July 7, 2003, 15:51:35; Search time 91 Seconds (without alignments) 6135.386 Million cell updates/sec
                                                                                                                                                                                                                        US-09-824-647-16
694
1 cgcaggcagaccatgtggac.....ataaagtttgtcacttctt 2095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /SIDS2/gogdata/geneseq/geneseqp-emb1/AA1990 DAT:*
/SIDS2/gogdata/geneseq/geneseqp-emb1/AA1990 DAT:*
/SIDS2/gogdata/geneseq/geneseqp-emb1/AA1991 DAT:*
/SIDS2/gogdata/geneseq/geneseqp-emb1/AA1993 DAT:*
/SIDS2/gogdata/geneseq/geneseqp-emb1/AA1993 DAT:*
/SIDS2/gogdata/geneseq/geneseqp-emb1/AA1994 DAT:*
/SIDS2/gogdata/geneseq/geneseqp-emb1/AA1995 DAT:*
/SIDS2/gogdata/geneseq/geneseqp-emb1/AA1997 DAT:*
/SIDS2/gogdata/geneseq/geneseqp-emb1/AA1997 DAT:*
/SIDS2/gogdata/geneseq/geneseqp-emb1/AA1999 DAT:*
/SIDS2/gogdata/geneseq/geneseqp-emb1/AA1999 DAT:*
/SIDS2/gogdata/geneseq/geneseqp-emb1/AA1999 DAT:*
/SIDS2/gogdata/geneseq/geneseqp-emb1/AA1999 DAT:*
/SIDS2/gogdata/geneseq/geneseqp-emb1/AA2000 DAT:*
/SIDS2/gogdata/geneseq/geneseqp-emb1/AA2001 DAT:*
/SIDS2/gogdata/geneseq/geneseqp-emb1/AA2001 DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1989.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1989.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1989.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DAT: *
GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

    protein search, using frame_plus_n2p model

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              seqs, 133250620 residues
                                                                                                                                                                                                                                                                                                                   OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A_Geneseq_101002:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Minimum DB seq length: 0
Maximum DB seq length: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Command line parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            908470
                                                                                                                                                                                                                                                     Perfect score:
                                                                                                                                                                                                                                                                                                                        Scoring table:
                                                                                    OM nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Word size:
                                                                                                                                                                                                                                                                          Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jatabase
                                                                                                                                    Run on:
```

Synthetic peptide Synthetic peptide HLA binding TADG-1 HLA binding TADG-1 HLA binding TADG-1 HLMan NY-ESO-1 HLA Immunogenic peptid

Cytomodulating lip Human cancer antig Human cancer antig

New bradykinin ana TSK protein tyrosi Chlamydial MOMP VD

D-form Interleukin

0.9 10 20 AAW3379 Peptide sensor TUK 0.9 10 20 AAW93872 Bifidobacterium bi 0.9 10 20 AAW74014 C. trachomatis MOM 0.9 10 22 AAG67204 Cancer testis tumo	ALIGNMENTS	T 1 077 AAR35077 standard; protein; 15 AA.		(first entry)	N-terminal amino acid sequence of human granulin A.	Transforming frowth factor e; cell proliferation; mitogen.				92WO-US08417.
		1 7 R35077 sta	AAR35077;	09-AUG-1993	terminal a	ansforming	Homo sapiens.	WO9307173-A.	15-APR-1993.	02-OCT-1992;
444		AR35077	2	60	ż	Tr	e H	<u>8</u>	15	03

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ACOLOGICA CONTRACTOR C

```
8; Page 45; 86pp; English.
                                                                                                                                                                                                Best Local Similarity:
                                                                                                                                             14 AA;
                                                                                                                                                                                         Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                  Homo saptens
                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-JUL-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-JUL-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Leukaemia(s)
                                                                                                                                                                                                                                                                                                                                                                                                                  WO9201000-A.
                                                                                                                                                                                                                                                                                                                                            19-MAY-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                   23-JAN-1992.
                                                                                                                                                               Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Scott RW,
                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                            AAR20737;
 Example
                                                                                                                                                                                                            Query Match:
                                                                                                                                                                          ..
Q
                                                                                                                                                                                                                                                                                         RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                        Composition containing antagonist of growth factor GP88 - useful for treating cancer and viral diseases and also for diagnosing disease
                                                                                                                                    Tighe is a glycoprotein with an Mr of about 25,000. The partial amino acid sequence of purified bother Tighe indicated no homology to other known growth factors. However the N-terminal sequence exhibits considerable amino acid sequence identity to the deduced N-terminal amino acid sequence of human granulin A and the N-terminus
                                                                                                                                                                                                                                                                                                                                                                                                                                   ranulin; epithilin; human; growth factor; autocrine; tumour; viral infection; antagonist; therapy; diagnosis; antigen;
                                                                                 Transforming growth factor E produced in commercial quantities used for wound healing and burns treatment, comprises monomeric protein which acts as mitogen for fibroblasts
                                                                                                                                                                                                                                                                                                             853 GATGTGAAATGTGACATGGAGGTGAGCTGCCCAGATGGCTATACC 897
                                                                                                                                                                                                                                                                                                                                                                                                                    Human GP88 autocrine growth factor antigenic peptide A14R.
                                                                                                                                                                                                                                                                                                                       0000
                                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                  Indels:
                                                                                                                                                                                                                                                                            Gaps:
                                                                                                                                                                                                                                                                                             US-09-824-647-16 (1-2095) x AAR35077 (1-15)
                              (UYGE-) UNIV GEORGIA RES FOUND INC.
                                                                                                                                                                                                                                                                                                                                                                   Z
                                                Parnell PG;
                                                                                                                      Example; Page 49; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                 AAW85481 standard; Peptide; 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               from altered GP88 expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                970S-0991862.
970S-0863079.
                                                                                                                                                                                                                                4.48e-05
15.00
100.00%
100.00%
2.16%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98WO-US10555
              91US-0770585.
                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-045276/04.
                                                 Mcgraw RA,
                                                                  WPI; 1993-134386/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ġ
                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                      15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SERR/) SERRERO
                                                                                                                                                                                                                                                                                                                                                                                                                                       granulin;
                                                                                                                                                                                      of epithelin 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-DEC-1997;
23-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9852607-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                     15-MAR-1999
                                                                                                                                                                                                                        Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-NOV-1998.
              03-OCT-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                  Halper J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          antibody.
                                                                                                                                                                                                                                                                                                                                                                                    AAW85481;
                                                                                                                                                                                                                                                                                                                               _
                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                  cancer;
                                                                                                                                                                                                                                                                  Query Match:
DB:
                                                                                                                                                                                                                                  ..
9
                                                                                                                                                                                                                                                                                                                                                                                                                                        GP88;
                                                                                                                                                                                                                                                                                                                                                  RESULT 2
                                                                                                                                                                                                                                                                                                                                                           AAW85481
                                                                                                                                                                                                                                           Score:
                                                                                                                                                                                                                                                                                                                                                                     ð
                                                                                                                                                                                                                                                                                                                               음
```

```
A patient with a form of chronic myelogenous leukemia underwent two treatments of cytophoresis from which basophils were recovered. These were used to search for novel basophil granule proteins (BGP). The proteins were fractioned. Ca. 25 peaks were identified. Several fractions were pure enough to allow for the determination of a single amino acid sequence. The N-terminal sequences of eight
This is the amino acid sequence of peptide A14R, comprising amino acid residues A566-R579 of human GPB8 (see AAMB5475). GPB8 is an 88 kbg ajvoprotein autocrine growth factor that is expressed in a tightly regulated manner in normal cells, is overexpressed and unregulated in highly tumorigenic cells derived from normal cells, and which acts as a stringently required growth stimulator for the tumorigenic cells. A14K was used in an attempt to raise neutralising antibodies to GPB8 (see also AAWB5480). Anteagonists to GPB8, such as anti-GPB8 antibodies, are used to treat diseases associated with increased expression of GPB8, particularly cancer but also viral infections. Anti-GPB8 antibodies can also be used
                                                                                                                                                                                                                                                                                                                         but also viral infections. Anti-GP88 antibodies can also be used as diagnostic reagents and to deliver toxins or other compounds to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New basophil granule proteins obtd. from cytoplasmic granules for diagnosis and treatment of pathologies involving inflammat and IgE-mediated responses, infection, hypersensitivity and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1708 GCACGCAGGGGTACCAAGTGTTTGCGCAGGGGGCCCCGGCGC 1749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Basophil granule protein; chronic myelogenous leukemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     770000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-824-647-16 (1-2095) x AAW85481 (1-14)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR20737 standard; Protein; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wilde GG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 2; Page 22; 28pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.000408
14.00
100.008
100.008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91WO-US04869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  900S-0551263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BGP N-terminal fraction 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (INCY-) INCYTE PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gleich GJ,
                                                                                                                                                                                                                                                                                                                                                                                            GP88-expressing cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1992-056828/07
```

ð

2 3 5

```
TGFe is a glycoprotein with an Mr of about 25,000. The partial amino acid sequence of purified bowine TGFe indicated no homology to other known growth factors. However the N-terminal sequence exhibits considerable amino acid sequence identity to the deduced N-terminal amino acid sequence of human granulin A and the N-terminus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transforming growth factor E produced in commercial quantities -
used for wound healing and burns treatment, comprises monomeric
protein which acts as mitogen for fibroblasts
                                                                                                                                                                                                                                                                                                      Transforming frowth factor e; cell proliferation; mitogen.
                                N-terminal âmino acid sequence of epithelin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UYGE-) UNIV GEORGIA RES FOUND INC
                                                                                                                                               AAR35078 standard; protein; 14 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example; Page 49; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9103-0770585.
                                                                                                                                                                                                                   09-AUG-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Halper J, Mcgraw RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1993-134386/16:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of epithelin 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity
                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-OCT-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                W09307173-A.
                                                                                                                                                                                                                                                                                                                                                                                                                        15-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-JAN-2001
                                865
                                                                                                                                                                                     AAR35078;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB14948;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No.:
                                                                                                          RESULT 5
AAR35078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB14948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR51665 shows an N-terminal sequence of a basophil granule protein. The BGP can be extracted from human basophil granules by treatment at pH 9.0 or greater. This can be used to generate its corresponding nucleic acid an antibodies. Anti-BGPs are useful for the diagnosis of prepathologic conditions as well as chronic and acute diseases, such as parasitic infection and leukaemia, where there is a change in the amount or distribution of BGPs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New human basophil granule proteins - and related nucleic acid, expression systems, antibodies, etc., for diagnosis and treatment of e.g. inflammation, parasitic infection, leukaemia etc.
such fractions are represented in AAR20736-42 and AAR22455.
                                                                                                        0000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0000
                                                                                                                                        Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                         865 GACATGGAGGTGAGCTGCCCAGATGGCTATACC 897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ophil granule protein; N-terminal sequence; specific antibodies; Antibodies; Leukaemia
                                                                                                                                                                                                                                                                                              Basophil granule protein N-terminal sequence
                                                                                                      Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
                                                                                                                                                                                                       Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps:
                                                                                                                                                                                                                                   US-09-824-647-16 (1-2095) x AAR20737 (1-15)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-824-647-16 (1-2095) x AAR51665 (1-15)
                                                                                                                                                                                                                                                                                                                                                                                          AAR51665 standard; protein; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gleich GJ, Scott RW, Wilde CG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 2; Page 34; 55pp; English.
                                                                                                0.296
11.00
100.008
1.598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93WO-US08511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92US-0943813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.00%
100.00%
1.59%
15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-OCT-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (INCY-) INCYTE PHARM INC. (MAYO-) MAYO FOUNDATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.296
11.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1994-118398/14
                                                                                                                                                             Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
Query Match:
                                            15 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15 AA;
                                                                                                                                      Percent Similarity:
                                                                              Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-SEP-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9406829-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-MAR-1994
                                            Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR51665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Basoph11
                                                                                                                                                                               Query Match:
                                                                                                    ..
№
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..
2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BGP
                                                                                                                                                                                                                                                                                                                                                                          AAR5166
                                                                                                                                                                                                                                                                                                                                                        RESULT
```

Parnell PG

```
Porphyromonas gingivalis; protective epitope; antiinflammatory; vaccine;
 9 0 0
         Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                  Porphyromonas gingivalis PrtR27 peptide #6.
Length:
                                      Indels:
                                                                                  Gaps:
                                                                US-09-824-647-16 (1-2095) x AAR35078 (1-14)
                                                                                                                                            AA.
                                                                                                                                           AAB14948 standard; peptide; 13
24.3
9.00
100.00%
100.00%
1.30%
                                                                                                                                                                                  (first entry)
                                                                                                                                                    XXEXEX XXXX
```

Score:

```
The present sequence is one of twenty overlapping peptides corresponding to the N-terminal 148 residues of the PrtR27 adhesin from Porphyromonas coingivalis. Antibodies directed towards the PrtR27 adhesin were found to provide protection against periodontitis in a human patient and immunoprotected mice. The peptides were used for epitope mapping of the prtR37 adhesin. Peptides comprising at least one P. gingivalis epitope are useful in the treatment and prevention of periodontal disease, particularly periodontitis, which is associated with P. gingivalis particularly periodontitis, which is associated with P. gingivalis infection. The peptides are useful as immunosens in vaccine formulations infection. The peptides are useful as immunosens in vaccine formulations incontain an include operation and peptide-specific antiserum useful for passive immunisation, and to generate polycional or monoclonal antibodies. The immunisation and antibodies against the peptides can be used in diagnostic tests to detect P. gingivalis infection. The antibodies can also be used in oral compositions such as toothpaste and mouthwash to neutralise the
periodontal disease; periodontitis; immunogen; infection; PrtR27 adhesin.
                                                                                                                                                                                                                                                                                                                              New compositions comprising at least one peptide with an epitope of Arg-specific proteinase associated with Lys-specific proteinase protein complex for treating and preventing periodontitis-associated Porphyromonas ginglyalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ranulin; epithilin; mouse; growth factor; autocrine; tumour; viral infection; antagonist; therapy; diagnosis; antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse GP88 autocrine growth factor antigenic peptide S14R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-824-647-16 (1-2095) x AAB14948 (1-13)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1029 GGGCCCCTGTTCACAGGTACC 1009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ź
                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; Page 21; 62pp; English.
                                                                                                                                                                                                                                     (VICT-) VICTORIAN DAIRY IND ASSOC.
                                                                                                                                                                                                                                                                        O'Brien-Simpson NM, Reynolds EC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW85479 standard; Peptide; 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antigen and prevent disease
                                                                                                                                                                        99AU-0008939.
                                                                                                                                       01-MAR-2000; 2000WO-AU00142.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.00%
100.00%
1.02%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2e+03
7.00
                                       Porphyromonas gingivalis
                                                                                                                                                                                                         UYME ) UNIV MELBOURNE.
                                                                                                                                                                                                                                                                                                         WPI; 2000-579275/54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GP88; granulin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
                                                                                                                                                                                                                            CSL LTD
                                                                         WO200052041-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
                                                                                                                                                                          01-MAR-1999;
                                                                                                        08-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cancer; vi
antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW85479;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..
⊗
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW85479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
```

Composition containing antagonist of growth factor GP88 - useful for treating cancer and viral diseases and also for diagnosing disease from altered GP88 expression

WPI; 1999-045276/04.

Serrero G;

970S-0991862. 970S-0863079.

16-DEC-1997; 23-MAY-1997;

(SERR/) SERRERO G.

98WO-US10555

22-MAY-1998; 26-NOV-1998

WO9852607-A1.

Mus sp.

Example 8; Page 45; 86pp; English.

```
Human; neuroprotective; nootropic; gene therapy; vaccine;
Alzheimer's disease; Alzheimer's Disease-Associated Feature; AF;
Alzheimer's Disease-Associated Protein Isoform; API; tryptic digest;
Expression Reference Protein Isoform; ERPI; proteolysis.
                                                                                                                                                                                                                                                                                This is the amino acid sequence of peptide S14R, comprising amino acid residues S562-R575 of murine GP88 (see AAW85474). GP88 is an KDa glycoprotein autocrine growth factor that is expressed in a tightly regulated manner in normal cells, is overexpressed and unregulated in highly tumorigenic cells derived from normal cells, uncrigenic cells. S14R was used to raise neutralising antibodies to GP88. Antagonists to GP88, such as anti-GP88 antibodies are used to treat diseases associated with increased expression of GP88, particularly cancer but also viral infections. Anti-GP88 antibodies can also be used as diagnostic reagents and to deliver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7,0000
                                                                                                                                                                                                                                                                                                                                                                                                                     other compounds to GP88-expressing cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human API-108 tryptic digest peptide #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-824-647-16 (1-2095) x AAW85479 (1-14)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1714 AGGGGTACCAAGTGTTTGCGC 1734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB52180 standard; Peptide; 14 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.98e+03
7.00
100.00%
100.00%
1.01%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                14 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200175454-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-0CT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABB52180;
                                                                                                                                                                                                                                                                                                                                                                                                                           oxins or
                                                                                                                                                                                                                                                                                                                                                                                                                                                Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..
92
.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABB52180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
```

healthy persons

```
The present invention relates to oligonucleotides (see AAL26793-AAL34659) encoding polymorphic variants of proteins related to amylases, amyloid proteins, angiopoletin, apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes, histones, kinases, colony stimulating factors, complement related proteins, cytochromes, kinesins, cytokines, interferons, interleukins, G-protein coupled receptors and thiosesterases. The present sequence is a peptide encoded by one such oligonucleotide. The oligonucleotides and the peptides encoded by them may be used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              prevention, diagnosis and treatment of diseases associated with inappropriate expression of the proteins listed above. Disorders that ma be prevented, diagnosed and/or treated include multifactorial diseases with a genetic component, such as autoimmune diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes, systemic lupus erythromatosus and Grave's disease), inflammation, cancer (e.g. cancers of the bladder, brain, breast, colon and kidney, leukaemia), diseases of the nervous system and an infection of pathogenic organisms.
                                                                                                                                                                                                                                                               Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases, oncogenes and histones, useful for diagnosing and treating, e.g. cancer, autoimmune diseases and infections -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         platelet derived growth factor; PDGF; smooth muscle; mimic; interaction site; constrained conformation; inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PDGF inhibitor (PGF-3), contg. proline brackets.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps:
                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 3902; 4143pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-824-647-16 (1-2095) x AAM97797 (1-14)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 264 CCCCTTCCCAGAGGCCGTGGC 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR67120 standard; peptide; 8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 ProLeuProArgGlyArgGly
                                                               28-DEC-1999; 99US-0173419.
27-DEC-2000; 2000US-0173419.
                     28-DEC-2000; 2000WO-US35498.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.98e+03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.00%
100.00%
1.01%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94WO-US04294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93US-0051741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-JUN-1995 (first entry)
                                                                                                                                                                           Leach M;
                                                                                                                                 (CURA-) CÜRAGEN CORP.
                                                                                                                                                                                                                     WPI; 2001-465210/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
                                                                                                                                                                           Shimkets RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9425482-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-NOV-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR67120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR67120
neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer; amyloid protein; antimicrobial; gene therapy; vaccine; amylase; cancer; cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor; complement related protein; cytochrome; kinase; colony stimulating factor; interleuklin; G-protein coupled receptor; thioesterase; inflammation; nervous system disease; autoimmune disease; infection;
                                                                                                                                                                                                                                                                                                                               Screening for Alzheimer's disease in a mammal, by making two-dimensional array of a feature whose relative abundance correlates with disease, and comparing with abundance of the feature in samples of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         order to determine whether a patient is suffering from, or has a predisposition to, Alzheimer's Disease. The relative abundance of the AFs and APIs correlates with the severity of Alzheimer's Disease. The present sequence is a peptide produced from an API by proteolysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to methods for the screening, diagnosis and prognosis of Alzheimer's disease. The methods involve the detection of Alzheimer's Disease-Associated Features (AFS) and Alzheimer's Disease-Associated Protein Isoforms (APIS) in cerebrospinal fluid, serum or plasma. The abundance of the AFS and APIS is then normalised to an Expression Reference Protein Isoforms (BEPI) in
                                                                                                                                                                                           Ourham KL, Friedman DL, Herath HWAC, Kimmel LH, Parekh RB; Potter DM, Rohlff C, Silber BM, Stiger TR, Sunderland PT; Pownsend RR, White F, Williams SA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human peptide #1072 encoded by a SNP oligonucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4,0000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-824-647-16 (1-2095) x ABB52180 (1-14)
                                                                                                                            (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1009 GGTACCTGTGAACAGGGGCCC 1029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAM97797 standard; Peptide; 14 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GlyThrCysGluGlnGlyPro 7
                                                                                                                                                                                                                                                                                                                                                                                                                                             Example; Page 29; 162pp; English
                03-APR-2001; 2001WO-US10908.
                                                          03-APR-2000; 2000US-194504P.
28-NOV-2000; 2000US-253647P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.98e+03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.00%
100.00%
1.01%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                           Durham KL, Friedman DL,
                                                                                                                                                                                                                                                                                  WPI; 2001-639384/73
                                                                                                                                                 (PFIZ ) PFIZER INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14 AA;
```

Alignment Scores:

Score:

Query Match:

Sequence

40200147944-A2

05-JUL-2001

Homo sapiens

24 - JAN - 2002

AAM97797;

6 AAM97.797 RESULT

셤

4,0000

may

```
Example 1; Page 11; 54pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
Best Local Similarity:
                                                                                                                                                                            Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-MAY-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-NOV-1994.
                                                                                                                                 Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                       27-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9426900-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sednence
                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                           AAR66383;
                                                                                                                                                                                                            Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..
Q
                                                                                                                                                   Pred. No.:
                                                                                                                                                                                                                                                                                                                                                 RESULT 12
                                                                                                                                                                                                                                                                                                                                                              AAR66383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score:
                                                                                                                                                                    Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
X & X O O O X & &
                                                                                                                                                                                                                         are derive from PDGF peptides that contain proline or proline/cysteine brackets. These peptides that contain proline or proline/cysteine brackets. These peptides contain one or more interaction sites of interest. The dose is 5-5000 microcomoles. The peptides interact with specific receptors and inhibit the migration of macrophages, and thus inhibits the pro-inflammatory effects of the interleukin. The data collected demonstrates that interaction sites possess activity when present in a polypeptide that differs from the native form. Inclusion of conformation-constraining moleties can have desirable effects on an interaction site. (Also see AR&FOIN-117 and AAR&FOIL-52 for analogues of other biologically active peptides contg. an interaction site flanked by conformation constraining 9ps., eg. RGD peptides.)
                                                                                                                                    Peptide homologue or analogue with constrained conformation - has proline residues flanking the interaction site to impart greater, or more stable, biological activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel polypeptide(s) having affinity for the human TSH receptor antibody - used in detection of the TSH antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       thyroid stimulating hormone receptor; TSH; human; Homo sapiens; antibody; affinity; detection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MITP ) MITSUBISHI PETROCHEMICAL CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-824-647-16 (1-2095) x AAR67120 (1-8)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human TSH receptor (residues 47-54).
                                                                                                                                                                                                     Example 3; Page 39; 57pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR73224 standard; Peptide; 8 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               270 CCCAGAGGCCGTGGCATG 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93JP-0240853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93JP-0240853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6.00
100.00%
100.00%
0.86%
      93US-0143364.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3.31e+07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1995-167251/22.
                                                                                                           WPI; 1994-358186/44.
                                  (EVAN/) EVANS H J. (KINI/) KINI R M.
                                                                              Evans HJ, Kini RM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 8 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JP07089991-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-DEC-1995
      29-OCT-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR73224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local S.
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score:
```

셤 ò

```
Peptides with affinity to human TSH (thyroid stimulating hormone) receptor antibody are used for detection of the antibody: (See also AAR73201-592).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nseq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                To obtain a pollovirus-1 (PV1)/Chlamydial hybrid, the PV1 Mahoney CDNA clone pT7XLD was modified to encode epitopes from C. trachomatis ser. A MOMP VDI. The VOI sequence was not restricted to the known epitope given in AAR66356, or to the sequence given in AAR66383 (expressed in previously described hybrids), but instead included adjacent sequences from VDI.
                                                                                            Š.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New hybrid picornaviruses expressing chlamydial epitopes to develop prods. for vaccination, diagnosis, treatment of chlamydial infections and prodn. Of immunological reagents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chlamydial epitope; variable domain; MOMP; major outer membrane protein; picorna virus; vaccine; PV1; diagnostic; therapeutic; poliovirus; capsid protein.
                                                                                                                                                   890000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                            Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oomen RP
                                                                                                                                                   Length:
Matches:
                                                                                                                                                                                                                                                            Gaps:
                                                                                                                                                                                                                                                                                                   (1-8)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caldwell HD, Klein MH, Murdin AD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 19; 99pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR66383 standard; peptide; 8 AA.
                                                                                                                                                                                                                                                                                                                                           1517 CCCAGCCTGCCACCTTCC 1534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chlamydia trachomatis serovar A.
                                                                                                                                                                                                                                                                                                     US-09-824-647-16 (1-2095) x AAR73224
                                                                                                                                                                                                                                                                                                                                                                   ProserteuProProSer 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3.31e+07
6.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94WO-CA00262.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    930S-0060978
                                                                                                                                                        3.31e+07
6.00
                                                                                                                                                                                          100.00%
100.00%
0.86%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CONN-) CONNAUGHT LAB LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chlamydial VDI epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1995-006796/01
                                                                                                                                                                                                                        Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 AA;
                                                                                            8 AA;
```

AAY13573 standard; peptide; 8 AA

(first entry)

30-JUL-1999

AAY13573;

```
Human; oestrogen receptor activity inhibitor; anti-oestrogen; diagnosis;
breast cancer; estrogen; tumour; phosphotyrosyl peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes a composition comprising an isolated oestrogen receptor activity inhibiting (anti-oestrogen) peptide. The peptides used in the composition comprise sequences of human oestrogen receptor (OR) surrounding Tyr537 and steroid receptor co-activator-1 (SCR-1). The peptide compositions, nucleic acids and vectors of the present invention can reduce OR activity in a cell, reduced OR polypeptide dimerisation in a cell and reduce the binding of SRC-1 polypeptide to an OR polypeptide dimer in a cell. They can be used for killing cancer cells and treating cancers, particularly breast cancer. The present sequence represents a specifically claimed anti-oestrogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New anti-oestrogen peptide compositions - comprise sequences based on oestrogen receptor and steroid receptor co-activator-1 sequences, used for treating cancers
                                                                                                                                                                                                                                                                                                               breast cancer; estrogen; tumour; phosphotyrosyl peptide; malonyltyrosyl peptide; steroid receptor co-activator-1.
    00
                                                                                                                                                                                                                                                                Destrogen receptor activity inhibiting peptide #1.
 Indels:
Gaps:
                                        US-09-824-647-16 (1-2095) x AAR66383 (1-8)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 157; 182pp; English.
                                                                                                                                                                    AAW82944 standard; peptide; 8 AA
                                                                           1279 GTGGCTGGACTGGAGAG 1296
                                                                                         2 ValAlaGlyLeuGluLys 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98WO-US07711.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         970S-0043545
                                                                                                                                                                                                                                  04-FEB-1999 (first entry)
0.86%
16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1998-594522/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 AA;
                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                            409846250-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                           22-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pietras RJ;
                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                     AAW82944;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No.:
                                                                                                                                       RESULT 13
                                                                           å
```

```
bloactive compounds. To ensure specificity and optimize binding, the sensor is generally present at sub-micromolar concentration and the binding reaction occurs in solution. The sensor peptide obviates the need to include a natural coactivator protein of the receptor in the mixture. Sequences AAX1371-587 represent examples of sensor peptides that can be used in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hormone receptor function. The methods use a sensor peptide covalently coupled to a detectable label, that provides direct, in vitro ligand-dependent binding to a nuclear hormone receptor. Panels of predetermined or randomized candidate sensors are readily screened for receptor binding. The methods and compositions provide for efficient screening of modulators of nuclear hormone receptor function, without the use of cell- or gal-based steps. The methods are amenable to automated, cost-effective high throughput screening of chemical libraries for
                                 Nuclear hormone receptor; sensor peptide; receptor binding; screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention provides methods for screening of modulators of
                                                                                                                                                                                                                                                                                                                                                 Shan B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    800000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                 Lustig K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                      Nuclear hormone receptor drug screens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-824-647-16 (1-2095) x AAY13573 (1-8)
                                                                                                                                                                                                                                                                                                                                                 Chen J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW67665 standard; peptide; 8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 7; Page 17; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1131 CTCCTCCGATACCTGCTG 1148
                                                                                                                                                                                                                                              980S-0163713
                                                                                                                                                                                                                                                                      97US-0975614.
                                                                                                                                                                                                           .98WO-US24969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 LeuLeuArgTyrLeuLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3.31e+07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.00%
100.00%
0.86%
                                                                                                                                                                                                                                                                                                                                               Baeuerle P, Beckmann H,
Peptide sensor TUK-1390.
                                                                                                                                                                                                                                                                                                         (TULA-) TULARIK INC.
                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-347794/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
                                                                                                                              WO9927365-A1
                                                                                                                                                                                                           :0-NOV-1998;
                                                                                                                                                                                                                                                                    21-NOV-1997;
                                                                                                                                                                                                                                                  30-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alignment Scores:
                                                                                                                                                                     03-JUN-1999.
                                                         modulator.
                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW67665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW67665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred.
```

Conservative: Mismatches: Indels:

100.00% 100.00% 0.86%

Percent Similarity: Best Local Similarity:

Score:

Query Match:

US-09-824-647-16 (1-2095) x AAW82944 (1-8)

1131 CTCCTCCGATACCTGCTG 1148

ð

Length: Matches:

3.31e+07

ă.

/note= "H4/D4 nicotinylated"

Location/Qualiflers

Escherichia coli.

Key Modified-site

50S; L17; protein sequencing; protein quantitation.

```
into sequence tepteseuts on mandam nucted protein. This peptide in the DNA binding domain (DBD) of the SRCia protein. This peptide corresponds to amino acids 748-75 of SRCia-DBD. The invention relates to the identification of inhibitor compounds capable of reducing the interaction between a region on a nuclear protein (RI) and a region on a nuclear protein (RI) and a region on a nuclear protein (RI) and a region on a nuclear protein satisfic (II) R2 is the region capable of interacting with the nuclear protein by binding the signature motif; (II) the nuclear protein is a bridging factor responsible for interaction between a liganded nuclear receptor and a responsible for interaction between a liganded nuclear receptor and transcription initiation complex involved in gene expression regulation; (IV) the nuclear experts in a transcription factor; (V) the signature of a nuclear protein which binds to a liganded nuclear receptor during of a nuclear protein which binds to a liganded nuclear receptor during a citivation or repression of target genes. The inhibitors are expected to be useful in the treatment of any disease mediated through any interaction between a signature motif on a nuclear protein and a nuclear receptor, for example inflammation and cancer.
                                                                             cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence represents an LXXLL nuclear protein signature motif found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identification of inhibitors of nuclear protein/nuclear receptor interaction - useful for, e.g. treatment of disease mediated through the interaction such as inflammation and cancer
                                                                         Nuclear protein; signature motif; receptor protein; inflammation; interaction; inhibitor; inhibition; transcription factor; ligand.
                                LXXLL signature motif #5 from protein SRC1a DNA binding domain.
                                                                                                                                                                                                                                                                                                                                                                     (IMCR ) IMPERIAL CANCER RES TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Fig 1A; 60pp; English.
                                                                                                                                                                                                                                                                                98WO-GB01238.
                                                                                                                                                                                                                                                                                                                              97GB-0008676
16-MAR-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                   Heery DM, Parker MG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-034672/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 AA;
                                                                                                                                                                                                                                                                                                                              30-APR-1997;
                                                                                                                                                                                                                                                                                     28-APR-1998;
                                                                                                                                                         Homo saptens
                                                                                                                                                                                                  W09849561-A1
                                                                                                                                                                                                                                         05-NOV-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
```

This sequence represents a peptide fragment of the E.Coli 50s ribosomal subunit L17 identified and characterised using a novel method of the invention. The invention comprises a method for labeling a protein by protecting epsilon-amino groups of Lys, cleaving the protein to produce a mixture of peptides and treating these with a labeling agent that binds to the N-terminal amino acid. The method is used for identifying proteins, e.g. for analysis of proteins expressed by cells in different expression states. The method makes possible relative protein againstitation in one- or two-dimensional gel separations, even when separation is only partial, and facilitates de novo sequencing and automated interpretation of mass spectra. Protection of Lys sidechains ensures specific labeling of the N-termina, increases the intensity of belong the communication of the store of the sidechains and protein the sequence of the sidechains are communicated to the sequence of the sidechains are communicated to the sequence of the sidechains and protein the sequence of the sidechains are communicated to the sequence of the sequence of the sidechains are communicated to the sequence of the sidechains are communicated to the sequence of the sidechain are communicated to the sequence of the s

Method for labeling proteins, useful for identification, particularly in expression analysis, by blocking lysine sidechains, proteclysis and N-terminal labeling of peptide fragments

(PROT-) PROTEOME SYSTEMS LTD 03-APR-2000; 2000AU-0006643.

WPI; 2002-017393/02.

James P;

03-APR-2001; 2001WO-AU00366,

WO200174842-A1 11-0CT-2001. Disclosure; Fig 2A; 27pp; English.

```
b-ions (permitting full-length sequence coverage for peptides of m/z over 1000) and allows differentiation between Lys and Glu. The use of different isotopic labels allows different proteins in the same gel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vascular endothelial growth factor receptor-2 peptide modulator #121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vascular endothelial growth factor receptor-2; VEGFR-2; VEGF modulator; psoriasis; rheumatoid arthritis; retinopathy;
                                                                                                                                                                                                                                                                                                                                                                                                           890000
                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (1-8)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-824-647-16 (1-2095) x AAU09998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      839 GCAGGCAGCTTAGTGAGG 822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU73544 standard; Peptide; 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 AlaGlySerLeuValArg
                                                                                                                                                                                                                                                                                                                                                                                                            3.31e+07
                                                                                                                                                                                                                                                                                                                                                                                                                   6.00
100.00%
100.00%
0.87%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                    spot to be quantified
                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                     8 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                      Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU73544;
                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                               М
Э
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU73544
                                                                                                                                                                                                                                                                                                                                                                                                                        score:
```

890000

Conservative: Mismatches: Indels: Length: Matches:

100.00% 100.00% 0.86% 20

Best Local Similarity:

Query Match:

Percent Similarity:

Aliqnment Scores:

Pred. No.:

Score:

3.31e+07 6.00

Gaps:

(1-8)

1131 CTCCTCCGATACCTGCTG 1148

ö g

US-09-824-647-16 (1-2095) x AAW67665

E.Coli 50S ribosomal subunit L17 peptide.

(first entry)

12-MAR-2002

XXXEXEX

AAU09998;

AAU09998 standard; peptide; 8 AA

RESULT 16 AAU09998 Slingluff CL;

Hunt DF, Shabanowitz J,

Engelhard VH,

95WO-0S01991

94US-0197399

94US-0234784

```
Melanoma-specific immunogen comprises epitope(s) homologous with pMel.17 - are highly potent stimulators of HLA-A2+CTL's useful in
                                                                                                                                                                                                                                    (UYVI-) UNIŅ VIRGINIA PATENT FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                      Example 8; Page 52; 148pp; English
                                                                                                                                                                                                                                                                                                                                                                                         adoptive 1mmuno-therapy
                                                                                                                                                                                                                                                                                                              WPI; 1995-302688/39.
                           Homo sapiens
                                                             W09522561-A2
                                                                                                                                        6-FEB-1995;
                                                                                                                                                                             29-APR-1994;
                                                                                                                                                                                               16-FEB-1994;
                                                                                                  24 - AUG-1995.
                                                                                                                                                                                                                                                                          COX AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW42528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       condition and provided and displayed and which acts as modulator of VEGF function. The compound is useful for: treating a modulator of VEGF function. The compound is useful for: treating a patient suffering from psoriasis, rhemmatoid arthritis, retinopathy and cancer; for imaging and assessing necvascularisation during angiogenesis; for detecting VEGFR-2 receptor or related receptor on living cells, as a calbration standard for quantitating the activities of candidate VEGFR-2 antagonists in a variety of functional assays; as probes for affinity screening; as blocking reagent in random peptide screening i.e. in screening for new families of VEGFR-2 peptide ligands; in the co-crystallisation with VEGFR-2; in inhibiting or decreasing the proliferation and growth of vascular endothelial cell growth configuration and diagnostic applications where VEGFR-2 is antagonised. Agonists are useful for the treatment of diseases such as coronary artery disease. This sequence is a peptide modulator of the cyascular endothelial growth factor receptor-2 (VEGF-2) based on the community peptide sequence ANS73422, described in the method of the
                                                                                                                                                                                                                                                                                                                                                           Novel compounds having affinity for vascular endothelial growth factor receptor-2 useful for treating cancer, retinopathy, rheumatoid arthritis, psoriasis and as angiogenesis imaging agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             invention describes a compound having affinity for vascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Melanoma; immunogen; epitope; homologue; vaccine; immunotherapy;
cytotoxic T cell; lymphocyte; HLA-A2.
cancer; cytostatic; ophthalmological; neovascularisation; anglogenesis; coronary artery disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Melanoma-specific mutant immunogen epitope 9mer peptide.
                                                                                                                                                                                                                                                                                        Mozsgai CA, Balu P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            890000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-824-647-16 (1-2095) x AAU73544 (1-8)
                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 19; Page 40; 101pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR82184 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1832 TGGGGTCCCGAGGCTGC 1815
                                                                                                                                                                                                                                                                                        Piplani S,
                                                                                                                                                                   27-APR-2001; 2001WO-US13598.
                                                                                                                                                                                                           28-APR-2000; 2000US-0561470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TrpGlyProGluGlyCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6.00
100.00%
100.00%
0.87%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3.31e+07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                GLAX ) GLAXO GROUP LTD
                                                                                                                                                                                                                                                                                      Chen M,
                                                                                                                                                                                                                                                                                                                       WPI; 2002-075158/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
                                                                                          WO200183693-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
                                                                                                                              08-NOV-2001
                                                                                                                                                                                                                                                                                      Schatz PJ,
                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR82184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR82184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score:
                                     à
```

```
A melanoma-specific immunogen homologous with pwel-17 comprises one or more CTL (cytotoxic T lymphocyte) epitopes from the group AAR82098-AAR82194 capable of eliciting a CTL response. The epitopes AAR82098-AAR82108 are of particular interest. The immunogen can be used for partial protection in mammals against melanoma peptides which are homologous with pwel-17 are highly potent stimulators of HiA-A2+CTLs in several cell lines and can be used in immunotherapy or incorporated into immunogenic conjugates as vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Metastatic melanoma; peptide analogue; vaccine; cancer; diagnosis; antigen; CTL; immunogenic; viral disease; gp 100; Melan A/MART-1.
                                                                                                                                                                                                                                                                                    600000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Melan A/MART epitope (residues 27-35) analogue #5.
                                                                                                                                                                                                                                                                                                                             Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                  Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                (1-9)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1982 TTACAAGCTGCCATCCCC 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW42528 standard; peptide; 9 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-824-647-16 (1-2095) x AAR82184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 LeuGlnAlaAlaIlePro 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97WO-EP03712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96EP-0201945
                                                                                                                                                                                                                                                                                  2.94e+07
                                                                                                                                                                                                                                                                                                                        100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-JUN-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                          0.868
                                                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo saptens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38-JUL-1997;
                                                                                                                                                                                                                                                             Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       409802538-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW42528;
                                                                                                                                                                                                                  Sequence
```

```
This sequence is shown in the specification. The invention relates to peptides, which are immunogenic with lymphocytes directed against metastatic melanomas. They are characterised in that they comprise at least a part of the following sequence, where the amino acid at position 2 or 8 is substituted: Lys-Thr-Tpr-Gly-Gln-Tyr-Trp-Gln-Val. Vaccines comprising the peptide, an epitope of the peptide, nucleotide sequence encoding the peptide, or an antigen presenting cell preloaded with the peptide or antibody as above, are useful for cancer, particularly melanoma, treatment. The peptides can also be used to generate antigen reactive tumour infiltrating lymphocytes, which can also be used in reactive tumour infiltrating lymphocytes, which can also be used in cracines. The peptides can be exploited to elicit native epitope-reactive CTL. Usage of the peptides with improved immunogenicity may contribute to the development of CTL-epitope based vaccines in viral disease and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identifying agonists or antagonists for ligand-induced activation of
                                                                                   associated peptide analogues - useful in vaccines against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oestrogen receptor beta; ER-beta; MBP; binding; detection;
ligand-dependent nuclear receptor; coactivator interaction;
hybrid system; corepressor; ligand binding domain; LBD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Coactivator leucine charged domain peptide #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (1-9)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Schatz PJ;
                                                                                                                                 Example 1; Page 28; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY42208 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-824-647-16 (1-2095) x AAW42528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99WO-US07168.
                                                                                                                                                                                                                                                                                                                                                                                                                                          2.94e+07
6.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.00%
100.00%
0.87%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GLAX ) GLAXO GROUP LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Northrop JP, Hart CP,
(ALKU ) AKZO NOBEL NV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-591374/50.
                             Figdor, CG;
                                                          WPI; 1998-110586/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                               9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9950664-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-0CT-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                  Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY42208;
                                 Adema GJ,
                                                                                           felanoma
                                                                                                        melanoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match:
                                                                                                                                                                                                                                                                                                                                                                    cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score:
```

```
The present invention describes the use of a ligand binding domain (LBD) transcription factor (TRX) fusion protein in methods for identifying transcription of actor (TRX) fusion protein in methods for identifying agonists or antagonists for ligand-induced activation of a predetermined auchies areceptor having a LBD. Also describes are: (1) a positive hybrid nuclear receptor signal transduction system, comprising an infact comprising a reverse hybrid reporter host cell; (2) a nuclear receptor signal transduction system, comprising a reverse hybrid reporter host cell; (3) a multiplexed format assay for identifying nuclear receptor ligands; (4) identifying a candidate pharmaceutical agent from a library of test agents; (5) a confidate pharmaceutical agent from a library of test agents; (5) a confidate pharmaceutical agent from a library of test agents; (5) a confidance nuclear receptor, typically by interaction with a binding to a nuclear receptor at which naturally occurring to a nuclear receptor at which naturally occurring a coactivators and/or corepressors bind; and (6) an agonist ligand of a coactivator and/or corepressors bind; and (6) an agonist ligand of a custom femiliar acceptor having a LBD. The present activation of a predetermined nuclear receptor having a LBD. The present sequence represents a coactivator leucine charged domain peptide, used in an example from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human; leukaemia; non-Rodgkins lymphoma; Hodgkins lymphoma; lung cancer; metastasis; melanoma; adenocarcinoma; thymoma; colon cancer; reterine cancer; cancer; prostate cancer; ovarian cancer; cervical cancer; bladder cancer; kidney cancer; pancreatic cancer liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
predetermined nuclear receptor having ligand binding domain (LBD)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human cancer antigen NY ESO-1/CAG-3 HLA peptide motif.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        vaccine; human leukocyte antigen; HLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-824-647-16 (1-2095) x AAY42208 (1-9)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1131 CTCCTCCGATACCTGCTG 1148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY06031 standard; Peptide; 9 AA
                                                  Example 1; Fig 1; 67pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98WO-US19609.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97US-0061428.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LeuLeuArgTyrLeuLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.94e+07
6.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.00%
100.00%
0.86%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rosenberg SA, Wang RF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-277270/23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9918206-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-APR-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY06031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY06031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score:
```

```
Example 10; Page 43; 88pp; English.
   This peptide was identified as an HLA peptide motif following a screen for epitopes from the coding region of human ESO-1/CAG-3 ORF1 (see AAX5859). 30 Epitopes (see AAX60814-47) were identified.

The present peptide (ranked 14) corresponds to amino acid residues 153-160 of CAG-1 ORF1 (see AAX05965). CAG-1 is a new and potent tumour antigen capable of eliciting an antigen specific immune response by T cells. Cancer peptides (see AAX05967-87) derived from CAG-3, portions of CAG-3 and their variants, are useful as cancer capacities. A claimed method of preventing or inhibiting cancer involves administering a cancer peptide, with or without an HLA molecule. The cancer peptides form part of, or are derived from cancers corers such as primary or metastatic melanoma, thymoma, Important cancer, cervical cancer, liver cancer, leuksemia, uterine cancer, cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such as breast, prostate, ovarian, pancreatic and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human; leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer; metastasis; melanoma; adenocarcinoma; thymoma; colon cancer; uterine cancer; breast cancer; prostate cancer; ovarian cancer; cervical cancer; bladder cancer; kidney cancer; pancreatic cancer; liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human cancer antigen NY ESO-1/CAG-3 HLA peptide motif.
                                                                                                                                                                                                                                                                                                  690000
                                                                                                                                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                 Indels:
                                                                                                                                                                                                                                                                                                                                                           Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vaccine; human leukocyte antigen; HLA
                                                                                                                                                                                                                                                                                                                                                                                 US-09-824-647-16 (1-2095) x AAY06031 (1-9)
                                   Example 10; Page 43; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY06039 standard; Peptide; 9 AA
                                                                                                                                                                                                                                                                                                                                                                                                       1119 CAGCAGCTGTCCCTCCTC 1136
                                                                                                                                                                                                                                                                                                                                                                                                                     2 GlnGlnLeuSerLeuLeu 7
            Cancer antigen NY ESO1/CAG-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cancer antigen NY ESO1/CAG-3
                                                                                                                                                                                                                                                                                              2.94e+07
6.00
100.008
100.008
0.868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98WO-US19609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97US-0061428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wang RF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-277270/23
                                                                                                                                                                                                                                                                                                                                   Best Local Similarity:
                                                                                                                                                                                                                                                             9 AA;
                                                                                                                                                                                                                                       thyroid cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rosenberg SA,
                                                                                                                                                                                                                                                                                                                       Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9918206-A2.
                                                                                                                                                                                                                                                                                  Aliqnment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-APR-1999
                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY06039;
                                                                                                                                                                                                                                                                                                                                              Query Match:
                                                                                                                                                                                                                                                                                                 ..
No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY06039
õ
                                                                                                                                                                                                                                                                                                                                                                                                                               셤
```

```
screen for epitopes from the coding region of human EGO-1/CAG-3 (CAR-1 (See AAX5659). 30 Epitopes (see AAX0618-47) were identified. The present peptide (ranked 22) corresponds to amino acid residues 152-160 of CAG-1 ORF1 (see AAX05965). CAG-1 is a new and potent tumour antigen capable of eliciting an antigen specific immune response by T cells. Cancer peptides (see AAX05967-87) derived from CAG-3, portions of CAG-3 and their variants, are useful as cancer c vaccines. A claimed method of preventing or inhibiting cancer involves administering a cancer peptide, with or without an HLA molecule. The cancer peptides form part of, or are derived from, cancers such as primary or metastatic melanoma, thymoma, Iymphoma, sarcoma, lung cancer, leukaemia, uterine cancer, cervical cancer, bladder cancer, leukaemia, uterine cancer, cervical cancer, broader cancer, leukaemia, uterine cancer, cervical cancer, broader cancer, leukaemia, pancreatic and adenocarcinomas such as breast, prostate, ovarian, pancreatic and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; Jung cancer; metastasis; melanoma; adenocarcinoma; thymoma; colon cancer; uterine cancer; breast cancer; prostate cancer; ovarian cancer; cervical cancer; bladder cancer; kidney cancer; pancreatic cancer; liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy; vaccine; human leukocyte antigen; HLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
                                                         This peptide was identified as an HLA peptide motif following a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human cancer antigen NY ESO-1/CAG-3 HLA peptide motif.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (1-9)
Example 10; Page 43; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY06025 standard; Peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1119 CAGCAGCTGTCCCTCCTC 1136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-824-647-16 (1-2095) x AAY06039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cancer antigen NY ESO1/CAG-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GlnGlnLeuSerLeuLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98WO-US19609.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97US-0061428.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.00%
100.00%
0.86%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.94e+07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-AUG-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wang RF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-277270/23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              thyroid cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rosenberg SA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9918206-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-APR-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY06025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY06025
```

This peptide was identified as an HLA peptide motif following a screen for epitopes from the coding region of human ESO-17CAG-3 ORF1 (see AAX58599). 30 Epitopes (see AAV06018-47) were identified. The present peptide (ranked 8) corresponds to amino acid residues 154-162 of CAG-1 ORF1 (see AAY05965). CAG-1 is a new and potent tumour antigen capable of eliciting an antigen specific immune response by T cells. Cancer peptides (see AAV05967-87) derived from CAG-3, portions of CAG-3 and their variants, are useful as cancer vaccines. A claimed method of preventing or inhibiting cancer involves administering a cancer peptides (var with or without an HLA molecule. The cancer peptides form part of, or are derived from, cancers such as primary or metastatic melanoma, thymoma, lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer, cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such as breast, prostate, ovarian, pancreatic and thyroid cancers.

Sequence 9 AA;

Conservative: Mismatches: Indels: Length: Matches: Gaps: 2.94e+07 6.00 100.00% 100.00% 0.86% Best Local Similarity: Query Match: Percent Similarity: Alignment Scores: .. Q Score:

(1-9)US-09-824-647-16 (1-2095) x AAY06025

1119 CAGCAGCTGTCCCTCCTC 1136 GlnGlnLeuSerLeuLeu 6

AAY13578 RESULT

AAY13578 standard; peptide; 9 AA. 30-JUL-1999 (first entry) AAY13578;

Peptide sensor TUK-1472

Nuclear hormone receptor; sensor peptide; receptor binding; screening; modulator.

Synthetic.

03-JUN-1999

98WO-US24969 20-NOV-1998;

98US-0163713. 97US-0975614. 21-NOV-1997; 30-SEP-1998;

(TULA-) TULARIK INC.

X, Lustig Chen J, Beckmann H, WPI; 1999-347794/29. Baeuerle P,

'n, Shan

Nuclear hormone receptor drug screens

Claim 7; Page 18; 29pp; English.

hormone receptor function. The methods use a sensor peptide covalently coupled to a detectable label, that provides direct, in vitro ligand-dependent binding to a nuclear hormone receptor. Penels of predetermined or randomized candidate sensors are readily screened for receptor The invention provides methods for screening of modulators of nuclear

modulators of nuclear hormone receptor function, without the use of cell- or gel-based steps. The methods are amenable to automated, cost-effective high throughput screening of chemical libraries for bioactive compounds. To ensure specificity and optimize binding, the sensor is generally present at sub-micromolar concentration and the binding reaction occurs in solution. The sensor peptide obviates the need to include a natural coactivator protein of the receptor in the mixture. Sequences AR13571-587 represent examples of sensor peptides that can be used in the method of the invention. binding. The methods and compositions provide for efficient screening of Cytotoxic T-lymphocyte response; CTL; antigen; lymphatic system; immunisation; tumour; infectious disease; immunotherapy; cancer; malignant melanoma; viral disease; hepatitis; AIDS. 00000 Conservative: Mismatches: Matches: Indels: Length: HLA Class I motif peptide SEQ ID NO:463. US-09-824-647-16 (1-2095) x AAY13578 (1-9) AAY10533 standard; Peptide; 9 AA 1131 CTCCTCCGATACCTGCTG 1148 1 LeuLeuArgTyrLeuLeu 2.94e+07 6.00 100.00% 100.00% 0.86% 98WO-US14289 12-MAY-1999 (first entry) Percent Similarity: Best Local Similarity: Query Match: 9 AA; Homo sapiens. WO9902183-A2. 10-JUL-1998; Alignment Scores: 21-JAN-1999 Sequence Synthetic AAY10533; AAY10533 RESULT 888888888888

The present invention describes a method of inducing and/or sustaining an immunological cytotoxic T lymphocyte (CTL) response in a mammal. The method comprises: (a) delivering an antigen to the mammal at a level to induce an immunological CTL response in the mammal; and (b) maintaining the level of the antigen in the mammal's lymphatic system to maintaining the inventoologic CTL response. The method can be used for the delivery of e.g. a differentiation antigen, a tumour-specific multilineage antigen, an embryonic antigen, an oncogene antigen, a mutated tumour-suppressor of antigen in the lymphatic system of a mammal so as to provide a sustained CTL response, used to treat, e.g. AIDS Disclosure; Page 45; 199pp; English. (CTLI-) CTL IMMUNOTHERAPIES CORP. 97US-0988320. Simard JJL; WPI; 1999-120514/10. 10-DEC-1997; 10-JUL-1997; Kuendig TM,

×...

690000

Length:
Matches:
Conservative:
Mismatches:
Indels:

2.94e+07 6.00

red. No.:

100.008 100.008 0.868

Percent Similarity: Best Local Similarity:

Query Match:

Gaps:

US-09-824-647-16 (1-2095) x AAG67189 (1-9)

1119 CAGCAGCTGTCCCTCCTC 1136

GlnGlnLeuSerLeuLeu

```
disease such as cancer, e.g. malignant melanoma or infectious disease, e.g. viral disease such as hepatitis or AIDS. Sustained antigen delivery to the lymphatic system provides for potent CTL stimulation that takes place in the milieu of the lymphoid organ, and it sustains stimulation that is necessary to keep CTL active, cytotoxic and recirculating through the body. AAY10071 to AAY10639 represent examples of peptide antigens given in the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cancer testis tumour antigen; NY-ESO-1; LAGE-2; human leukocyte antigen; HLA; HLA binding peptide; major histocompatibility complex; MHC; tumour; cancer; testis tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tumour associated antigen EY-ESO-1 (LAGE-2) useful
                                                                                                                                                                                                                                                                                                                                                                                                                           Cancer testis tumour antigen NY-ESO-1 derived peptide.
                                                                                                                                                                   Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                          Length:
                                                                                                                                                                                                                        Gaps:
                                                                                                                                                                                                                                            US-09-824-647-16 (1-2095) x AAY10533 (1-9)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genomic sequences of tumour associ
for diagnosing testicular tumours
                                                                                                                                                                                                                                                                                                                                              AAG67189 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                       918 GGCCTGGGGCTGCTGCCC 935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (LUDW-) LUDWIG INST CANCER RES.
                                                                                                                                                                                                                                                                                    22-FEB-2000; 2000US-0510635.
                                                                                                                                                                            100.00%
100.00%
0.86%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-JAN-2001; 2001WO-US02126
                                                                                                                                                       2.94e+07
                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lethe B, Boon-Falleur T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-550091/61.
                                                                                                                                                                                            Best Local Similarity:
                                                                                                                   9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200162917-A1
                                                                                                                                                                               Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                          Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                   13-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                          AAG67189;
                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genomic
                                                                                                                                                                                                         Query Match:
                                                                                                                                                                                                                                                                                                                                      AAG67189
                                                                                                                                                                                                                                                                                                                         RESULT
  8888888888888888
```

Tauopathy; phospho-tau (181); neurological marker; antibody; BT2; AT120; HT7; AT270; nootropic; neuroprotective; cerobroprotective; epitope.

18-JAN-2001; 2001WO-EP00560

NO200155725-A2. Homo sapiens.

Synthetic.

02-AUG-2001

Synthetic peptide immunoreactive with tau antibody HT7

29-OCT-2001 (first entry)

AAB85641;

AAB85641 standard; peptide; 9 AA

```
individual that comprises determining the ratio of phospho-tau (181)/
total tau. Tau and phospho tau are useful as neurological markers for the
manufacture of a diagnostic kit for the diagnosis of a tauopathy and/or
the differential diagnosis of a tauopathy versus a non tauopathy. A
phospho-peptide liable to form an immunological complex with monoclonal
antibody HT7 and MAD AT270 comprising at least the minimal epitope of HT7
or AT270 is useful to measure phospho-tau levels and diagnose a tauopathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and/or for the differential diagnosis of a tauopathy versus a non tauopathy. The kit is useful for the diagnosis of Alzheimer's disease, Pick's disease, sporadic Frontotemporal dementia and/or Frontotemporal dementia and/or Frontotemporal dementia with Parkinsonism linked to chromosome 17, Creutzfeldt Jacob disease, stroke and/or neurotoxicity in patients with leukemia. The prosphopeptide kits and methods are useful for therapeutic monitoring and for determining the effectiveness of a treatment. Sequences ABBS5641-64 represent synthetic peptides immunoreactive to tau antibodies HT7, taul,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Determining the ratio of phospho-tau / total tau is useful for diagnosing a tauopathy i.e. Alzheimer's disease or Pick's disease, versus a non tauopathy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention provides a method of diagnosis of tauopathies in an
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vanmechelen E, Vanderstichele H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; Fig 1; 71pp; English.
                                                                                                                                                                                                                                                                                                                                             24-JAN-2000; 2000EP-0870008
27-JAN-2000; 2000US-0178391.
22-NOV-2000; 2000EP-0870280
                                                                                                                                                                                                                                                                                                                                                                                                                      (INNO-) INNOGENETICS NV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3T2, AT120 and AT270.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-476242/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
```

bind to human leukocyte antigens (HLAS). NY-ESO-1 is a molecule that is processed to at least one human leukocyte antigen (HLA) binding peptide, which binds to class I and class II major histocompatibility complex (HGC). NY-ESO-1 is expressed in tumour mRNA and in testis, but not normal colon, kidney, liver or brain tissue. The presence or level of expression of NY-ESO-1 may be assayed for the diagnosis of

especially

cancer,

Alignment Scores:

Sequence

AAG67169-AAG67206 represent peptides which are derived from cancer testis tumour antigen NY-ESO-1 (also called LAGE-2). The peptides

Example 13; Page 26; 50pp; English.

Conservative: Mismatches:

Indels:

Gaps:

GGGCCACCCCCAGGA 448

465

ă

(first entry)

9

```
TADG-16; ovarian carine protease; tumour antigen derived gene-16; prostate cancer; HIA type.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New tumour antigen-derived gene-16 protein, useful for diagnosis and treatment of ovarian, breast, lung, colon and prostate cancer
                                                                                            US-09-824-647-16 (1-2095) x AAB85642 (1-9)
                                                                                                                                                                                                                                             AAU02257 standard; Peptide; 9 AA
                                                                                                                                                                                                                                                                                                                                                         HLA binding TADG-16 peptide #33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-OCT-2000; 2000WO-US28558.
Percent Similarity: 100.008
Best Local Similarity: 100.008
Ouery Match: 0.878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UYAR-) UNIV ARKANSAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-273769/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40200127257-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-APR-2001.
                                                                                                                                                                                                                                                                                                                      29-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               O'Brien TJ,
                                                                                                                                                                                                                                                                                  AAU02257;
                                        Query Match:
                                                                                                                                                                                                                              AAU02257
                                                                                                                                                                                                                                                                                    The invention provides a method of diagnosis of tauopathies in an individual that comprises determining the ratio of phosphortau (181)/
total tau. Tau and phospho tau are useful as neurological markers for the manufacture of a diagnosit kit for the diagnosis of a tauopathy and/or the differential diagnosis of a tauopathy versus a non tauopathy and/or phospho-peptide liable to form an immunological complex with monoclonal antibody HT7 and MAD AT270 comprising at least the minimal epitope of HT7 or AT270 is useful to measure phospho-tau levels and diagnose a tauopathy and/or for the differential diagnosis of a tauopathy versus a non tauopathy. The kit is useful for the diagnosis of Alzheimer's disease, pick's disease, sporadic Frontotemporal dementia and/or Frontotemporal dementia and/or neurotoxicity in patients with leukemia. The phosphopeptide kits and methods are useful for therapeutic monitoring and for determining the effectiveness of a treatment. Sequences AMBSS641.64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    represent synthetic peptides immunoreactive to tau antibodies HT7, taul,
                                                                                                                                                                                                                                                                                                                                                                                                                    Tauopathy; phospho-tau (181); neurological marker; antibody; BT2; AT120;
HT7; AT270; nootropic; neuroprotective; cerobroprotective; epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Determining the ratio of phospho-tau / total tau is useful for diagnosing a tauopathy 1.e. Alzheimer's disease or Pick's disease, versus a non tauopathy -
                                                                                                                                                                                                                                                                                                                                                                                Synthetic peptide immunoreactive with tau antibody HT7
           90000
                       Conservative:
Mismatches:
Indels:
Gaps:
           Matches:
                                                                                                                   (1-9)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vanmechelen E, Vanderstichele H;
                                                                                                                                                                                                                                                                    AAB85642 standard; peptide; 9 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Fig 1; 71pp; English.
                                                                                                                     US-09-824-647-16 (1-2095) x AAB85641
                                                                                                                                                     24-JAN-2000; 2000EP-0870008.
27-JAN-2000; 2000US-0178391.
22-NOV-2000; 2000EP-0870280.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-JAN-2001; 2001WO-EP00560.
       6.00
100.00%
100.00%
0.87%
                                                                                                                                                                                                                                                                                                                                           29-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (INNO-) INNOGENETICS NV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BT2, AT120 and AT270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-476242/51.
                     Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200155725-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                         465
                                                                                                                                                                                                                                                                                                         AAB85642;
                                                                                                                                                                                                                                  RESULT 28
             Score:
```

Shigemasa K;

Underwood LJ,

```
AAU02225-AAU02384 represent TADG-16 peptides which are tested for their binding affinity to the 8 haplotypes HLA A0201, HLA A0205, HLA A1, HLA B24, HLA B27, HLA B2702, and HLA B40203. Tumour antigen derived gene-16 protein, TADG-16 (AAU02223), is a novel human extracellular serine protease. TADG-16 (AAU02223), is a novel human conserved catalytic triad, His-Asp-Ser, and a signal secretion sequence characteristic of the serine protease family. An antisense oligonucleotide having a complementary sequence to the TADG-16 nucleic acid is useful for treating various cancers, including ovarian, breast, antibodies specific to TADG-16 nucleic acid, TADG-16 protein and antibodies specific to TADG-16 nucleic acid, TADG-16 protein and antibodies specific to TADG-16 are useful for the diagnosis of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-824-647-16 (1-2095) x AAU02257 (1-9)
Example 8; Page 53; 124pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.94e+07
6.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                 ä
                                                                                                                                                                                                                                                                                                                                                                           against TADG-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..
Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred.
```

Length: Matches:

2.94e+07 6.00

Alignment Scores: Pred. No.: Score:

```
AAU02225-AAU02384 represent TADG-16 peptides which are tested for their binding affinity to the 8 haplotypes HLA A0201, HLA A0205, HLA A0201, HLA B07. December the A0201 THA B07. December the A0202 THA B07. DECEMBER THA B
                                                                                                                                                                                                                                                                                                                                                protease; tumour antigen derived gene-16;
breast cancer; lung cancer; colon cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New tumour antigen-derived gene-16 protein, useful for diagnosis and treatment of ovarian, breast, lung, colon and prostate cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shigemasa K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-824-647-16 (1-2095) x AAU02355 (1-9)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 8; Page 55; 124pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU02360
ID AAU02360 standard; Peptide; 9 AA.
                                                                                                                                             AAU02355 standard; Peptide; 9 AA
                                                                                                                                                                                                                                                                                          HLA binding TADG-16 peptide #131
884 GGGCAGCTCACCTCCATG 867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; extracellular serine
TADG-16; ovarian carcinoma;
prostate cancer; HLA type.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-OCT-2000; 2000WO-US28558.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0418527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94e+07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.00%
100.00%
0.87%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Underwood LJ,
                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UYAR-) UNIV ARKANSAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-273769/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200127257-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-OCT-1999;
                                                                                                                                                                                                                                            29-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 O'Brien TJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-APR-2001
884
                                                                                                                                                                                             AAU02355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                              RESULT 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 31
                                                                                                                        AAU02355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred.
                                                                                                                                                                    Š
```

```
oligonucleotide having a complementary sequence to the TADG-16 nucleic acid is useful for treating various cancers, including ovarian, breast, lung, colon and prostate. The TADG-16 nucleic acid, TADG-16 protein and antibodies specific to TADG-16 are useful for the diagnosis of cancer. TADG-16 protein or its fragments are useful for vaccinating an individual
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU02225-AAU02384 represent TADG-16 peptides which are tested for their binding affinity to the 8 haplotypes HLA A0201, HLA A0205, HLA A1, HLA A24, HLA B7, HLA B8, HLA B2702, and HLA B4403. Tummour antigen derived gene-16 protein, TADG-16 (AAU02223), is a novel human extracellular serine protease. TADG-16 is expressed in normal ovaries and testes and in certain ovarian carcinomas. TADG-16 contains the conserved catalytic triad, HLS-A5P-Ser, and a signal secretion sequence characteristic of the serine protease family. An antisense
                                                                                                                                      Human; extracellular serine protease; tumour antigen derivéd gene-16;
TADG-16; ovarian carcinoma; breast cancer; lung cancer; colon cancer;
prostate cancer; HLA type.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                diagnosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New tumour antigen-derived gene-16 protein, useful for diagnos
treatment of ovarian, breast, lung, colon and prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                00000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shigemasa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (1-9)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human NY-ESO-1 HLA binding motif #21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 8; Page 55; 124pp; English.
                                                                                                HLA binding TADG-16 peptide #136.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB69921 standard; Peptide; 9 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-824-647-16 (1-2095) x AAU02360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.94e+07
6.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 GlyGlnLeuThrSerMet
                                                                                                                                                                                                                                                                                                                                                                                                                13-OCT-2000; 2000WO-US28558.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     884 GGGCAGCTCACCTCCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-OCT-1999; 99US-0418527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.00%
100.00%
0.87%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Underwood LJ,
                                                29-AUG-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-APR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UYAR-) UNIV ARKANSAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-273769/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            against TADG-16
                                                                                                                                                                                                                                                                                                       WO200127257-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Aliqnment Scores:
                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                           19-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       O'Brien TJ,
AAU02360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB69921;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB69921
```

のからは、これのないのでは、これのないからないのできないないのできないないのできないないないないないないないないないないないないないないないないできないないないできないないないできないないないできない

```
AAP90829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HLA-A2.1 binding peptide; cytostatic; virucide; anti-HIV; hepatotropic; human immunodeficiency virus; antiinflammatory; antibacterial; vaccine; protozoacide; immunosuppressant; immunogenic peptide; T cell activation; human leucocyte antigen binding silte; cytotoxic T cell response; viral infection; hepatitis; bystein Barr virus; papilloma virus; human immunodeficiency virus; HIV; Kaposi sarcoma; Lassa fever virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is given in a specification relating to a method for determining the status of a cancerous condition in a patient with a tumour that expresses NY-ESO-1. The method comprises assaying a sample taken from the patient for antibodies that specifically bind to the NY-ESO-1 and comparing the value obtained to a prior value obtained form assay of a prior sample taken from the patient. Any difference between the values is indicative of a change in status of the cancerous condition. The method is useful for determining whether a cancerous in patients receiving treatment for a melanoma, adenocarcinoma, non-small cell lung carcinoma or bladder carcinoma.
                                                                                                                                                                                                                                                                                                                                                       Method useful for determining the status (e.g. progression, regression or stability of the disease) of a cancerous condition, involves determining the levels of NY-ESO-1 specific antibodies in a sample
 Human; NY-ESO-1; HLA; human leukocyte antigen; CTL; cytotoxic T cell; HLA-A2; HLA-DR53; melanoma; adenocarcinoma; bladder carcinoma; non-small cell lung carcinoma; tumour status determination.
                                                                                                                                                                                                                                                                                           Scanlan M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Immunogenic peptide with (HLA)-A2.1 binding site #16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60000
                                                                                                                                                                                                                                                                                             chen Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
                                                                                                                                                                                                                                                                                             Knuth A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps:
                                                                                                                                                                                                                            (LUDW-) LUDWIG INST CANCER RES.
(SLOK ) SLOAN KETTERING INST CANCER RES.
(CORR ) CORNELL RES FOUND INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (1-9)
                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 14; Page 25; 50pp; English:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU95803 standard; Peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1119 CAGCAGCTGTCCCTCCTC 1136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-824-647-16 (1-2095) x AAB69921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                              old LJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GinginLeuSerLeuLeu
                                                                                                                                                                    14-JUL-2000; 2000WO-US19220..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.94e+07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.00%
100.00%
0.86%
                                                                                                                                                                                                99US-0359503.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8
                                                                                                                                                                                                                                                                                                Stockert E,
                                                                                                                                                                                                                                                                                                                                                                                                            taken from a patient
                                                                                                                                                                                                                                                                                                                              WPI; 2001-182822/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 AA;
                                                                                                      40200107917-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-JUL-2002
                                                                                                                                                                                                     23-JUL-1999;
                                                                        Homo sapiens
                                                                                                                                      01-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAU95803;
                                                                                                                                                                                                                                                                                                  Jager E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU95803
```

à

```
The invention describes a composition comprising an immunogenic peptide having a human leucocyte antigen (HLA)-A2.1 binding site. The peptides bind specifically to HLA-A2.1, to cause T cell activation and thus a cytotoxic T cell response. The peptides and the nucleic acids that cytotoxic T cell response. The peptides and the nucleic acids that encodes them, are used, in vivo or ex vivo, for treatment of viral infections (hepatitis B or C; Epstein-Barr; human immune deficiency; infections (hepatitis B or C; Epstein-Barr; human immune deficiency; Kaposi sarcoma: human papiliona; Lassa fever or dytomegaloviruses); theoris in human papiliona; Lassa fever or dytomegaloviruses); clumours including prostate cancer, renal carcino-embryonal antigen, directed to prostate-specific antigen, p53, carcino-embryonal antigen, corporace directed to trypanosome surface antigen); and condlylome or protozoa directed to trypanosome surface antigen); and condlylome cauminatum. The peptides are suitable for use in peptide-based vaccines. This sequence represents an immunogenic peptide with the human leucocyte antigen (HLA)-A2.1 binding site, described in the
cytomegalovirus; tumour; prostate cancer; renal carcinoma; lymphona; prostate-specific antigen; p53; carcino-embryonal antigen; melanoma antigen; Mycobacterium tuberculosis; protozoa; trypanosome surface antigen; condlyloma acuminatum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Immunogenic peptide with human leucocyte antigen-A2.1 binding site, useful for treating e.g. viral infection or tumours
                                                                                                                                                                                          Æ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New bradykinin analogue with D-beta-(2-napththyl)-Ala,
beta-(2-thienyl)-Ala and D-Phe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    690000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bradykinin analogue; bradykinin antagonist.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                      Ś
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Southwood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (1-9)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ...J
Misc-difference 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-824-647-16 (1-2095) x AAU95803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGGACGGCAGCAGCTGTA 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAP90829 standard; protein; 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 24; 35pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Grey HM, Sette A, Sidney J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.94e+07
6.00
100.00%
100.00%
0.87%
                                                                                                                                                                                                                                                                                        01-SEP-2000; 2000WO-US24102.
                                                                                                                                                                                                                                                                                                                                                 01-SEP-2000; 72000WO-US24102.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-JUN-1990 (first entry)
                                                                                                                                            Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                 (EPIM-) EPIMMUNE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-351766/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 AA;
                                                                                                                                                                                                   WO200220616-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
                                                                                                                                                                                                                                                       14-MAR-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . ednence .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAP90829;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 34
```

Zoller MJ

```
The sequences given in AAR93272-342 represent peptides which are SH3 ligands/SH3 binding agents. They represent a biased phage library which comprises six random amino acids flanking the tetrapeptide phich which was identified as a recognition sequence for the src SH3 domain. These sequences were identified using the method of the invention. The method comprises contacting the SH3 domain with a mixture of peptides under conditions permitting a ligand to bind to an SH3 domain to form a complex. Any unbound peptides are removed and the complexed peptide ligands are dissociated from the complexes. The selected peptides are enriched by re-contacting them with the SH3 domain and then candidates which bind to the SH3 domain are detected. The isolated SH3 binding peptides may be used in the diagnosis, prevention and treatment of conditions or diseases resulting from cellular processes mediated by an SH3-based interaction. Such diseases include Paget's disease. Other conditions treatable with these peptides include restenosis, rheumatoid arthritis, gout and other problems in which an SH3 of neutrophil oxidase p47 and p67 complex is
                                                                                                                                                                                                                                                                                                                                                                             Identification of peptide(s) binding specifically to SH3 domains for use in inhibiting interactions mediated by SH3 domains in treatment of e.g. osteoporosis and cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chlamydial epitope; variable domain; MOMP;
major outer membrane protein; picornavirus; poliovirus; PV1;
diagnostic; therapeutic; capsid protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps:
                                                                                                                                                                                                                                                                             Rickles RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-824-647-16 (1-2095) x AAR93340 (1-10)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 1; 74pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTCCCTCCGATACCT 1144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chlamydia trachomatis serovar A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR66370 standard; peptide; 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 ValProProProllePro 10
                                                                                                                                                   95US-0369832.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.88e+04
6.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chlamydial MOMP VDI epitope.
                                                                                                     95WO-US03208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.00%
100.00%
0.86%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-JUN-1995 (first entry)
                                                                                                                                                                                                                                                                             Brugge JS,
                                                                                                                                                                                                                            PHARM INC
                                                                                                                                                                                                                                                                                                                               WPI; 1995-328231/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   implicated, etc.
                                                                                                                                                                                                                               (ARIA-) ARIAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity
                                                                                                                                                   06-JAN-1995;
11-MAR-1994;
                                                                                                  13-MAR-1995;
     W09524419-A1
                                                                                                                                                                                                                                                                             Botfleld MC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
                                                      14-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9426900-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR66370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR66370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            It may be prepd. by conventional liq. - or solid-phase peptide synthesis methods. It is useful for treating local pain, inflammation and swelling, rhinitis, hypotension, asthma, arthritis, diarrhoea, irritable bowel syndrome, carcinoid syndrome, angina pain, and anaphylactic or septic shock: Pharmaceutical compsns. can be made with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SH3 ligand; SH3 binding agent; blased phage library; recognition sequence; src SH3 domain; Paget's disease; restenosis; rheumatoid arthritis; gout; neutrophil oxidase; tyrosine kinase; p67; complex; chronic myelogenous leukaemia; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New peptide bradykinin analogues -
with D-amino acid in 7 position, useful as bradykinin antagonists
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TSK protein tyrosine kinase derived peptide #4.
/label=OTHER
/note="D-beta-(2-naphthyl)-Ala"
                                                                                                                                                                        'note="beta-(2-thienyl)-Ala"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-824-647-16 (1-2095) x AAP90829 (1-10)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR93340 standard; peptide; 10 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 10; page 52; 54pp; English.
                                                                      /label=OTHER
/note="As above"
                                                                                                                                                                                                                                                 'note="As above"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             462 GCAGCACCCCAGGAGCC 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label=OTHER
                                                                                                                                              /label=OTHER
                                                                                                                                                                                                                                                                                                  /label=D-Phe
                                                                                                                                                                                                                                                                                                                                                                                                                                                   88WO-US02960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     870S-0091995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88e+04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.00%
100.00%
0.87%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vavrek RJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1989-085401/11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (STEW/) STEWART JM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ¥,
                                                 Misc-difference
                                                                                                                       Misc-difference
                                                                                                                                                                                                Misc-difference
                                                                                                                                                                                                                                                                   Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-SEP-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 39-AUG-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
                                                                                                                                                                                                                                                                                                                                              WO8901781-A.
                                                                                                                                                                                                                                                                                                                                                                                                  09-MAR-1989.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Stewart JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR93340;
```

Query Match:

Pred

RESULT 35 AAR93340

ö

```
(SANG-) SANGSTAT MEDICAL CORP
WPI; 1997-480355/44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-FEB-1998;
11-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W09846633-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW82826;
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW82826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                    Mahoney CDNA clone PTXID was modified to encode epitopes from C. trachomatis ser. A MOMP VDI. The mutagenesis cartridge was contained between PV nucleotides 2753-91 (given in AAQ79003) which encode PV amino acids 1092-1104 (AAR66375) which include the BC loop of capsid protein VP1 (AAR66386). The polio-specific DNA within the cartridge, encoding the sequence given in AAR66366, was replaced by eligonucleotides encoding VDI peptides AAR66370-74. Viable PV expressing chlamydial immunostimulatory epitope was expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteriophage peptide library;peptide epitope; therapeutic target;
variegated compound library; interleukin-8; IL-8.
                                                                                                                                                                              nseq
                                                                                                                                                                           New hybrid picornaviruses expressing chlamydial epitopes - to develop prods. for vaccination, diagnosis, treatment of chlamydial infections and prodn. of immunological reagents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               D-form Interleukin-8 peptide ligand consensus sequence 2.
                                                                                                                                                                                                                                                         obtain a poliovirus-1 (PV1)/chlamydial hybrid, the PV1
                                                                                                                                                                                                                                                                                                                                                                                                                                             00000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative:
Mismatches:
Indels:
                                                                                                                          Oomen RP;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-824-647-16 (1-2095) x AAR66370 (1-10)
                                                                                                                          Klein MH, Murdin AD,
                                                                                                                                                                                                                                Disclosure; Page 15; 99pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW42311 standard; Peptide; 10 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96US-0622338
                                            94WO-CA00262.
                                                                                                                                                                                                                                                                                                                                                                                                                                             1.88e+04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.00%
100.00%
0.86%
                                                                     93US-0060978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                               (CONN-) CONNAUGHT LAB LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HARD ) HARVARD COLLEGE
                                                                                                                                                   WPI; 1995-006796/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                        10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W09735194-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-MAR-1996;
                                                                                                                          Caldwell HD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-APR-1998
                                            12-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
                                                                      3-MAY-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Forster AC;
                                                                                                                                                                                                                                                                                                                                                                              Vero cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW42311;
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW42311
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
```

```
target molecule, and comprises contacting a screening molecule with a target molecule, and comprises contacting a screening molecule with a variegated compound library, where the screening molecule is chiral.

Target molecule, or the enantioner if the target molecule is chiral.

Compounds which have a desired interaction with the target molecule are selected, and the ability of their enantioner to interact with the target molecule is tested. Ligands for a target protein can be identified by combining a D-fanationer of a target protein can be identified by complining a D-fanationer of a target protein (a D-target protein), and a variegated compound library, and then selecting one or more compounds from the library which have a desired binding interaction with the cartagonists of targets such as receptors, enzymes, DNA binding proteins or signal transduction proteins. The methods can provide a structurally selective approach in addition to scoring for interaction of functional groups. They provide a powerful selection method that allows for the production of ligands with the same diversity as peptides but with the sealty improved pharmacokinetic profiles needed for drug activity.
                                                                                                                                                                                                                       The present sequence represents a consensus sequence obtained after several rounds of selection and amplification of a 6-mer peptide library. The consensus sequence is derived from peptide ligands of a D-enantiomer of interleukin-8 (IL-8), and was obtained using the method of the invention. This novel method identifies compounds which interact with a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cytomodulating lipophilic oligopeptide; immune system; inflammation; cytotoxic; lymphocytic; inhibition; cytokine; autoimmune disease; T (B cell; mononuclear phagocyte; septic shock; rheumatoid arthritis; Crohn's disease; colitis; allergy; transplant.
Identifying compounds which interact with target molecules - using enantiomers of the target molecules and testing of enantiomers of selected compounds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               00000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cytomodulating lipophilic oligopeptide (w).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (1-10)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW82826 standard; peptide; 10 AA.
                                                                                                                                                      English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-824-647-16 (1-2095) x AAW42311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  741 GTGATCGGAGCAGCAGGT 724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 valileGlyAlaAlaGly 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98WO-US07231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98US-0028083,
97US-0838916,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.88e+04
6.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.00%
100.00%
0.87%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-JAN-1999 (first entry)
                                                                                                                                                             Disclosure; Fig 8; 89pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ä
```

us-09-824-647-16.lim.rag

```
08-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY06009
    AAW82804 to AAW82829 are cytomodulating lipophilic oligopeptides. The oligopeptides are used to inhibit: (i) activity of lymphocytes cligopeptides are used to inhibit: (i) activity of lymphocytes.

(particularly cytotoxic T cells, but also natural killers, Becals and monouclear phagocytes); (ii) production of inflammatory cytokines, and (iii) an inflammatory response in mammals (e.g. in cases of septic.

Shock, rheumatoid arthritis (RA), Crohn's disease, colitis and allergy). They are also used for modulating activity of haem-containing enzymes and for delaying onset of autoimmune disease (specifically insulin-dependent diabetes mellitus, RA and systemic lupus erythematosus). In all cases the oligopeptides may be generated from nucleic acids, and treatments are in vitro or in vivo. A specific application is treatment of organs or calls for transplantation, or of the recipient of such treasplants.

The part from therapeutic use, the oligopeptides can be used to study mechanisms of T cell (de)activation and to raise antibodies (used to identify oligopeptides and to raise anti-idiotypic antibodies that are competitors of the oligopeptides. The oligopeptides are administered by the oligopeptides increases the life of the oligopeptides increases the life of
                                                                  New lipophilic peptide(s) that inhibit activation of immune system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy; vaccine; human leukocyte antigen; HLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human; leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer; metastasis; melanoma; adenocarcinoma; thymoma; colon cancer; uterine cancer; breast cancer; prostate cancer; ovarian cancer;
                                                                                  cells - used for, e.g. production of cytokine(s) and the inflammatory response, and also for modulating haem-containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human cancer antigen NY ESO-1/CAG-3 HLA peptide motif.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   00000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-824-647-16 (1-2095) x AAW82826 (1-10)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY05999 standard; Peptide; 10 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1131 CTCCTCCGATACCTGCTG 1148
                                                                                                                                         Claim 7; Page 37; 48pp; English.
              Grassy G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98WO-US19609.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.88e+04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.86%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
                                         WPI; 1998-594558/50.
              B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity:
              Calas
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W09918206-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                             ransplants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-APR-1999
              ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY05999;
                                                                                                               enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match:
DB:
              Buelow
                                                                                   cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY05999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score
á
```

```
coreen for epitopes from the coding region of human ESO-1/CAG-3

ORF1 (see AAX58599). 30 Epitopes (see AAX0588-Y06017) were identified.

The present peptide (ranked 12) corresponds to amino acid residues

152-161 of CAG-1 ORF1 (see AAY05965). CAG-1 is a new and potent
tumour antigen capable of eliciting an antigen specific immune
cresponse by T (cells. Cancer peptides (see AAX05967-87) derived from
CAG-3, portions of CAG-3 and their variants, are useful as cancer
vaccines. A claimed method of preventing or inhibiting cancer
involves administering a cancer peptide, with or without an HLA
molecule. The cancer peptides form part of, or are derived
from, cancers such as primary or metastatic melanoma, thymoma,
C lymphoma, sarcoma, lung cancer, ilver cancer, leukaemia, uterine
cancer, cervical cancer, bladder cancer, kidney cancer and
adenocarcinomas such as breast, prostate, ovarian, pancreatic and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer; detastasis; melanoma; adenocarcinoma; thymoma; colon cancer; uterine cancer; breast cancer; prostate cancer; ovarian cancer; cervical cancer; bladder cancer; kidney cancer; pancreatic cancer; liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                peptide; antigen; human;
                                                                                                                                                                                                                                                                                                                                               this peptide was identified as an HLA peptide motif following
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human cancer antigen NY ESO-1/CAG-3 HLA peptide motif.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               00000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
                                                     (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NY ESO-1/CAG-3 gene; CAG-3 gene; cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-824-647-16 (1-2095) x AAY05999 (1-10)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        vaccine; human leukocyte antigen; HLA
                                                                                                                                                                                                                                                                                      Example 10; Page 42; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY06009 standard; Peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1119 CAGCAGCTGTCCTCTC 1136
                                                                                                                                                                                                                                Cancer antigen NY ESO1/CAG-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.88e+04
6.00
100.00$
100.00$
0.86$
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GlnGlnLeuSerLeuLeu
97US-0061428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97US-0061428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98WO-US19609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-AUG-1999 (first entry)
                                                                                                              Wang RF
                                                                                                                                                                    WPI; 1999-277270/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               thyroid cancers
                                                                                                           Rosenberg SA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
08-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9918206-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5-APR-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY06009;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
```

07:45:06 2003

Tue Jul

WPI; 1999-277270/23

Rosenberg SA,

(USSH) US DEPT HEALTH & HUMAN SERVICES

Rosenberg SA, Wang RF; WPI; 1999-277270/23.

JS-09-824-647-16 (1-2095) x AAY06009 (1-10) Example 10; Page 42; 88pp; English. AAY05997 standard; Peptide; 10 AA. Cancer antigen NY ESO1/CAG-3 Percent Similarity: Best Local Similarity: 10 AA; thyroid cancers 16-AUG-1999 Alignment Scores: Sequence AAY05997; 1119 Query Match: DB: RESULT Score: ò

0000

This peptide was identified as an HLA peptide motif following a screen for epitopes from the coding region of human ESO-1/CAG-3 ORF1 (see AAY0598-Y06017) were identified.

C ORF1 (see AAY0596). COTESPONDS to amino acid residues to more peptide (ranked 22) corresponds to amino acid residues (tumour antigen capable of elliciting an antigen specific immune response by T cells. Cancer peptides (see AAY05967-87) derived from CAG-3, portions of CAG-3 and their variants, are useful as cancer vaccines. A claimed method of preventing or inhibiting cancer (involves administering a cancer peptide, with or without an HLA molecule. The cancer peptides form part of, or are derived from cancers such as primary or metastatic melanoma, thymoma, acroma, lung cancer, liver cancer, leukaemia, uterine cancer, cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such as breast, prostate, ovarian, pancreatic and

Matches: Conservative: Mismatches: Length: Indels: Gaps: 100.00% 100.00% 0.86% 1.88e+04

CAGCAGCTGTCCTCCTC 1136 GlnGlnLeuSerLeuLeu 6

AAY05997 ID AAY

(first entry)

Human cancer antigen NY ESO-1/CAG-3 HLA peptide motif.

NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human; leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer; metastasis; melanoma; adenocarcinoma; thymoma; colon cancer; uterine cancer; breast cancer; prostate cancer; ovarian cancer; cervical cancer; bladder cancer; kidney cancer; pancreatic cancer; liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy; vaccine; human leukocyte antigen; HLA

domo sapiens

WO9918206-A2

15-APR-1999.

98WO-US19609 21-SEP-1998;

970S-0061428 08-OCT-1997;

(USSH) US DEPT HEALTH & HUMAN SERVICES.

This peptide was identified as an HLA peptide motif following a screen for epitopes from the coding region of human ESO-1/CAG-3 coren for epitopes (see AAY0598-706017) were identified.

CORFI (see AAX5859) 30 Epitopes (see AAY0598-706017) were identified.

The present peptide (ranked 10) corresponds to amino acid residues is a new and potent tumour antigen capable of eliciting an antigen specific immune response by T cells.

CAG-3, portions of CAG-3 and their variants, are useful as cancer vaccines. A claimed method of preventing or inhibiting cancer involves administering a cancer peptide, with or without an HLA molecule. The cancer peptides form part of, or are derived from cancers such as primary or metastatic melanoma, thymoma, from, cancers such as primary or metastatic melanoma, thymoma, cancer, cervical cancer, ludge cancer, ludge cancer, ludge cancer, cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such as breast, prostate, ovarian, pancreatic and Example 10; Page 42; 88pp; English. Cancer antigen NY ESO1/CAG-3 10 AA; thyroid cancers. Sequence

Conservative: Mismatches: Indels: Length: Matches: Gaps: 1.88e+04 6.00 100.00% 100.00% 0.86% Percent Similarity: Best Local Similarity: Query Match: Alignment Scores: .. Q Score:

US-09-824-647-16 (1-2095) x AAY05997 (1-10)

CAGCAGCTGTCCCTCCTC 1136 1119

AAY13579 RESULT

AAY13579 standard; peptide; 10 AA.

AAY13579;

30-JUL-1999 (first entry)

Peptide sensor TUK-1473.

Nuclear hormone receptor; sensor peptide; receptor binding; screening; modulator.

W09927365-A1 Synthetic:

03-JUN-1999

98WO-US24969. 20-NOV-1998; 98US-0163713. 97US-0975614. 30-SEP-1998; 21-NOV-1997;

(TULA-) TULARIK INC.

Chen J, Lustig K, Baeuerle P, Beckmann H,

WPI; 1999-347794/29.

Nuclear hormone receptor drug screens

```
binding reaction occurs in solution. The sensor peptide obviates the need to include a natural coactivator protein of the receptor in the mixture. Sequences AAY13571-587 represent examples of sensor peptides that can be
                                                         hormone receptor function. The methods use a sensor peptide covalently coupled to a detectable label, that provides direct, in vitro ligand-dependent binding to a nuclear hormone receptor. Panels of predetermined or randomized candidate sensors are readfly screened for receptor binding. The methods and compositions provide for efficient screening of modulators of nuclear hormone receptor function, without the use of cell- or gel-based steps. The methods are amenable to automated, cost-effective high throughput sorreening of chemical libraries for bloactive compounds. To ensure specificity and optimize binding, the sensor is generally present at sub-micromolar concentration and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bacteria; fungi; yeast; protozoa; virus; mycoplasma; filaria; plasmodia;
infection; inflammation; microbial induced tumour; degenerative disorder
diarrhoea; colic; oral microflora; intestinal microflora; caries;
                                                 screening of modulators of nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This invention describes milk-derived bifidogenic peptides and their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bifidogenic peptide; protease; treatment; microbe-related disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Milk-derived peptides that stimulate Bifidobacterium bifidus
                                                                                                                                                                                                                                                                                                                                                          000000
                                                                                                                                                                                                                                                                                                                                                                                        Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bifidobacterium bifidus stimulating peptide 8.
                                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                         Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (4-10)
                                                                                                                                                                                                                                                                         used in the method of the invention
                                               The invention provides methods for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW93872 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zucht H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1131 CTCCTCCGATACCTGCTG 1148
             Claim 7; Page 18; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-824-647-16 (1-2095) x AAY13579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 2; Page 3; 25pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98WO-EP05899.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98DE-1005385.
97DE-1040604.
                                                                                                                                                                                                                                                                                                                                                                                       100.00%
                                                                                                                                                                                                                                                                                                                                                        1.88e+04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-JUN-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                         0.868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Liepke C,
                                                                                                                                                                                                                                                                                                                                                                         8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bifidobacterium bifidus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (FORS/) FORSSMANN W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-244022/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vaginal microflora.
                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                         10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W09914231-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Forssmann W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-FEB-1998;
16-SEP-1997;
                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-MAR-1999
                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW93872;
                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW93872
                                                                                                                                                                                                                                                                                                                                                                           Score:
                                                                                                                                                                                                                                                                                                                                                            Pred.
```

```
chemical coupling. Such are produced from bovine or human milk by chemical coupling. Such are produced from bovine or human milk by treatment for 2 hr with proceases, then centrifuging to remove fat and caidifying to pH 2 to precipitate proteins. The solution phase is then subjected to reverse-phase high-performance liquid chromatography (HPLC) and cation-exchange HPLC, the fractions adjusted to salt content below can cation-exchange HPLC, the fractions adjusted to salt content below growing Bifidobacterium bifidus and Escherichia coll in pregence of the fractions. Those fractions for which (Bw-B0). (Ew-E0) is at least 0.15 are selected where Bw = germ count after 16 hr culture of B. Difidus in 50 Biliker broth containing peptide at 0.2 mg/ml, BO = germ count under similar conditions in a peptide-free control. Bw = germ count after 16 hr culture of B. Difidus in 50 Biliker, broth containing peptide similar conditions in a peptide-free control. The peptides Aaw93865-W93888 are used to treat microbe-related control. The peptides Aaw93865-W93888 are used to treat microbe-related shoots and plasmodia, e.g. infections, inflammation, microbially induced tumours or degenerative disorders, diarrhees, colic, abnormalities in oral, intestinal or vaginal microflora, or caries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Variable domain; MOMP; major outer membrane protein; subunit vaccine; C. trachomatis infection; serotyping; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence represents an epitope of the major outer membrane protein (MOMP) of Chlamydia trachomatis. The invention relates to variable domain fragments of the MOMP of Chlamydia trachomatis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chlamydia trachomatis peptides - and DNA fragments encoding them
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Watkins NG, Ying Y, Zhang Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Column 11-12; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-824-647-16 (1-2095) x AAW93872 (1-10)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW74014 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C. trachomatis MOMP epitope A-20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1379 GCTGCCCGAGCCAGGGTG 1396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92US-0853359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 AlaAlaArgAlaArgVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          890S-0324664
920S-0853359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6:00
100.00%
100.00%
0.86%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .88e+04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chlamydia trachomatis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-152876/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                        10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Caldwell HD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-MAR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-MAR-1989;
16-MAR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JS5869608-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW74014;
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW74014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                $$$$$$$$$$$$$$$$$$$$$$$$$$
```

```
Cancer testis tumour antigen; NY-ESO-1; LAGE-2; human leukocyte antigen; HLA; HLA binding peptide; major histocompatibility complex; MHC; tumour; cancer; testis tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genomic sequences of tumour associated antigen EY-ESO-1 (LAGE-2) useful for diagnosing testicular tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAG67169-AAG67206 represent peptides which are derived from cancer testis tumour antigen NY-ESO-1 (also called LAGE-2). The peptides bind to human leukocyte antigens (HLAS). NY-ESO-1 is a molecule that is processed to at least one human leukocyte antigen (HLA) binding peptide, which binds to Class I and Class II major histocompatibility complex (MHC). NY-ESO-1 is expressed in tumour mRNA and in testis, but not normal colon, kidney, liver or brain tissue. The presence or level of expression of NY-ESO-1 may be assayed for the diagnosis of
serovar Ba, serovar D, serovar E, serovar F, serovar G, serovar H, serovar I, serovar J, serovar K, and serovar L3, and to DNA sequences encoding them. The peptides are useful in diagnostic tests for C trachomatis infections, serological tests for serotyping, and as subunit vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cancer testis tumour antigen NY-ESO-1 derived peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10
6
0
                                                                                                                                               00000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
                                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                              Gaps:
                                                                                                                                                                                                                                                        US-09-824-647-16 (1-2095) x AAW74014 (1-10)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 13; Page 26; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cancer, especially testis tumours.
                                                                                                                                                                                                                                                                                                                                                                                         AAG67204 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                          1279 GTGGCTGGACTGGAGAG 1296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (LUDW-) LUDWIG INST CANCER RES.
                                                                                                                                                                                                                                                                                                            2 ValAlaGlyLeuGluLys 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.88e+04
6.00
100.00%
                                                                                                                                        1.88e+04
6.00
100.00%
100.00%
0.86%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-JAN-2001; 2001WO-US02126.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-FEB-2000; 2000US-0510635
                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Boon-Falleur T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-550091/61.
                                                                                                                                                                                          Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A);
                                                                                               10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200162917-A1
                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
Pred. No.:
                                                                                                                              Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                       AAG67204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lethe B,
                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                           RESULT 45
                                                                                                                                                                                                                                                                                                                                                                           AAG67204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88888888
                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                          δ
```

```
Best Local Similarity: 100.00% Mismatches:
Ouery Match: 0.86% Indels:
DB: 22 Gaps:
US-09-824-647-16 (1-2095) x AAG67204 (1-10)
Oy 1119 CAGCAGCTGCCCTCCT (136
I GINGINLEUSErLeuLeu 6
Search completed: July 7, 2003, 16:07:23
Job time: 94 secs
```

us-09-824-647-16.lim.rapb

```
Sequence 5, Appli
Sequence 108, Appli
Sequence 143, Appli
Sequence 5, Appli
Sequence 7, Appli
Sequence 195, App
Sequence 5, Appli
                                                                                                                                                                                                                                                               1060,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3851,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7, Application US/09824647

Sequence 7, Application US/09824647

Publication No. US20020183270A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REFERENCE: 29996.488/P001-A

CURRENT PILING DATE: 2001-04-04

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/991,862

PRIOR RILING DATE: EARLIER FILING DATE: 1998-08-17

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/863,862

PRIOR FILING DATE: EARLIER FILING DATE: 1997-05-23

NUMBER: OF SOI DATE: AND APPLICATION NUMBER: 08/863,862
                                                                                                                                                                                                                                      Sequence 55,
Sequence 375
Sequence 379
Sequence 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (1)...(14)

OTHER INFORMATION: Internal peptide of human GP88 used to develop

OTHER INFORMATION: neutralizing anti-human GP88 monoclonal antibody
US-09-824-647-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                   Sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence seq
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
Sequence
Sequence
                                                                                                              0 US-09-813-1156-5

0 US-09-824-807-5

0 US-09-865-446A-143

0 US-09-731-449-55

0 US-09-731-449-55

0 US-09-731-449-55

0 US-09-572-404B-375

0 US-09-572-404B-379

0 US-09-572-404B-403

0 US-09-572-404B-403

0 US-09-572-404B-419

0 US-09-572-404B-419

0 US-09-572-404B-500

0 US-09-572-404B-500

0 US-09-572-404B-500

0 US-09-572-404B-2101

0 US-09-572-404B-2101

0 US-09-572-404B-2103

0 US-09-572-404B-326

0 US-09-572-404B-3673

0 US-09-572-404B-3673

0 US-09-572-404B-3673

0 US-09-572-404B-3673

0 US-09-572-404B-3673

0 US-09-572-404B-3673

0 US-09-572-404B-3673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Human granulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : Patentin Ver.
  NAME/KEY: PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alignment Scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JS-09-824-647-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0 0 0 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             000
                                                                                                                                                                                                                                                                 \circ \circ \circ \circ \circ \circ \circ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -MODEL-frame+_n2p.model -DEV-x1p
-Q-Cgn2_1/USPTO_spool/US09824647/runat_07072003_154800_26675/app_query.fasta_1.2247
-Q-Cgn2_1/USPTO_spool/US09824647/runat_07072003_154800_26675/app_query.fasta_1.2247
-Q-Cgn2_1/USPTO_spool/US09824647/runat_07072003_154800_26675/app_query.fasta_1.2247
-LOOPCL-0 -LOOPEXT-0 -UNITS-bits -STARR-1 -END-1 -MATRIX-oligo
-TRANS-human40.cd1 -LIST-45 -DOCALIGN-200 -THR_SCORE-quality -THR_MIN-1
-ALIGN-45 -MODE-LOCAL -OUTFWT-pto -NORM-ext -HEAPSIZE=500 -MINLEN-0 -MAXLEN-15
-USER-US9924647_@CG1_1_24_@runat_07072003_154800_26675 -NCPU-6 -ICPU-3
-NO_MMAP -LARGEQUERY -NGS_SCORES-0 -WAIT -DSPBLOCK-100 -LONGICG
-DEV_TIMEOUT-120 -WARN_TIMEOUT-30 -THRRADS-1 -XGAPOP-60 -XGAPEXT=60 -FGAPOP-6
-FGAPEXT=7 -YGAPOP-60 -YGAPEXT=60 -DELOP-6 -DELDEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 7, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 7, Appli
                                                                                                                                                                                          (without alignments)
6257.407 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                             1 cgcaggcagaccatgtggac.....ataaagtttgtcactttctt 2095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | Cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
| Cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US00_PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
                                                                                                                                                               7, 2003, 16:04:42; Search time 77 Seconds
                      GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                   protein search, using frame_plus_n2p model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-824-647-7
US-10-218-509-7
US-10-281-160-7
US-09-813-156-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   440863 seqs, 114992915 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Published_Applications_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                60.0
60.0
7.0
7.0
                                                                                                                                                                                                                                                                                                                                                                                , Ygapext 6
, Ygapext 6
, Fgapext
, Delext
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . 6 6 6 1
                                                                                                                                                                                                                                                       US-09-824-647-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1144
                                                                                                                                                                                                                                                                                                                                                                                60.0
60.0
6.0
6.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Minimum DB seq length: 0
Maximum DB seq length: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Command line parameters:
                                                                                                                                                                                                                                                                                                                                                                             Xgapop
Ygapop
Fgapop
Delop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0000
                                                                                                                                                                 July
                                                                                                                                                                                                                                                                                                                                                         OFIGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score
                                                                                                                                                                                                                                                            Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                       Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7777
                                                                                                                   OM nucleic -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Word size:
                                                                                                                                                                                                                                                                                                           Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Searched:
                                                                                                                                                                 Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Result
No.
```

```
ORGANISM: Human granulin
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
                                                                                                                                                                                                                                           Alignment Scores;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 5
US-09-824-807-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-813-156-7
                                                                                                                                                                                  US-10-281-160-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 7
LENGTH: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                   Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No.:
                                                                                                                                                                                                                                                                         Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7, Application US/10281160
Publication No. US20030108950A1
GENERAL INFORMATION:
APPLICANT: Serrero, Ginette
APPLICANT: Serrero, Ginette
TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REPERBACE: 29996.488/PP001-A
CURRENT APPLICATION NUMBER: US/10/281,160
CURRENT FILING DATE: 2002-10-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT INTEGRATION OF THE APPLICANT SETTED OF THE APPLICANT SETTED OF TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL OF APPLICATION NUMBER: US/91,862 PRIOR APPLICATION NUMBER: US/91,862 PRIOR FILING DATE: 1999-05-17 PRIOR FILING DATE: 1999-05-13 NUMBER OF SEQ ID NOS: 17 SOFTWARE: PATENTIN VOTAL OF TOTAL OF TOT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18 used to develop
monoclonal antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1708 GCACGCAGGGGTACCAAGTGTTTGCGCAGGGAGGCCCCGCGC 1749
                                                                                                                                                                                                                                                                                                             440000
                  0000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: (1)..(14)
OTHER INFORMATION: Internal peptide of human GP88
OTHER INFORMATION: neutralizing anti-human GP88 mc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches:
Conservative:
Mismatches:
Indels:
                                                                     Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-824-647-16 (1-2095) x US-10-218-509-7 (1-14)
                                                                                                                                                                                                                   US-09-824-647-16 (1-2095) x US-09-824-647-7 (1-14)
               Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps:
                                                                                                                                                               Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 1998-08-17
PRIOR FILING DATE: 1998-08-17
PRIOR PRILING DATE: 1997-05-23
NUMBER OF SEQ ID NOS: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7, Application US/10218509 Publication No. US20030092661A1 GENERAL INFORMATION:
            0.000925
14.00
100.00%
100.00%
2.02%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.000925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14.00
100.00$
100.00$
2.02$
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Human granulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity:
Query Match:
                                                                        Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 3
US-10-281-160-7
                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-218-509-7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-218-509-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGIH: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: 1
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
                                                                                                                                    Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score:
                                                   Score:
                     Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            q
                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                        셤
```

```
Sequence 7, Application US/09824807
Sequence 7, Application US/09824807
Patent No. US20020094966A1
GENERAL INFORMATION:
APPLICANT: Serrero, Ginette
TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REFERENCE: 29996.488/PP001-A
CURRENT APPLICATION NUMBER: US/09/824,807
CURRENT FILING DATE: 2001-04-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Serrero, Ginette
TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
TITLE DEPERENCE: 2996.488/P001-A
CURRENT APPLICATION NUMBER: US/09/813,156
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 08/991,862
PRIOR FILING DATE: 1997-12-16
PRIOR FILING DATE: 1997-05-23
KUMBER OF SEQ ID NOS: 17
SOFTWARE: PATENTIN OF 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (1)..(14)
OTHER INFORMATION: Internal peptide of human GP88 used to develop
OTHER INFORMATION: neutralizing anti-human GP88 monoclonal antibody
                                GP88 used to develop
988 monoclonal antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1708 GCACGCAGGGGTACCAAGTGTTGCGCAGGGAGGCCCCGCGC 1749
                                                                                                                                                                                                                                                                                                               1708 GCACGCAGGGGTACCAAGTGTTTGCGCAGGGAGGCCCCGCGC 1749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0000
                                                                                                                                    770000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                Length:
Matches:
Conservative:
Mismatches:
Indels:
NAME/KEY: PEPTIDE
LOCATION: (1)..(1)..(1)..OPD
OTHER INFORMATION: Internal peptide of human GP8
OTHER INFORMATION: neutralizing anti-human GP88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-824-647-16 (1-2095) x US-09-813-156-7 (1-14)
                                                                                                                                                                                                                                                                       US-09-824-647-16 (1-2095) x US-10-281-160-7 (1:14)
                                                                                                                                                                                                                                      Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                               US-09-813-156-7
; Sequence 7, Application US/09813156
; Patent No. US20020061859A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.000925
14.00
100.00%
100.00%
2.02%
                                                                                                                                    0.000925
                                                                                                                                                      14.00
100.00%
100.00%
2.02%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Human granulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
NAME/KEY: PEPTIDE
```

```
Alignment Scores:
                                                                                                                                                                            US-09-824-647-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-824-647-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-218-509-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No.:
                                                                              ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Williams, Stephen A.

TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and
TITLE OF INVENTION: Uses Therefor, Including Diagnosis and Treatment of
TITLE OF INVENTION: Alzheimer's Disease
FILE REFERENCE: 2572-1-001 NZ
CURRENT APPLICATION NUMBER: US/09/826,290
CURRENT FILING DATE: 2001-04-30
PRIOR APPLICATION NUMBER: US 60/194,504
PRIOR APPLICATION NUMBER: US 60/253,647
PRIOR APPLICATION NUMBER: US 60/253,647
PRIOR FILING DATE: 2000-01-128
NUMBER OF SEQ ID NOS: 492
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 195
LENGTH: 14
                                                                                                                                                                                      NAME/KET: PEPTIDE

LOCATION: (1)..(14)

COTHER INFORMATION: Internal peptide of human GP88 used to develop

OTHER INFORMATION: neutralizing anti-human GP88 monoclonal antibody.
US-09-824-807-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 195, Application US/09826290
Patent No. US20020164668A1
GENERAL INFORMATION:
APPLICANT: Durham, L. Kathryn
APPLICANT: Friedman, David L.
APPLICANT: Herath, Herath, Mudiyanselage Athula Chandrasiri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-824-647-16 (1-2095) x US-09-824-807-7 (1-14)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
              PRIOR FILING DATE: 1997-12-16
PRIOR APPLICATION NUMBER: 08/863,862
PRIOR FILING DATE: 1997-05-23
NUMBER OF EXQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
SRQ ID NO 7
LENGTH: 14
TYPE: PRT
CRGANISM: Human granulin
FRATRRE:
PRIOR APPLICATION NUMBER: 08/991,862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Parekh, Rajesh Bhikhu
Potter, David M.
Rohlff, Christian
Silber, B. Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Stiger, Thomas R.
Sunderland, P. Trey
Townsend, Robert Reid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2.44e+03
7.00
100.00$
100.00$
                                                                                                                                                                                                                                                                                                                                            0.000925
14.00
100.008
100.008
2.028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lmmel, Lida H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  White, Frost
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: homo sapien
US-09-826-290-195
                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
Ouery Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-826-290-195
                                                                                                                                                                                                                                                                                                                              Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No.:
                                                                                                                                                                                                                                                                                                                                                Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                    Score:
```

```
Sequence 5, Application US/10218509;
Publication No. US20030092661A1;
GENERAL INFORMATION:
APPLICANT: Serrero, Ginette
TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS;
FILE REFERENCE: 29996.488/P001-A;
CURRENT FILING DATE: 20996-015;
PRIOR PELICATION NUMBER: 08/991,862;
PRIOR FILING DATE: 1999-08-17;
PRIOR PELICATION NUMBER: 08/991,862;
PRIOR PELICATION NUMBER: 08/991,862;
PRIOR FILING DATE: 1999-05-23;
NUMBER OF SEQ ID NOS: 17;
SOFTWARE: Patentin Ver: 2.0
                                                                                                                                                                       Sequence 5, Application US/09824647

Publication No. US20020183270A1

GENERAL INFORMATION:

APPLICANT: Serrero, Ginette

TITLE OF INVENTION:

ELLE REFERENCE: 19996.488/P001-A

CURRENT APPLICATION NUMBER: US/09/824,647

CURRENT FILING DATE: 2001-04-04

PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-17

PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-17

PRIOR FILING DATE: EARLIER FILING DATE: 1999-05-23

NUMBER OF SEQ ID NOS: 17

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 5

LENGTH: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (1)..(14)
OTHER INFORMATION: Internal peptide of mouse GP88 used to raise the OTHER INFORMATION: antisera against the GP88 used in the OTHER INFORMATION: immunoaffinity step.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4,0000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
US-09-824-647-16 (1-2095) x US-09-826-290-195 (1-14)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-824-647-16 (1-2095) x US-09-824-647-5 (1-14)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps:
                                            1009 GGTACCTGTGAACAGGGGCCC 1029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1714 AGGGGTACCAAGTGTTTGCGC 1734
                                                                 1 GlyThrCysGluGlnGlyPro 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 ArgGlyThrLysCysLeuArg 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.44e+03
7.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.00%
100.00%
1.01%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: mouse granulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: mouse granulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)..(14)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KEY: PEPTIDE
```

```
RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
                                                                                                                                                                                                                                                                                                                                                                                core
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5, Application US/10281160
; Sequence 5, Application US/10281160
; Publication No. US20303108950A1
; GENERAL INFORMATION:
APPLICANT: Serrero, Ginette
; TITE OF INVENTION: 88 RAD TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
; FILE REPERENCE: 29996.488/P001-28
; CURRENT APPLICATION NUMBER: US/10/281,160
; PRIOR PILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 08/863,862
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 08/863,862
; PRIOR SPLING DATE: 1997-05-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PATENTIN VET: 2.0
; SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Serrero, Ginette
TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
FILE REPERENCE: Z9996.488/P001-A
CURRENT APPLICATION NUMBER: US/09/813,156
CURRENT FILING DATE: 2001-03-21
; OTHER INFORMATION: Internal peptide of mouse GP88 used to raise the ; OTHER INFORMATION: antisera against the GP88 used in the ; OTHER INFORMATION: immunoaffinity step. US-10-218-509-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to raise the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: (1)...(14)
OTHER INFORMATION: Internal peptide of mouse GP88 used to OTHER INFORMATION: antisera against the GP88 used in the OTHER INFORMATION: immunoaffinity step.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-824-647-16 (1-2095) x US-10-281-160-5 (1-14)
                                                                                                                                                                                                                                                                           US-09-824-647-16 (1-2095) x US-10-218-509-5 (1-14)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps:
                                                                                                                                                                                                                                                                                                                 1714 AGGGGTACCAAGTGTTTGCGC 1734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT FILING DATE: 2001.03-21
PRIOR APPLICATION NUMBER: 08/991,862
PRIOR FILING DATE: 1997-12-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 ArgGlyThrLysCysLeuArg 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5, Application US/09813156 Patent No. US20020061859Al GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.44e+03
7.00
100.00%
100.00%
                                                                                                                                  2.44e+03
7.00
                                                                                                                                                                      100.00%
100.00%
1.01%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: mouse granulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alignment Scores:
                                                                                                               Aliqument Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-813-156-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match:
                                                                                                                                                                                                              Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No.:
                                                                                                                                      Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 9
                                                                                                                                                         Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                     ð
```

```
US-09-814-807-5

US-09-814-807-5

Sequence 5, Application US/09824807

Patent No. US2002094966A1

GENERAL INFORMATION:

TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS

TITLE OF INVENTION NUMBER: US/09/824,807

CURRENT FILING DATE: 2090-0484

PRIOR FILING DATE: 1997-12-16

PRIOR FILING DATE: 1997-12-16

PRIOR FILING DATE: 1997-05-23

NUMBER OF SEQ ID NOS: 17
                                                                                                                              FEATURE:
NAME/RET: PETIDE
LOCATION: (1)..(14)
OTHER INFORMATION: antisera against the GP88 used to raise the
OTHER INFORMATION: antisera against the GP88 used in the
OTHER INFORMATION: immunoaffinity step.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)..(14).
OTHER INFORMATION: Internal peptide of mouse GP88 used to raise the
OTHER INFORMATION: antisera against the GP88 used in the
OTHER INFORMATION: immunoaffinity step.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4,0000
                                                                                                                                                                                                                                                                               40000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-824-647-16 (1-2095) x US-09-824-807-5 (1-14)
                                                                                                                                                                                                                                                                                                                                                                                               US-09-824-647-16 (1-2095) x US-09-813-156-5 (1-14)
                                                                                                                                                                                                                                                                                                                                                                Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                               1714 AGGGGTACCAAGTGTTTGCGC 1734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1714 AGGGGTACCAAGTGTTTGCGC 1734
PRIOR APPLICATION NUMBER: 08/863,862
PRIOR FILING DATE: 1997-05-23
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                3 ArgGlyThrLysCysLeuArg 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.44e+03
7.00
100.00%
100.00%
1.01%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.44e+03
7.00
100.00$
100.00$
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: mouse granulin
                                                                                                 TYPE: PRT 'ORGANISM: mouse granulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity:
                                                                                                                                                                                                                                                                                                                               Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                 Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alignment Scores:
                                                                                                                                                                                                                                                                Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match:
                                                                                                                                                                                                                                                                                 ..
9
```

```
DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED PROTEIN TAU, HYBRIDOMAS SECRETING THESE ANTIBODIES, ANTIGEN RECOGNITION BY THESE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                      VAN DE VOORDE, ANDRE
TITLE OF INVENTION: MONOCLONAL ANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-824-647-16 (1-2095) x US-09-790-148-5 (1-9)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 14-DEC-1992
APPLICATION NUMBER: EP/92/403403.6
FILING DATE: 14-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 13-JUN-1994
PPILICATION NUMBER: 08/244,951
FILING DATE: 10-DEC-1993
APPLICATION NUMBER: PCT/EP93/03499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 410.003-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: ASCII
CURRENT APPLICATION NUMBER: US/09/790,148
PILING DATE: 21-Feb-2001
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: BIERMAN & MUSERLIAN STREET: 600 THIRD AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 27-JUN-1994
APPLICATION NUMBER: 08/256,167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE DESCRIPTION: SEQ ID NO: 5:
                                                                                                           RESULT 14
US-09-790-148-5
US-09-790-148-5
; Sequence 5, Application US/09790148
; Patent No. US20020001857A1
; GENERAL INFORMATION:
; APPLICANT: VANDERMEEREN, MARC;
; MERCKEN, MARC;
; VANDEREL, EUGEEN;
VANDERELLE, EUGEEN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSERLIAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ELEPHONE: (212) 661-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: FLOPPY DISK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION
                         1638 CTGCTGTCCCTACGCCCA 1655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ELEFAX: (212) 661-8002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            465 GGGCAGCACCCCCAGGA 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: Unknown TOPOLOGY: Unknown
                                                                  2 LeuLeuSerLeuArgPro 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.55e+07
6.00
                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.00%
100.00%
0.87%
                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 10016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-790-148-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No.:
                                                                8
                                                                                                   APPLICANT: Beer, Ilan
APPLICANT: ZIV, Tamar
APPLICANT: Admon Arie
TITLE OF INVENTION: METHOD OF IDENTIFYING PEPTIDES CAPABLE OF BINDING TO MHC MOLECULE
TITLE OF INVENTION: PEPTIDES IDENTIFIED THEREBY AND THEIR USES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Peptide with peptide binding sequence retrieved from phage biopar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Belcher, Angela M
APPLICANT: Smalley, Richard E.
APPLICANT: Syan, Esther
APPLICANT: Ryan, Esther
TITLEONT: Lee, Seung-Wuk
TITLE OF INVENTION: BIOLOGICAL CONTROL OF NANOPARTICLES
FILE REFERENCE: 119927-1066
CURRENT APPLICATION NUMBER: 08/10/254,446A
CURRENT FILING DATE: 2003-02-19
PRIOR PELLING DATE: 2001-09-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-824-647-16 (1-2095) x US-09-865-548A-108 (1-9)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-824-647-16 (1-2095) x US-10-254-446A-143 (1-9)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels:
                                                                                                                                                                                                    FILE REFERENCE: 01/22080
CURRENT APPLICATION NUMBER: 05/09/865,548A
CURRENT FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: 05 60/290,958
PRIOR FILING DATE: 2001-05-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps:
                       Application US/09865548A o. US20030096298A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 143, Application US/10254446A Publication No. US20030113714A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: synthetic peptide US-09-865-548A-108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                459 CTGCCCCATGCCCCAGGC 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 LeuProHisAlaProGly 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 245
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: artificial sequence
                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 204
SOFTWARE: Patentin version 3.1
SEQ ID NO 108
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.55e+07
6.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.55e+07
6.00
100.00%
100.00%
0.86%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.868
                                                                                 APPLICANT: Barnea, Eilon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                   Sequence 108, Applica
Publication No. US200
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
US-09-865-548A-108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-254-446A-143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JS-10-254-446A-143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 143
                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATORE:
                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           red. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..
Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ð
```

```
FEATURE:
CTHER INFORMATION: sequence located in NPR3 OR ANPRC at 34-43 and may interact
CTHER INFORMATION: Sequence 390 in this patent.
US-09-572-404B-389
                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Sequence located in NPR3 OR ANPRC at 33-42 and may interact correct information: Sequence 380 in this patent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-572-404B-389
US-09-572-404B-389
US-09-572-404B-389
Sequence 389, Application US/09572404B
Sequence 389, Application Wor US20030078374A1
GENERAL INFORMATION:
APPLICANT: Proteom Lid
TITLE OF INVENTION: Complementary peptide ligands from the human genome
FILE REPREBENCE: Human patent
CURRENT APPLICATION NUMBER: US/09/572,404B
CURRENT APPLICATION NUMBER: 2000-05-17
NUMBER OF SEQ ID NOS: 4203
SEQ ID NO 389
LENGTH: 10
                                   RESULT 17
US-09-572-404B-379
US-09-572-404B-379
Sequence 379, Application US/09572404B
Sequence 379, Application Wo. US20030078374A1
SERMERAL INFORMATION:
APPLICANT: Proteom Lid
TITLE REFERENCE: Human patent
CURRENT APPLICATION NUMBER: US/09/572,404B
CURRENT PILING DATE: 2000-05-17
NUMBER OF SEQUENCE: 2000-05-17
NUMBER OF SEQUENCE: Protebatent version 1.0
SEQ ID NO 379
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90000
                                                                                                                                                                                                                                                                                                                                                                                                                                                             00000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-824-647-16 (1-2095) x US-09-572-404B-389 (1-10)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-824-647-16 (1-2095) x US-09-572-404B-379 (1-10)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1146 GCAGGTATCGGAGGAGGG 1129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1146 GCAGGTATCGGAGGAGGG 1129
4 AlaGlyIleGlyGlyGly 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.11e+04
6.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 AlaGlyIleGlyGlyGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.00%
100.00%
0.87%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6.00
100.00%
100.00%
0.87%
                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.\11e+04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo Saptens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                               Aliqnment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence located in NPR3 OR ANPRC at 33-42 and may interact with Sequence 376 in this patent.
                                                                                                                                   PAPLICANT: Busifield, Samantha J.

PILLE OF INVENTION: NOVEL SECRETED IMMUNMODULATORY PROTEINS AND USES THEREOF FILE REFERENCE: 07334-32001.

CURRENT APPLICATION NUMBER: US/09/731,449

CURRENT FILING DATE: 1999-09-30

PRIOR APPLICATION NUMBER: US 09/410,350

PRIOR APPLICATION NUMBER: US 09/163,523

PRIOR PILING DATE: 1999-09-30

NUMBER OF SEQ ID NOS: 62

SOFTWARE: FESSERE for Windows Version 4.0

SEQ ID NO 55

LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 375, Application US/09572404B
Publication No. US20030078374A1
GENERAL INFORMATION:
APPLICANT: Proteom Ltd
TITLE OF INFORMATION: Complementary peptide ligands from the human genome FILE REFERENCE: Human patent
CURRENT APPLICATION NUMBER: US/09/572,404B
CURRENT FILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 4203
SOFTWARE: ProtPatent version 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-824-647-16 (1-2095) x US-09-572-404B-375 (1-10)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-824-647-16 (1-2095) x US-09-731-449-55 (1-10)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
                                                               US-09-731-449-55; Sequence 55, Application US/09731449; Patent No. US20020155526A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1146 GCAGGTATCGCAGGAGGG 1129
                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Fusion protein US-09-731-449-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GlyAlaAlaProProGly 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2.11e+04
6.00
100.008
100.008
                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.11e+04
6.00
100.00%
100.00%
0.86%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION:
OTHER INFORMATION:
US-09-572-404B-375
                                                                                                                       GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-572-404B-375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ର. ଶ
         a
```

```
CTHER INFORMATION: sequence located in NPR3 OR ANPRC at 33-42 and may interactive OrHER INFORMATION: Sequence 416 in this patent.

US-09-572-404B-415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: sequence located in NPR3 OR ANPRC at 33-42 and may intera-
OTHER INFORMATION: Sequence 420 in this patent.
                APPLICANT: Proteom Ltd
TITLE OF INVENTION: Complementary peptide ligands from the human genome
FILE REFERENCE: Human patent
CURRENT APPLICATION NUMBER: US/09/572,404B
CURRENT FILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 4203
SEGTHARE: ProtPatent version 1.0
SEQ ID NO 415
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 419, Application US/09572404B
Ublication No. US20030078374A1
GENERAL INFORMATION:
APPLICAMY: Proteom Ltd
APPLICAMY: Proteom Ltd
TILLE OF INVENTION: Complementary peptide ligands from the human genome FILE REPERENCE: Human patent
CURRENT APPLICATION NUMBER: US/09/572,404B
CURRENT FILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 4203
SOFTWARE: Protebatent version 1.0
SEQ ID NO 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Proteom Ltd IIILE OF INVENTION: Complementary peptide ligands from the human genome
                                                                                                                                                                                                                                                                                                                                                              00000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-824-647-16 (1-2095) x US-09-572-404B-415 (1-10)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-824-647-16 (1-2095) x US-09-572-404B-419 (1-10)
                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches:
                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 500, Application US/09572404B Publication No. US20030078374A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1146 GCAGGTATCGGAGGAGGG 1129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.11e+04
6.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.11e+04
6.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.00%
100.00%
0.87%
                                                                                                                                                                                                                                                                                                                                                                                               .100.00%
100.00%
0.87%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo Sapiens
                                                                                                                                                                                                                    ORGANISM: Homo Saplens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
  GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-572-404B-419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-572-404B-500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-572-404B-419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
                                                                                                                                                                                                    TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                              Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: sequence located in NPR3 OR ANPRC at 33-42 and may interact with OTHER INFORMATION: Sequence 410 in this patent.
                                                                                                                                                                                                                                                                                                                    CHER INFORMATION: sequence located in NPR3 OR ANPRC at 33-42 and may interact with COTHER INFORMATION: Sequence 404 in this patent.

US-09-572-404B-403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NGS-09-572-404B-409
Sequence 409, Application US/09572404B
Sequence 409, Application US/09572404B
Publication No. US20030078374A1
GENERAL INFORMATION:
APPLICART: Proteom Ltd
TITLE OF INVENTION: Complementary peptide ligands from the human genome
CURRENT APPLICATION NUMBER: US/09/572,404B
CURRENT PILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 4203
SOFTWARE: ProtPatent version 1.0
                                                                           APPLICANT: Proteom Ltd
TITLE OF INVENTION: Complementary peptide ligands from the human genome
FILE REFERENCE: Human patent
CURRENT FILE REPERSORS: 1000-05-17
CURRENT FILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 4203
SOFTWARE: ProtPatent version 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                          0000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-824-647-16 (1-2095) x US-09-572-404B-409 (1-10)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-824-647-16 (1-2095) x US-09-572-404B-403 (1-10)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps:
                Sequence 403, Application US/09572404B Publication No. US20030078374A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-572-404B-415; Sequence 415, Application US/09572404B; Publication No. US20030078374A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1146 GCAGGTATCGGAGGAGGG 1129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1146 GCAGGTATCGGAGGAGGG 1129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 AlaGlyIleGlyGlyGly 9
                                                                                                                                                                                                                                                                                                                                                                                                                      2.11e+04
6.00
100.00%
100.00%
0.87%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.11e+04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6.00
100.00%
100.00%
0.87%
                                                                                                                                                                                                                                                                            ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-572-404B-409
US-09-572-404B-403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
                                                                                                                                                                                                                      SEQ ID NO 403
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 409
LENGTH: 10
                                                                                                                                                                                                                                                                TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       õ
```

```
; OTHER INFORMATION: sequence located in ITPKB at 1964-1973 and may interact with ; OTHER INFORMATION: 1059 in this patent.
US-09-572-404B-1060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTHER INFORMATION: sequence located in SG2NA at 48-57 and may interact with Sec; OTHER INFORMATION: in this patent. US-09-572-404B-2096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Protecom Ltd
TITLE OF INVENTION: Complementary peptide ligands from the human genome
FILE REFERENCE: Human patent
CURRENT APPLICATION NUMBER: US/09/572,404B
CURRENT FILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 4203
SEGTHARE: ProtPatent version 1.0
SEQ ID NO 2096
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Proteom Ltd
TITLE OF INVENTION: Complementary peptide ligands from the human genome
FILTL OF INVENTION: Complementary peptide ligands from the human genome
CURRENT EFFERENCE: Human patent
CURRENT FILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 2000-05-17
SOFTWARE: ProtPatent version 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               00000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-824-647-16 (1-2095) x US-09-572-404B-2096 (1-10)
                                                                                                                                                                                                                                                                                                                                                                                   JS-09-824-647-16 (1-2095) x US-09-572-404B-1060 (1-10)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                  Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                           Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
                                                                                                                                                                                                                                                                                                                                              Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2101, Application US/09572404B Publication No. US20030078374A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2096, Application US/09572404B Publication No. US20030078374A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1397 GGAGCTGGGCCTGCTGCC 1414
                                                                                                                                                                                                                                                                                                                                                                                                                            915 GGGGGCTGGGGCTGCTG 932
NUMBER OF SEQ ID NOS: 4203
SOFTWARE: ProtPatent version 1.0
SEQ ID NO 1060
LENGTH: 10
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 GlyGlyLeuGlyLeuLeu 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.11e+04
6.00
                                                                                                                                                                                                                                       2.11e+04
6.00
100.00$
100.00$
0.86$
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.00%
100.00%
0.86%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo Sapiens
                                                                                                   ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-572-404B-2101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-572-404B-2096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
                                                                                                                                                                                                                            Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 2101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match:
                                                                                                                                                                                                                                                                                                                         Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                 Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: sequence located in PTHR1 OR PTHR at 270-279 and may interact wit; OTHER INFORMATION: Sequence 501 in this patent.
US-09-572-404B-502
                                                                                                                                                                                                    sequence located in PTHR1 OR PTHR at 271-280 and may interact with Sequence 499 in this patent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-572-404B-502
US-09-572-404B-502
Sequence 502, Application US/09572404B
Sequence 502, Application US/09572404B
Sequence 502, Publication No. US20030078374A1
SEMERAL INFORMATION:
APPLICANT: Proteom Ltd
FILE REPRENCE: Human patent
FILE REPRENCE: Human patent
CURRENT APPLICATION NUMBER: US/09/572,404B
SUPRANE PLING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 4203
SOFTWARE: ProtPatent version 1.0
SEQ ID NO 502
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1060, Application US/09572404B
Dublication No. US20030078374Al
GENERAL INFORMATION:
APPLICANT: Proteom Ltd
TITLE OF INVENTION: Complementary peptide ligands from the human genome
TITLE APPLICANT: PLOTEOM US409572,404B
CURRENT APPLICATION UD4DER: US/09/572,404B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             00000
                                                                                                                                                                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-824-647-16 (1-2095) x US-09-572-404B-502 (1-10)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-824-647-16 (1-2095) x US-09-572-404B-500 (1-10)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                         Indels:
                        CURRENT APPLICATION NUMBER: US/09/572,404B CURRENT FILING DATE: 2000-05-17 NUMBER OF SEQ ID NOS: 4203 SOFWARE: ProtPatent version 1:0 SEQ ID NO 500
                                                                                                                                                                                                                                                                                                                                                                                                          Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         122 CCAGCTACAGCTGCTGCC 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          122 CCAGCTACAGCTGCTGCC 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ProAlaThrAlaAlaAla 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 ProAlaThrAlaAlaAla 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.11e+04
6.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.00%
100.00%
0.86%
                                                                                                                                                                                                                                                                                                                             6.00
100.00%
100.00%
0.86%
                                                                                                                                                                                                                                                                                                             2.11e+04
          FILE REFERENCE: Human patent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo Sapiens
                                                                                                                                                                ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                        OTHER INFORMATION:
COTHER INFORMATION:
US-09-572-404B-500
                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 25
US-09-572-404B-1060
                                                                                                                                                                                                                                                                                        Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
                                                                                                                                              TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                 Query Match:
DB:
                                                                                                                                                                                                                                                                                                         Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
```

ð a

```
; OTHER INFORMATION: sequence located in DDIT1 OR GADD45 at 104-113 and may in 15.0THER INFORMATION: Sequence 3063 in this patent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: sequence located in OXT OR OT at 88-97 and may interact w OTHER INFORMATION: 3255 in this patent.
                      sequence located in GUCY2D OR GUC2D OR RETGC1 OR RETGC OR CORD6 at 713-722 and may interact with Sequence 2774 in t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3256, Application US/09572404B
Publication No. US20030078374A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Proteom Ltd
TITLE OF INVENTION: Complementary peptide ligands from the human genome
TITLE OF INVENTION: Complementary peptide ligands from the human genome
TITLE REPERBNCE: Human patent
CURRENT FILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 4203
SOFTWARES Proteatent version 1.0
SEQ ID NO 3256
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3064, Application US/09572404B
Publication No. US20030078374A1
Publication No. US20030078374A1
APPLICANT: Protecom Ltd
TITLE OF INVENTION: Complementary peptide ligands from the human genome TITLE OF INVENTION: Complementary peptide ligands from the human genome CURRENT APPLICATION WUMBER: US/09/572,404B
CURRENT FILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 4203
SOFTWARE: Protepatent version 1.0
SEQ ID NO 3064
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20000
                                                                                                                          90000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-824-647-16 (1-2095) x US-09-572-404B-3064 (1-10)
                                                                                                                                                                                                                                                                 US-09-824-647-16 (1-2095) x US-09-572-404B-2773 (1-10)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative:
Mismatches:
Indels:
                                                                                                                                                               Conservative:
Mismatches:
                                                                                                                          Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
                                                                                                                                                                                                         Indels:
                                                                                                                                                                                                                                                                                                      2.11e+04
6.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6.00
100.00%
100.00%
0.86%
                                                                                                                                                             100.00%
100.00%
0.86%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.11e+04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo Sapiens
                      CTHER INFORMATION:
CTHER INFORMATION:
US-09-572-404B-2773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                               Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 31
US-09-572-404B-3256
                                                                                                                                                                                                                                                                                                                                                                                                        US-09-572-404B-3064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
                                                                                                       Alignment Scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
                                                                                                                                                                                                         Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No.:
                                                                                                                              Pred. No.:
                                                                                                                                               Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score:
                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ď
                                                                              ; OTHER INFORMATION: sequence located in CNTFR at 323-332 and may interact with Sequence OS-09-572-404B-2101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: sequence located in CNTFR at 322-331 and may interact with Sequen
OTHER INFORMATION: in this patent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Proteom Ltd
TITLE OF INVENTION: Complementary peptide ligands from the human genome
TITLE OF INVENTION: Complementary peptide ligands from the human genome
TITLE REPERENCE: Human patent
CURRENT APPLICATION NUMBER: US/09/572,404B
CURRENT FILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 4203
SOFTWARE: ProtPatent version 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2773, Application US/09572404B
Publication No. US20030078374A1
Publication No. US20030078374A1
APPLICANT: Protecom Ltd
TITLE OF INVENTION: Complementary peptide ligands from the human genome FILE REPERENCE: Human patent
CURRENT APPLICATION NUMBER: US/09/572,404B
CURRENT FILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 4203
                                                                                                                                                                                                                                                                                                                         US-09-824-647-16 (1-2095) x US-09-572-404B-2101 (1-10)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-824-647-16 (1-2095) x US-09-572-404B-2103 (1-10)
                                                                                                                                                                                                                     Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                  Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-572-404B-2103
Sequence 2103, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                              1859 TCCCTAGCACCTCCCCCT 1876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1859 TCCCTAGCACCTCCCCCT 1876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: ProtPatent version 1.0 SEQ ID NO 2773 LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 SerLeuAlaProProPro 8
                                                                                                                                                                                2.11e+04
6.00
100.00%
100.00%
0.86%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.11e+04
6.00
100.008
100.008
0.868
                    TYPE: PRT
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-572-404B-2103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-572-404B-2773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
                                                                                                                                                               Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 2103
LENGTH: 10
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
                                                                                                                                                                                red. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ð
```

```
CTHER INFORMATION: sequence located in PKD1 at 316-325 and may interact with Sicorder INFORMATION: in this patent.

US-09-572-404B-3586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Proteom Ltd
TITLE OF INVENTION: Complementary peptide ligands from the human genome
FILE REFERENCE: Human patent
                                                                                                                                                                                                                                                                                                                        APPLICANT: Protecom Ltd
TITLE OF INVENTION: Complementary peptide ligands from the human genome
FILE REFERENCE: Human patent
CURRENT APPLICATION NUMBER: US/09/572,404B
CURRENT FILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 4203
SEQ ID NO 3262
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTHER INFORMATION: sequence located in AVP OR ARVP OR VP at 87-96; OTHER INFORMATION: Sequence 3261 in this patent.
US-09-572-4048-3262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10
6
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              00000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-824-647-16 (1-2095) x US-09-572-404B-3262 (1-10)
                                                                                                                             US-09-824-647-16 (1-2095) x US-09-572-404B-3260 (1-10)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
Conservative:
                                    Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
 Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/572,404B CURRENT FILING DATE: 2000-05-17 NUMBER OF SEQ ID NOS: 4203 SOFTWARE: ProtPatent version 1.0 SEQ ID NO 3586 LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3586, Application US/09572404B Publication No. US20030078374A1
                                                                                                                                                                                                                                                                         Sequence 3262, Application US/09572404B Publication No. US20030078374A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAGGCTTGTGGGTCTGGC 1074
                                                                                                                                                                 4 LysAlaCysGlySerGly 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.11e+04
6.00
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.11e+04
6.00
2.11e+04
6.00
100.00%
100.00%
0.87%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.00%
100.00%
0.87%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
                                  Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-572-404B-3586
                                                                                                                                                                                                                                                              JS-09-572-404B-3262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No.:
       ored. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: sequence located in OXT OR OT at 87-96 and may interact with Sequ
SOTHER INFORMATION: 3257 in this patent.
US-09-572-404B-3258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Sequence located in AVP OR ARVP OR VP at 88-97 and may interact; OTHER INFORMATION: Sequence 3259 in this patent.
US-09-572-404B-3260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Proteom Ltd
TTLE OF INVENTION: Complementary peptide ligands from the human genome FILE REFERENCE: Human patent US/09/572,404B
CURRENT APPLICATION NUMBER: US/09/572,404B
CURRENT FILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 4203
SOFTWARE: ProtPatent version 1.0
SEQ ID NO 3260
                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Proteom Ltd
TILE OF INVENTION: Complementary peptide ligands from the human genome
FILE REPERENCE: Human patent
CURRENT APPLICATION NUMBER: US/09/572,404B
CURRENT FILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 4203
SECTUMENE: ProtPatent version 1.0
SEQ ID NO 3258
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-824-647-16 (1-2095) x US-09-572-404B-3258 (1-10)
                                                                                                                                                                                           US-09-824-647-16 (1-2095) x US-09-572-404B-3256 (1-10)
                                                            Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels:
                                                                                                                                                           Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-572-404B-3260
; Sequence 3260, Application US/09572404B
; Publication No. US20030078374A1
                                                                                                                                                                                                                                                                                                                        5-09-572-404B-3258
Sequence 3258, Application US/09572404B
Publication No. US20030078374A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1091 AAGGCTTGTGGGTCTGGC 1074
                                                                                                                                                                                                                                 1091 AAGGCTTGTGGGTCTGGC 1074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 LysAlaCysGlySerGly 9
                                                                                                                                                                                                                                                  3 LysAlaCysGlySerGly 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.11e+04
6.00
100.00%
100.00%
                                                            2.11e+04
6.00
100.00%
100.00%
0.87%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
                                                                                              Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
           JS-09-572-404B-3256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
                                                 Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                   ò
```

Alignment Scores:

and may inter

us-09-824-647-16.lim.rapb

```
sequence located in Unknown at 96-105 and may interact wi
3675 in this patent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: sequence located in Unknown at 94-103 and may interact wird other information: 3674 in this patent.
US-09-572-404B-3675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Proteon Ltd
TTLE OF INVENTION: Complementary peptide ligands from the human genome FILE REPERENCE: Human patent CURRENT APPLICATION NUMBER: US/09/572,404B
CURRENT FILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 4203
SOFTWARE: ProtPatent version 1.0
SEQ ID NO 3675
                                                                                                                                                                                                                                         APPLICANT: Proteom Ltd
TITLE OF INVENTION: Complementary peptide ligands from the human genome
TITLE OF INVENTION: Complementary peptide ligands from the human genome
TITLE REPERMENT: Human patent
CURRENT APPLICATION NUMBER: US/09/572,404B
CURRENT FILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 4203
SOFTWARE: ProtPatent version 1.0
SEQ ID NO 3674
LENGTH: 10
                                                                                                                                       1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0000
                       US-09-824-647-16 (1-2095) x US-09-572-404B-3673 (1-10)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-824-647-16 (1-2095) x US-09-572-404B-3674 (1-10)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-824-647-16 (1-2095) x US-09-572-404B-3675 (1-10)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels:
                                                                                                                                                                                Sequence 3674, Application US/09572404B Publication No. US20030078374A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3675, Application US/09572404B Publication No. US20030078374A1 GENERAL INFORMATION:
                                                               1042 AGGGCACCTGGTGGGGCC 1025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1042 AGGCCACCTGGTGGGGCC 1025
                                                                              3 ArgAlaProGlyGlyAla 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 ArgAlaProGlyGlyAla 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.11e+04
6.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3.11e+04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.00%
100.00%
0.87%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.00%
100.00%
3.87%
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo Saplens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
Sest Local Similarity:
                                                                                                                                                                   JS-09-572-404B+3674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-572-404B-3675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-572-404B-3674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: sequence located in Unknown at 95-104 and may interact with Seque; OTHER INFORMATION: 3672 in this patent.
US-09-572-4048-3673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence located in Unknown at 95-104 and may interact with Seque 3673 in this patent.
                                                                                                                                                                                                                                                                                                    APPLICANT: Proteom Ltd
TILLE NET INVENTION: Complementary peptide ligands from the human genome
TILLE REPERENCE: Human patent
CURRENT APPLICATION NUMBER: US/09/572,404B
CURRENT FILING DATE: 2000-05-17
CURRENT FILING DATE: 2000-05-17
SOFTWARE: ProtPatent version 1.0
SEQ ID NO 3672
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Proteom Ltd
TITLE OF INVENTION: Complementary peptide ligands from the human genome
FILE REFERENCE: Human patent
                                                                              US-09-824-647-16 (1-2095) x US-09-572-404B-3586 (1-10)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-824-647-16 (1-2095) x US-09-572-404B-3672 (1-10)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches:
Conservative:
Mismatches:
Indels:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ength:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION UNBER: US/09/572,404B CURRENT FILING DATE: 2000-05-17 NUMBER OF SEQ ID NOS: 4203 SOFTWARE: ProtPatent version 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3673, Application US/09572404B Publication No. US20030078374A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                             Sequence 3672, Application US/09572404B Publication No. US20030078374A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1042 AGGGCACCTGGTGGGGCC 1025
                                                                                                                        1400 GCTGGGCCTGCTGCCAGT 1417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 ArgAlaProGlyGlyAla 8
                                                                                                                                            2.11e+04
6.00
100.00%
100.00%
0.87%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.11e+04
6.00
100.008
100.008
Best Local Similarity: 100.00%
Query Match: 0.86%
DB: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo Sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTHER INFORMATION:
CTHER INFORMATION:
US-09-572-404B-3672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                              JS-09-572-404B-3672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-572-404B-3673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 3673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
              Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            red. No.:
                                                                                                                                                                                                       RESULT 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 37
```

```
APPLICANT: Valuel, Jean-Charles
APPLICANT: Cerottini, Jean-Charles
APPLICANT: Romero, Pedro
TITLE OF INVENTION: To Him Molecules, and the Use Thereof
TITLE OF INVENTION: TO Him Molecules, and the Use Thereof
TITLE OF INVENTION: TO HIM MOLECULES, and the Use Thereof
TITLE OF TRIBNE DATE: 2001-02-21
CURRENT APPLICATION NUMBER: US/09/789,649
FRIOR PELLOR DATE: 1998-06-18
PRIOR FILING DATE: 1998-06-18
PRIOR FILING DATE: 1998-06-16
PRIOR FILING DATE: 1998-06-16
PRIOR FILING DATE: 1998-06-16
PRIOR FILING DATE: 1998-06-16
PRIOR FILING DATE: 1998-06-18
PRIOR FILING DATE: 1998-06-18
PRIOR FILING DATE: 1998-06-18
SEQ ID NO 27
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: sequence located in CCKBR OR CCKRB at 310-319 and may intera OTHER INFORMATION: Sequence 3850 in this patent.
                           Sequence 3851, Application US/09572404B
Sequence 3851, Application US/09572404B
Sequence 3851, Correction No. US20030078374A1
SEMENAL INFORMATION:
APPLICANT: Proteom Ltd
TITLE OF INVENTION: Complementary peptide ligands from the human genome
FILE REPERBNGE: Human pare: US/09/572,404B
CURRENT APPLICATION NUMBER: US/09/572,404B
CURRENT PILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 4203
SOFTWARE: ProtPatent version 1.0
SEQ ID NO 3851
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                00000
                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.0000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-824-647-16 (1-2095) x US-09-572-404B-3851 (1-10)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-824-647-16 (1-2095) x US-09-789-649-27 (1-10)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Derivative of SEQ ID NO:1 US-09-789-649-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 27, Application US/09789649
Publication No. US20030082804A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1393 CCTGGCTCGGGCAGCAGG 1376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 ProGlySerGlySerArg 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.11e+04
6.00
100.00%
100.00%
0.87%
                                                                                                                                                                                                                                                                                                                                                                                                                                                          2:11e+04
6.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.00%
100.00%
0.87%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Valmori, Danila
                                                                                                                                                                                                                                                                                                                ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                 US-09-572-404B-3851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-789-649-27
                                                                                                                                                                                                                                                                                                 TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: sequence located in CCKBR OR CCKRB at 310-319 and may interact wi ; OTHER INFORMATION: Sequence 3851 in this patent.
US-09-572-404B-3850
                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: sequence located in ATP5Al at 456-465 and may interact with Seque
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3850. Application US/09572404B
Publication No. US20030078374A1
CENERAL INFORMATION:
APPLICANT: Protecom Ltd
TITLE OF INVENTION: Complementary peptide ligands from the human genome FILE REFERENCE: Human patent
CURRENT PAPLICATION NUMBER: US/09/572,404B
CURRENT FILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 4203
SOFTWARE: Proteatent version 1.0
SEQ ID NO 3850
LENGTH: 10
                                                                                                          Sequence 3688, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
   APPLICANT: Proteom Ltd
   TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT APPLICATION NUMBER: US/09/572,404B
; SOFTWARE: Protebatent version 1.0
; SOFTWARE: Protebatent version 1.0
; SOFTWARE: Protebatent version 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-824-647-16 (1-2095) x US-09-572-404B-3850 (1-10)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-824-647-16 (1-2095) x US-09-572-404B-3688 (1-10)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                             . OTHER INFORMATION: 3689 in this patent.
US-09-572-404B-3688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1393 CCTGGCTCGGCCAGCAGG 1376
1042 AGGCACCTGGTGGGGCC 1025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               972 CTGCTGTCCCGCGGGTT 989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 ProGlySerGlySerArg 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 LeuLeuSerArgGlyVal 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.11e+04
6.00
100.00%
100.00%
0.87%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.11e+04
6.00
100.00%
100.00%
0.86%
                  4 ArgAlaProGlyGlyAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-572-404B-3850
                                                                                                US-09-572-404B-3688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                               LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 41
                                                                                 RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                     g
  ð
```

```
Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                         US-09-824-647-16 (1-2095) x US-10-216-122-80 (1-10)
                                                                                                Indels:
                                                                                                                                                                                                                                                                                                 Search completed: July 7, 2003, 16:14:55 Job time: 81 secs
                                                                                                                                                                                                 1164 GGAGTGGGGCTGCTGTCC 1181
                  2.11e+04
6.00
                                                                                                                                                                                                                      4 GlyValGlyLeuLeuSer
                                                    100.00%
100.00%
0.86%
                                                      Percent Similarity:
Best Local Similarity:
Alignment Scores:
Pred. No.:
                                                                                                Query Match:
                                            Score:
                                                                                                                                                                                                     ò
                                                                                                             US-10-254-426-55
Sequence 55, Application US/10254426
Sequence 55, Application US/10254426
BUBLication No. US20303113865A1
GENERAL INFORMATION:
APPLICANT: Busfield, Samantha J.
TITLE OF INVENTION: NOVEL SECRETED IMMUNOMODULATORY PROTEINS AND USES THEREOF
FILE REFERENCE: 07334-320001
CURRENT FILING DATE: 2002-09-25
PRIOR PELICATION NUMBER: US/09/731,449
PRIOR FILING DATE: 1999-09-30
PRIOR FILING DATE: 1999-09-30
PRIOR FILING DATE: 1999-09-30
PRIOR FILING DATE: 1999-09-30
PRIOR FILING DATE: 1998-09-30
NUMBER OF SEQ ID NOS: 62
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 55
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Ostertag, Efic.
TITLE OF INVENTION: COMPOSITIONS AND METHODS OF USE OF MAMMALIAN RETROTRANSPOSONS
FILE REFERENCE: 053893-5006-03
CURRENT APPLICATION NUMBER: US/10/216,122
PRIOR FILING DATE: 2002-09-01
PRIOR PELING DATE: 1997-04-28
PRIOR APPLICATION NUMBER: US 08/749,805
PRIOR APPLICATION NUMBER: US 08/749,805
PRIOR PILING DATE: 1996-11-15
PRIOR PILING DATE: 1996-11-16
PRIOR FILING DATE: 1996-11-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-824-647-16 (1-2095) x US-10-254-426-55 (1-10)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 80, Application US/10216122 Publication No. US20030121063A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
; FEATURE:
OTHER INFORMATION: Fusion protein
US-10-254-426-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   903 GCAGCAGGTATAGCCATC 886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2.11e+04
6.00
100.00%
100.00%
0.86%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Homo sapiens US-10-216-122-80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JS-10-216-122-80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              core:
                    ð
```

```
7, 2003, 16:02:12 ; Search time 76.5 Seconds (Without alignments) 5265.402 Million cell updates/sec
                                                                                                                                                                                          1 cgcaggcagaccatgtggac.....ataaagtttgtcactttctt 2095
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                              - protein search, using frame_plus_n2p model
                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                         96134422 residues
                                                                                                                                                                                                                                             60.0
60.0
7.0
7.0
                                                                                                                                                                                                                                          60.0 , Xgapext 6
60.0 , Ygapext 6
6.0 , Fgapext
6.0 , Delext
                                                                                                                                                             US-09-824-647-16
                                                                                                                                                                                                                                                                                                                         283224 seqs,
                                                                                                                                                                                                                                                                                                                                                                                                                          Minimum DB seq length: 0
Maximum DB seq length: 15
                                                                                                                                                                                                                                             Xgapop
Ygapop
Fgapop
Delop
                                                                                                                                                                                                                              OLIGO
                                                                                                                                                                                                                                                                                                                                                          -
                                                                                                                                                            Title:
Perfect score:
                                                                                                                                                                                                                            Scoring table:
                                                              OM nucleic
                                                                                                                                                                                                                                                                                                                                                          Word size:
                                                                                                                                                                                            Sequence:
                                                                                                                                                                                                                                                                                                                         Searched:
                                                                                               Run on:
```

Post-processing: Listing first 45 summaries

Command line parameters:

1: pir1:* 2: pir2:* pir3:* pir4:* PIR_73:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	dextransucrase (EC	phospholipase A2 (malate dehydrogena	H+-transporting tw	leucopyrokinin - M	hypothetical histo	thymic factor - pi	thymocyte growth p	xylose isomerase (macrophage cytotox	calpain (EC 3.4.22	Achatina cardio-ex	Ig H chain V-D-J r	retinoic acid rece
						-										
						•										
		ខ	PU0034	A29169	B60683	S70719	A23967	155411	YFPG	A60957	A31576	A60427	839392	A34662	PH1632	154081
		8	7	~	~	7	7	4	H	7	~	~	~	7	7	4
		Match Length DB	11	12	14	15	8	80	σ	σ	6	6	10	11	11	11
æ	Query	Match	0.9	6.0	6.0	6.0	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7
		Score	9	9	9	9	S	S	S	2	ហ	S	S	Ŋ	Ŋ	2
	ılt	<u>ي</u>	H	7	m	4	2	9	7	æ	6	10	11	13	13	14
	Result	- ;			O	υ	O				O	Ų	O	U		ပ

RESULT 1 PUOD34 dext.ansucrase (EC 2: 4.1.5) - Stref C: Accession: Put D3 3 RESULT 1 PUOD34 Absortiption: Purification and pre A: Accession: Put D3 4 Submitted to JIPID, October 1993 A; Reference number: Puod34 A; Residues: 1-11 CUE2> A	(EC 2:4.1.5) pptcoccus bov 10034 #sequence 112034 #sequence 1131034 #sequence 1131034 #sequence 1131034 #sequence 1131034 #sequence 1131034 #sequence 1131034 #sequence 11310334 #sequence 1131034 #sequence 1131034 #sequence 1131034 #sequence 1131034 #sequence	112 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	12 2 PH1175 12 2 A60528 7 12 2 A60528 7 12 2 A60528 7 12 2 C30503 7 12 2 A33520 7 12 2 A33520 7 13 2 A33734 7 13 2 B51438 7 13 2 B6143 7 13 2 B6143 7 13 2 B61233 7 13 2 B61233 7 14 2 PH1763 7 15 2 B9189 7 15 2 B9189 7 15 2 B9189 7 15 2 B9189 7 15 2 CACCOCCOCCOCCOCCOCCOCCOCCOCCOCCOCCOCCOCC	2 199990 accepted to photospho accepted to photospho accepted to a second accepted and a second accepted and a second accepted and a second a	acetylcholine rece T-cell receptor al insulin-like growt phosphorylase b - Ig gamma-2b chain inhibitory diffusi microcin B17 - Esc enkephalin precurs R-phycoerythrin ga potassium channel Ig kappa chain V-I T-cell antigen rec conceptus protein conceptus protein mastoparan M - hor malate dehydrogena conceptus protein conceptus protein T-cell receptor al T cell receptor de insulin-like growt i
	syltransfe	rase		hexosyltransferase	•
	-	.17e+04		Length: 11	

1331 GAGACATCGGCTGTGACC 1348 2 GluThrSerAlaValThr . qq

US-09-824-647-16 (1-2095) x PU0034 (1-11)

RESULT 2 A29169

phospholipase A2 (EC 3.1.1.4) precursor - sheep (fragment)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Species: Ov-Jun-1988 #sequence_revision 02-Jun-1988 #text_change 31-Oct-1997
C;Accession: A29169
R;Dutilh, C.E.; Van Doren, P.J.; Verheul, F.E.A.M.; De Haas, G.H.
Eur. J. Blochem. 53, 91-97, 1975

```
R;Nachman, R.J.; Holman, G.M.; Cook, B.J.
Biocham. Blophys. Res. Commun. 137, 936-942, 1986
A;Title: Active fragments and analogs of the insect neuropeptide leucopyrokinin: st.
A;Reference number: A23967; MUID:86269041; PMID:3015140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C.Accession: 155411
R.Ivanova, V. S.; Hatch, C.L.; Bonner, W.M.
J. Biol. Chem. 269, 24189-24194, 1994
J. Biol. Chem. 269, 24189-24194, 1994
J. Hille: Characterization of the human histone H2A.X gene. Comparison of its promot A; Reference number: 155411; MUID:95014156; PMID:7929075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross references: GB:S73863; NID:9765295; PIDN:AAD14141.1; PID:94261841
A;Note: this is a hypothetical translation of a sequence from the promotor region F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C.Species: Homo sapiens (man)
C.Date: 28-Jan-2000 #sequence_revision 28-Jan-2000 #text_change 28-Jan-2000
                                                                                                                                                                                                                                           leucopyrokinin - Madeira cockroach
C;Species: Leucophaea maderae (Madeira cockroach)
C;Date: 31-Mar-1988 *sequence_revision 26-May-1994 *text_change 11-Jul-1997
C;Accession: A22967
                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: protein
A; Residues: 1-8 <NAC>
Kreywords: amidated cabboxyl end; neuropeptide; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;8/Modified site: amidated carboxyl end (Leu) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Status: translation not shown; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ypothetical histone H2A.X (mistranslated) - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     840000
00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length: Matches: Conservative: Mismatches: Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels:
Indels:
                        Gaps:
                                                                 US-09-824-647-16 (1-2095) x S70719 (1-15)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (1-8)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (1-8)
                                                                                                        US-09-824-647-16 (1-2095) x I55411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-824-647-16 (1-2095) x A23967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1379 GCTGCCCGAGCCAGG 1393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1568 ACGTCCTTCACACCC 1554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.00%
100.00%
0.72%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.4e+07
5.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.4e+07
5.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 AlaAlaArgAlaArg 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.00%
100.00%
0.73%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-8 <IVA>
                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: A23967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: 155411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Gene: H2A.X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match:
    Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S70719
H1-transporting two-sector ATPase (EC 3.6.3.14) beta chain - Salmonella typhimurium (fra C; Species: Salmonella typhimurium (5.2) species: Salmonella typhimurium (5.2) species: Salmonella typhimurium (5.2) species: Salmonella typhimurium 17-Apr-1998 #text_change 03-Jun-2002 (5.3) species: S70719
R; Oi, S.Y.; Li, Y.; Szyroki, A.; Giles, I.G.; Moir, A.; O'Connor, C.D.
Mol. Microbiol. 17, 523-531, 1995
A; Title: Salmonella typhimurium responses to a bactericidal protein from human neutrophi A; Reference number: S70719; MUID: 96100451; PMID: 8559071
A; Molecule type: protein
A; Molecule type: protein
A; Molecule type: protein
A; Residues: 1-15 curs.
A; Residues: 1-15 curs.
C; Keywords: ATP binding; hydrogen ion transport; hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    malate dehydrogenase (decarboxylating) (EC 1.1.1.39) - millet (fragment)
C;Species: Panicum sp. (millet)
R;Murata, T; Ikeda, J; Takano, M; Ohsugi, R.
Plant.cell Physiol. 30, 429-437, 1989
A;Title: Comparative studies of NAD-malic enzyme from leaves of various C-4 plants.
A;Reference number: A60683
A;Rocession: B60683
A;Rolcule type: protein
A;Residues: 1-14 <a href="Mainto-Millet">Millet</a>
C;Keywords: oxidoreductase; photosynthesis
    A; Title: Isolation and properties of prophospholipase A2 from ox and sheep pancreas. A; Reference number: A94661
                                               A; Accession: A29169
A; Molecule type: protein
A; Residues: 1-12 < CDUT>
C; Superfamily: phospholipase A2
C; Keywords: carboxylic ester hydrolase; pyroglutamic acid
F; 1/Modified site: pyrrolidone carboxylic acid (Gln) *status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              000
                                                                                                                                                                                                                              00000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  00000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
                                                                                                                                                                                                                                                                                                                 Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps:
                                                                                                                                                                                                                                                                                                                                                                               US-09-824-647-16 (1-2095) x A29169 (1-12)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-824-647-16 (1-2095) x B60683 (1-14)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                462 GCAGCACCCCCAGGAGCC 445
                                                                                                                                                                                                                                                                                                                                                                                                                            GGCCTTAACAGCAGGGCT 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 AlaAlaProProGlyAla 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.12e+04
6.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.13e+04
6.00
100.00%
100.00%
0.87%
                                                                                                                                                                                                                         1.15e+04
6.00
100.00%
100.00%
0.86%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alignment Scores:
Pred. No.:
                                                                                                                                                                                                         Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                            36
                                                                                                                                                                                                                                                                                                                 Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No.:
                                                                                                                                                                                                                                Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                q
                                                                                                                                                                                                                                                                                                                                                                                                                            à
```

```
xylose isomerase (EC 5.3.1.5), intracellular - Streptomyces sp. (fragment) (;Species: Streptomyces sp. (c;Date: 31-Mar-1990 &sequence_revision 31-Mar-1990 #text_change 28-Apr-1993 C;Accession: A31576 R;Pawar, H.S.; Kannan, K.; Srinivasan, M.C.; Vartak, H.G. Biochem, Blophys, Res. Commun. 155, 411-417, 1988 A;Title: Purification and characterisation of glucose (xylose) isomerase from Charak, Reference number: A31576; WUID:88326335; PMID:3415697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       macrophage cytotoxicity-inducing factor, 29K - human (fragment)
C; Species: Homo sapiens (man)
C; Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 18-Jun-1993
C; Accession: A60427
R; Jones, C.M.; Prince, C.A.; Williams, J.S.
Exp. Hematol. 19, 704-709, 1991
Exp. Hematol. 19, 704-709, 1991
A; Title: Purification and amino acid analysis of a human macrophage cytotoxicity-A; Reference number: A60427; MUID:91372335; PMID:1909970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Note: the sequence from the text on page 706 is inconsistent with that from pact; Reywords: cytokine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                calpain (EC 3.4.22.17) II light chain - pig (fragment)
C;Species: Sus scrofa domestica (domestic plg)
C;Species: Sus Scrofa domestica (domestic plg)
C;Date: 18-Feb-1994 #sequence_revision 24-Jul-1998 #text_change 29-Sep-1999
C;Accession: S39392
R;Crawford, C.; Brown, N.R.; Willis, A.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: A31576
A; Molecule type: protein
A; Residues: 1-9 < PRW>
C; Keywords: intramolecular oxidoreductase; isomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (1-9)
  US-09-824-647-16 (1-2095) x A60957 (1-9)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-824-647-16 (1-2095) x A31576 (1-9)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1380 GCAGGTTCCGCCCAC 1366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-824-647-16 (1-2095) x A60427
                                                   1227 GGGCAGCAGTGCTG 1213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ·2.14e+07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.00%
100.00%
0.73%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.14e+07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GlyAlaAlaValLeu 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: protein A; Residues: 1-9 <JON>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..
SO::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 11
S39392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 10
                                                                                                                                                                    RESULT
                                                                                                                                                                                              A31576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A60427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred.
                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Superfamily: thymic factor
C;Reywords: blocked amino end; pyroglutamic acid
F;1/Modified site: pyrrolldone carboxylic acid (Glx) (in FTS) *status experimental
F;1/Modified site: blocked amino end (Glx) (in thymocyte growth peptide) *status experim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: protein
A; Residues: 'z',2-4,'z',6-9 <BAC>
C; Comment: This peptide induces DNA synthesis in immature thymocytes, but not peripheral
in a variety of immunoassays.
C; Comment: See PIR: A60957 (sheep) for discussion of another possible N-terminal modifica
C; Superfamily: thymic factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      thymocyte growth peptide - sheep
N;Contains: FTS (facteur thymique serique)
N;Contains: FTS (facteur thymique serique)
N;Contains: FTS (facteur thymique serique)
C;Species: Ovis orientails aries, Ovis ammon aries (domestic sheep)
C;Species: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 24-Nov-1999
C;Accession: A60957 ** Reference 10, 403-412, 1990
A;Fitle: Purification of thymocyte growth peptide (TGP) from sheep thymus. Relationship
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A.Accession: A60957
A.Molecule type: protein
A.Molecule type: Postein
A.Molecule type: PERN>
C.Comment: This peptide induces DNA synthesis in immature thymocytes, but not peripheral in a variety of immunoassays.
C.Comment: This peptide was isolated in two forms. One form contained the pyrrolidone car form (thymocyte growth peptide) contains a large, non-peptide blocking group with a hi
                                                                                                                                                                                                                                              a peptide isolated from pig seru
                                          W. Alternate names: FTS (facteur thymique serique)
(.) Species: Sus scrofa domestic pig)
(.) Species: Sus scrofa domestic pig)
(.) Date: 13-011-1881 #sequence_revision 13-Jul-1981 #text_change 07-May-1999
(.) Accession: A01523; A60983
(.) Accession: A01523; A60983 MGID: Blouquit, Y.; Bach, J.F.
(.) Biol. Cham. 252, 8045-8047, 1977
(.) Biol. Cham. 252, 8045-8047, 1977
(.) A; Title: Structural study of circulating thymic factor: a peptide isolated from A; Recession: A01523; MGID: 78026571; PMID: 914862
(.) A; Residues: 1-9 ForLe.
(.) A; Residues: 1-9 ForLe.
(.) Bach, J.F.; Dardenne, M.; Pleau, J.M.; Rosa, J.
(.) Nature 266, 55-57, 1977
(.) A; Title: Blochemical characterisation of a serum thymic factor.
(.) A; Reference number: A60983; MGID: 77123829; PMID: 300146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C:Reywords: pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-824-647-16 (1-2095) x YFPG (1-9)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1387 AGCCAGGGTGGGAGC 1401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.14e+07.
5.00
100.00$
100.00$
0.72$
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.14e+07
5.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 SerGlnGlyGlySer 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.72%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No.:
RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ŏ
```

: Si. .

w0000

```
R; Dong, S.; Geng, J.P.; Tong, J.H.; Wu, Y.; Cai, J.R.; Sun, G.L.; Chen, S.R.; Wang, Genes Chromosomes Cancer 6, 133-139, 1993
A; Title: Breakpoint clusters of the PML gene in acute promyelocytic leukemia: priman A; Reference number: 154081; MUID:93222087; PMID:7682097
A; Accession: 154081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporo A; Reference number: PN0160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               malate dehydrogenase (EC 1.1.1.37) - fungus (Fusarium sporotrichioides) (fragment) C;Species: Fusarium sporotrichioides C;Decies: Pasarium sporotrichioides C;Date: 05-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 11-Nov-1994 C;Accession: PNO162 #sequence_revision 05-Aug-1994 #text_change 11-Nov-1994 S;Fukaya, N; Chow, L.P.; Sugiura, Y.; Tsugita, A.; Ueno, Y.; Tabuchi, K. submitted to JIPID, May 1994
                                                                                                                                                                                                                                                                retinoic acid receptor alpha, exon 3 (mistranslated) - human (fragment) C;Species: Homo sapiens (man) C;Date: 04-Jun-1999 #sequence_revision 04-Jun-1999 #text_change 28-Jun-1999 C;Accession: I54081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:S57794; NID:g299073; PIDN:AAD13888.1; PID:g4261588 A;Note: the translation is from an incorrect reading frame
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches:
Conservative:
Mismatches:
Indels:
                 Conservative:
Mismatches:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
                                                         Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GDB:120337; OMIM:180240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (1-12)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (1-11)
                                                                                                                US-09-824-647-16 (1-2095) x PH1632 (1-11)
                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-824-647-16 (1-2095) x PN0162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-824-647-16 (1-2095) x I54081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1461 CGGCCAGCAGTGCTG 1447
                                                                                                                                                      1705 TGCGCACGCAGGGGT 1719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTCTTGGGGGCAGCA 748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.19e+05
5.00
100.00%
100.00%
0.73%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.18e+05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ArgalaAlaValLeu 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.00%
100.00%
0.73%
               100.00%
100.00%
0.72%
                                                                                                                                                                         8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GDB:120.
A;Map position: 17q12-17q12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Accession: PN0162
A;Molecule type: protein
A;Residues: 1-12 <FUK>
C;Keywords: oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
Query Match:
   Score:
Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-11 <DON>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Gene: GDB: RARA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Accession: PH1632
R;Levinson, D.A.; Campos-Torres, J.; Leder, P.
A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice
A;Reference number: PH1580; MUID:93301609; PMID:8315387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biochem. J. 296, 135-142, 1993
A; Title: Studies of the active site of m-calpain and the interaction with calpastatin.
A; Reference number: S39391; MUID:94071815; PMID:8250833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PH1632
IG H chain V-D-J region (clone B-less 209) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: O2-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C;Accession: PH1632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C:Reywords: amidated carboxyl end F:11/Modified site: amidated carboxyl end (Phe) #status experimental
                                                                                                                                    calmodulin repeat homology hand; hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0000
                                                                                                                                                                                                               00000
                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Experimental source: bone marrow pre-B lymphocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (1-11)
                                                                                                                                                                                                                                                                                                                                                 (1-10)
                                                                                                                                  C; Superfamily: calpain small chain; C; Keywords: cysteine proteinase; EF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-824-647-16 (1-2095) x A34662
                                                                                                                                                                                                                                                                                                                                                   US-09-824-647-16 (1-2095) x S39392
                                                                                                                                                                                                                                                                                                                                                                                   1.19e+05
5.00
100.00%
100.00%
0.73%
                                                                                                                                                                                                           1.21e+05
5.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGGCCACAGGGCAGA 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.19e+05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Keywords: immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-11 <FUJ>
                                                                                                  A; Molecule type: protein A; Residues: 1-10 <CRA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-11 <LEV>
                                                                               A; Status: preliminary
                                                             A; Accession: S39392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
Pred. No:
                                                                                                                                                                                               Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No.:
                                                                                                                                                                                                                   Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 13
                                                                                                                                                                                                                                     Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                         ð
```

0000

```
R;Luo, S.; Martin, B.L.; Senshu, T.; Graves, D.J.
Arch. Biocohem. Biophys. 318, 362-369, 1995
A;Title: Enzymatic deimination of 91;Yocogen phosphorylase and a peptide of the phoa. A;Reference number: S65626; MUID:95251385; PMID:7733664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rigilmore, G.L.; Bard, J.A.; Birshtein, B.K.
J. Immunol. 141, 1754-1761, 1988
A:Title: DNA rearrangements affecting both variable and constant regions of Ig
A;Reference number: A30503; MUID:88315788; PMID:2842402
A;Accession: C30503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ig gamma-2b chain C region (F5.5.1) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 16-Aug-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative:
Mismatches:
Indels:
                                                                                                                                               Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997
C;Accession: S65626
                                                                                                           Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
                                                                                                                                                                                                                                       (1-12)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-824-647-16 (1-2095) x S65626 (1-12)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-824-647-16 (1-2095) x C30503 (1-12)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Experimental source: myeloma cell line C; Keywords: immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                       phosphorylase b - rabbit (fragments)
                                                                                                                                                                                                                      US-09-824-647-16 (1-2095) x A60528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1394 GTGGGAGCTGGGCCT 1408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.18e+05
5.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.18e+05
                                                                                                           .18e+05
                                                                                                                                           100.00%
100.00%
0.72%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.00%
100.00%
0.73%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.00%
100.00%
0.72%
                                                                                                                                                                                                                                                                                               5 ValGlyAlaGlyPro 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-3;4-12 <LUO>
                     A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-12 <WAL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                       Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-12 <GIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
 A; Accession: A60528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: S65626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Accession: C30503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alignment Scores:
                                                                                           Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No.:
                                                                                                               Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Мо.:
                                                                                                                                                                                                                                                                                                                                                      RESULT 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C30503
                                                                                                                                Score:
                                                                                                                                                                                                                                                                                                                                                                         S65626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R.Walton, P.E.; Baxter, R.C.; Burleigh, B.D.; Etherton, T.D. Comp. Blochem. Physiol. B 92, 561-567, 1989
A;Title: Purification of the serum acid-stable insulin-like growth factor binding protein. A;Reference number: A60528; MUID:89209787; PMID:2468442
                                                                                                                                                           Ridhovilovic, M.; Mai, Y.; Herbstreith, M.; Rubboli, F.; Tarroni, P.; Clementi, F.; Ros Biochem. Blophys. Res. Commun. 197, 137-144, 1993
A;ritle: Splicing of an anti-sense Alu sequence generates a coding sequence variant for A;Reference number: 139390; MUID:94071933; PMID:8250918
A;Accession: 139390
                                                                                                         C.Species: Homo sapiens (man)
C.Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      insulin-like growth factor-binding protein, serum - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 11-May-2000
                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:L18973; NID:g441143; PIDN:AAA86792.1; PID:g441144
C;Keywords: alternative splicing; neurotransmitter receptor
                                                                                         cetylcholine receptor (alternative exon 5b) - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             00002
                                                                                                                                                                                                                                                                                                                                                                                         0000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps:
                                                                                                                                                                                                                                                        A; Status: preliminary; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-824-647-16 (1-2095) x I39390 (1-12)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (1-12)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-824-647-16 (1-2095) x PH1175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1952 CTGTCAGAAGGGGGT 1966
                                                                                                                                                                                                                                                                                                                                                                                   1.18e+05
5.00
100.00%
100.00%
0.73%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .18e+05
.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.00%
100.00%
0.72%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 LeuSerGluGlyGly 7
Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-12 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-12 <CAS>
                                                                                                                                             Accession: 139390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Accession: A60528
                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                       Pred. No.:
                                                     RESULT 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          đ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 음
```

00002

#text_change 13-Mar-1997

```
A;Cross-references: FlyBase:FBgn0003429
C;Keywords: alternative splicing; ion channel; potassium channel; transmembrane pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 potassium channel protein Slo G3 – fruit fly (Drosophila melanogaster) (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R-phycoerythrin gamma-B chain - red alga (Gastroclonium coulteri) (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Drosophila melanogaster
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Feb-1997
C;Accession: PSO443
R;Adelman, J.P.; Shen, K.Z.; Kavanaugh, M.P.; Warren, R.A.; Wu, Y.N.; Lagrul
Neuron 9, 209-216, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C:Species: Gastroclonium coulteri
C:Date: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 23-Mar-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Accession: G22565
R;Klotz, A.V.; Glazer, A.N.
J. Biol. Chem. 260, 4856-4863, 1985
A;Title: Characterization of the bilin attachment sites in R-phycoerythrin. A;Reference number: A22565; MUID:85182601; PMID:3886644
A;Recession: G22565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        calcium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
Conservative:
                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Wolecule type: mRNA
A;Residues: 1-13 <ADE>
C;Comment: This potassium channel is activated by
                                                                                                                                                                                                                                                                                                  Gaps:
                                                                                                                                                                                                                                                                                                                                             US-09-824-647-16 (1-2095) x A32734 (1-13)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (1-13)
                                                                                                                  C; Keywords: neuropeptide; opioid peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-824-647-16 (1-2095) x G22565
                                                                                                                                                                                                                                                                                                                                                                                       GGGGAGGTGCTAGGG 1860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.16e+05
5.00
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                525 GCAGAAGGCACCGTG 511
                                                                                                                                                                             1.16e+05
5.00
100.00%
100.00%
0.73%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.16e + 05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5.00
100.00%
100.00%
0.73%
                                                                                                                                                                                                                                                                                                                                                                                                                 GlyGluValLeuGly 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 AlaGluGlyThrVal 6
                                              A; Molecule type: protein
A; Residues: 1-13 <MIC>
C; Superfamily: proenkephalin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: protein
A; Residues: I-13 <KLO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
A; Accession: A32734
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Gene: FlyBase:slo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alignment Scores:
Pred. No.:
                                                                                                                                                               Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                         1874
                                                                                                                                                                                                                                                                             Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No.:
                                                                                                                                                                                    Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score:
                                                                                                                                                                                                              Score:
                                                                                                                                                        inhibitory diffusible factor - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Wus musculus (house mouse)
C;Date: 29-Jan-1990 #sequence_revision 29-Jan-1990 #text_change 30-Sep-1993
C;Accession: A33520
R;Blat, C.; Bohlen, P.; Villaudy, J.; Chatelain, G.; Golde, A.; Harel, L.
A;Blat, C.; Bohlen, P.; Villaudy, J.; Chatelain, G.; Golde, A.; Harel, L.
A;Title: Isolation and amino-terminal sequence of a novel cellular growth inhibitor (inh A;Reference number: A33520; MUID:89197888; PMID:2703477
A;Accession: A33520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A32734
A32734
Cispecias: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
Cispecies: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
Cispecies: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
Cispecies: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 21-Jan-2000
Cispecies: A37334
RiMicanovic, R:, Ray, P:; Kruggel, W.; Lewis, R.V.
Biochem. Biophys. Res. Commun. 118, 299-303, 1984
A;Title: Purification and sequence of an opioid peptide derived from ovine proenkephalin A;Reference number: A32734; MUID:84128045; PMID:6546517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Accession: A58375
R;Yorgey, P.; Lee, J.; Koerdel, J.; Vivas, E.; Warner, P.; Jebaratnam, D.; Kolter, R. Proc. Natl. Acad. Sci. U.S.A. 91, 4519-4523, 1994
A;Title: Posttranslational modifications in microcin B17 define an additional class of A;Reference number: A58375; MUD:94240167; PMID:8183941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           microcin B17 - Escherichia coli (fragment)
C;Species: Escherichia coli plasmid pPY113
C;Date: 19-Mar-1997 #sequence_revision 19-Dec-1997 #text_change 07-May-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-824-647-16 (1-2095) x A58375 (1-12)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-824-647-16 (1-2095) x A33520 (1-12)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1394 GTGGGAGCTGGGCCT 1408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1143 GGTATCGGAGGAGGG 1129
                            CGGACTTCTCCACGT 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .18e+05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.00
100.00%
100.00%
0.73%
                                                   .18e+05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.008
100.008
0.728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 ValGlyAlaGlyPro 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 GlylleGlyGlyGly 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-12 <YOR>
                                                                                                                                                                                                                                                                                                                                                                  A Status: preliminary
A Molecule type: protein
A Residues: 1-12 <BLA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
                            413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                            à
                                                                 요
```

0000

Y.N.; Lagrutta, A.;

s.

```
C;Accession: A01777
R;Hirai, Y.; Yasuhara, T.; Yoshida; H.; Nakajima, T.
Bibmed. Res. 2, 447-449, 1981
A;Title: A new mast cell degranulating peptide, mastoparan-M, in the venom of the A;Reference number: A01777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 1-14 <HIR>
C;Comment: This cytoactive peptide from hornet venom induces mast cell degranulat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Accession: B61233 **Convenue_revision vo-may-1994 **text_cnange 07-may-1999 C; Accession: B61233 **Convenue vo-may-1999 **C; Accession: B61233 **M.F.; Bazer, F.W.; Sisum, W.; Randal, B101. Reprod. 44, 108-120, 1991 **A; Title: Characterization of feline conceptus proteins during pregnancy. A; Reference number: A61233; MUID:91198359; PMID:2015342 **Accession: B61233
              conceptus protein 4 - cat (fragment)
C;Species: Felis silvestris catus (domestic cat)
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 07-May-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      conceptus protein 4 - cat (fragment)
C;Species: Felis silvestris catus (domestic cat)
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 07-May-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N;Alternate names: mast cell-degranulating peptide
C;Species: Vespa mandarinia
C;Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 08-Dec-1995
                                                                                                                     RiThatcher, M.J.D.; Shille, V.M.; Fliss, M.F.; Bazer, F.W.; Sisum, W.; R Biol. Reprod. 44, 108-120, 1991
A.fille: Characterization of felline conceptus proteins during pregnancy. A;Reference number: A61233; MUID:91198359; PMID:2015342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                113
                                                                                                                                                                                                                                                                                                                                                                                                           0000
                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-824-647-16 (1-2095) x B61233 (1-13)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (1-13)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Superfamily: mastoparan
C; Keywords: amidated carboxyl end; venom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mastoparan M - hornet (Vespa mandarinia)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-824-647-16 (1-2095) x B61233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1169 GGGCTGCTGTCCAA 1183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       756 GGGCAGCAGTGCAG 742
                                                                                                                                                                                                                                                                                                                                                                                                         1.16e+05
5.00
100.00%
100.00%
0.72%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.16e + 05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.008
100.008
0.738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 GlyAlaAlaValGln 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 GlyAlaAlaValGln 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-13 <THA>
                                                                                                                                                                                                                                                               A; Status: preliminary
A; Molecule type: protein
A; Residues: 1-13 <THA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: protein A; Residues: 1-14 <HIR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity:
                                                                                             C; Accession: B61233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: A01777
                                                                                                                                                                                                                                          A; Accession: B612
                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                         Score:
                                                                                                                                                                                                                                                                                                                                                                     C; Species: Homo sapiens (man)
C; Date: 15-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 16-Aug-1996
C; Date: 15-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 16-Aug-1996
C; Accession: B61458
R; Brouet, J.C.; Dellaqi, K.; Gendron, M.C.; Chevalier, A.; Schmitt, C.; Mihaesco, E.
J. Exp. Med. 170, 1551-1558, 1989
A; Exp. Med. 170, 1551-1558, House by human monoclonal IgM directed to myelin-asscation of a public idiotype by human monoclonal IgM directed to myelin-asscation of the myelin-asscatio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Treell antigen receptor VJ junction beta chain - human c.Species: Homo sapiens (man) (Johace: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999 (Johace: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999 (Johacession: 84738 R;Lehner, P.J. Submitted to the EMBL Data Library, August 1994 A;Description: Human HiA-A0201 restricted recognition of influenza A is dominated by T.A.Ccession: 847386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:235710; NID:9527515; PIDN:CAA84779.1; PID:9527516
C;Keywords: T-cell receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0000
              000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
Indels:
           Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                 Ig kappa chain V-I region (BLA) - human (fragment)
                                                                   Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-13 <BRO.
C;Reywords: heterotetramer; immunoglobulin
                                                                                                                        (1-13)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (1-13)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-824-647-16 (1-2095) x S47388 (1-13)
                                                                                                                     US-09-824-647-16 (1-2095) x PS0443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-824-647-16 (1-2095) x B61458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.16e+05
5.00
100.00%
100.00%
0.72%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.16e+05
5.00
100.00%
100.00%
0.73%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  160 CCCACACACTGAGC 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 ProThrThrLeuSer 12
        100.00%
0.73%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
Query Match:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-13 <LEH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 28
B61233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ð
```

s,

à

```
C;Species: Homo sapiens (man)
C;Species: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C;Accession: PH1767
C;Accession: PH1767
C;Accession: X; Yockey, C.E.; Brenner, M.B.; Balk, S.P.
J; Porcelli, S.; Yockey, C.E.; Brenner, M.B.; Balk, S.P.
J; Exp. Med. 178, 1-16, 1993
A;Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Accession: $57574
R; Burrows, S.R.; Silins, S.L.; Moss, D.J.; Khanna, R.; Misko, I.S.; Argaet, V.P. submitted to the EMBL Data Library, June 1995
A; Description: T cell receptor repertoire for a viral epitope in humans is diversif A; Reference number: $57494
A; Accession: $57574
                                                                                          C;Accession: PH1763
R;Porcelli, S.; Yockey, C.E.; Brenner, M.B.; Balk, S.P.
J. Exp. Med. 178, 1-16, 1993
A;Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral b.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cell receptor alpha chain V region (clone 2V alpha 7.2-2) - human (fragment)
                             receptor alpha chain V region (clone 1V alpha 23-2) - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T cell receptor V-J junctional alpha chain region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-Oct-1995 #sequence_revision 17-Nov-1995 #text_change 05-Nov-1999
                                                        C:Species: Homo sapiens (man)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                            40000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Reference number: PH1754; MUID:93301585; PMID:8391057
A; Accession: PH1767
A; Status: prellainary
A; Molecule type: mRNA
A; Residues: 1-14 < POR>
                                                                                                                                                                                             A; Reference number: PH1754; MUID: 93301585; PMID: 8391057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (1-14)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-824-647-16 (1-2095) x PH1763 (1-14)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-824-647-16 (1-2095) x PH1767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             947 CTGTGTGTGTGAGG 961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.15e+05
5.00
100.00%
100.00%
0.72%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        947 CTGTGTGTGTGAGG 961
                                                                                                                                                                                                                                                                                                                                          1.15e+05
5.00
                                                                                                                                                                                                                                                                                                                                                                              100.00%
100.00%
0.72%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 LeuCysAlaValArg 5
                                                                                                                                                                                                                A; Accession: PH1763
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-14 <POR>
                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Aliqnment Scores:
                                                                                                                                                                                                                                                                                                                         Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           red. No.:
                                                                                                                                                                                                                                                                                                                                            red. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 34
                                       cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Species: Alvinella pompejana
C; Species: Alvinella pompejana
C; Date: 13-3nn-1995 #sequence_revision 13-Jan-1995 #text_change 29-May-1998
C; Accession: S23376
R; Gaill, F.; Wiedemann, H.; Mann, K.; Kuehn, K.; Timpl, R.; Engel, J.
J. Mol. Biol. 221, 209-223, 1991
A; Title: Molecular characterization of cuticle and interstitial collagens from worms A; Reference number: S17581; MuID:92015209; PMID:1920405
A; Recession: S23376
A; Recession: S23376
A; Residues: 1-14 cGAI>
                                                                                                                                                                                                                                                                                                                                                                                                                                             Rimirata, T.; Ikeda, J.; Takano, M.; Ohsugi, R.
Plant Cell Physiol. 30, 429-437, 1989
A;Title: Comparative studies of NAD-malic enzyme from leaves of various C-4 plants.
                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Panicum sp. (millet)
C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 24-Feb-1994
C;Accession: B60683
                                                                                                                                                                                                                                                                                                                                                             malate dehydrogenase (decarboxylating) (EC 1.1.1.39) - millet (fragment)
F;14/Modified site: amidated carboxyl end (Leu) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           collagen alpha chain - polychaete (Alvinella pompejana) (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7.0000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40000
                                                                                              Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative:
Mismatches:
Indels:
                                                          Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
                                                                                                                                                             Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: protein
A;Residues: 1-14 <MUR>
C;Reywords: oxidoreductase; photosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-824-647-16 (1-2095) x B60683 (1-14)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (1-14)
                                                                                                                                                                                                     (1-14)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-824-647-16 (1-2095) x S23376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-824-647-16 (1-2095) x QMVHMM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1026 GCCCCACCAGGTGCC 1040
                                                                                                                                                                                                                                           571 CTGGCAAAGAAGCTC 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.15e+05
5.00
100.00%
100.00%
0.72%
                                                1.15e+05
5.00
100.00$
100.00$
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .15e+05
                                                                                                                                                                                                                                                                100.00%
100.00%
0.72%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 AlaProProGlyAla 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Reference number: A60683
A; Accession: B60683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                          Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
                                          Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
                                                             ::
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score:
                                                             Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
```

```
T-cell receptor delta chain V region (105.211) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Species: Mus musculus (house mouse)
C:Date: 31-Aug-1990 #sequence_revision 31-Aug-1990 #text_change 30-May-1997
C;Accession: D35141
R:Sim, G.K.; Augustin, A.
R:Sim, G.K.; Augustin, A.
A:Title: Daniantly inherited expression of BID, an invariant undiversified T cell A;Reference number: A35141; MUID:90242386; PMID:2110506
                                                                                                                                                                                Ricetinson, D. M.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A; Title: Molecular characterization of transgene-induced immunodeficiency in B-le
A; Reference number: PH1580; MUID:93301609; PMID:8315387
A; Accession: PH1639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ricevinson, D.A.; Campos-Torres, J.; Leder, P.
L. Exp. Med. 178, 317-329, 1993
A;Title: Molecular characterization of transgene-induced immunodeficiency in B-1¢
A;Reference number: PH1580; MUID:93301609; PMID:8315387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ig H chain V-D-J region (wild-type clone 304) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C;Accession: PH1597
                                                                                                 IG H chain V-D-J region (clone B-less 230) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change#17-Mar-1999
C;Accession: PH1639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        # v o o o o
                                                                                                                                                                                                                                                                                                                                                                                                                  40000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A) Accession: PH1597
A; Molecule type: DNA
A; Residues: 1.14 <LEV>
A; Experimental source: Done marrow pre-B lymphocyte
C; Reywords: immunoglobulin
                                                                                                                                                                                                                                                                                                                             Experimental source: bone marrow pre-B lymphocyte
                                                                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-824-647-16 (1-2095) x PH1597 (1-14)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (1-14)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-824-647-16 (1-2095) x PH1639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1705 TGCGCACGCAGGGGT 1719
                                                                                                                                                                                                                                                                                                                                                                                                         1.15e+05
5.00
100.008
Y: 100.008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.15e+05
5.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.00%
100.00%
0.72%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CysAlaArgArgGly 5
  3 GlyAlaAlaThrGly
                                                                                                                                                                                                                                                                                                                                                  C; Keywords: immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-14 <LEV>
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 40
                                                             RESULT
PH1639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Accession: JH0516
R; Coleman, M.E.; Pan, Y.C.E.; Etherton, T.D.
Riccheman, M.E.; Pan, Y.C.E.; Etherton, T.D.
R; Coleman, Blophys. Res. Commun. 181, 1131-1136, 1991
A; Title: Identification and NH2-terminal amino acid sequence of three insulin-like growth; Reference number: JH0515; MUID: 92109718; PMID: 1722398
A; Accession: JH0516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Accession: .JH0516
R; Coleman, M.E.; Pan, Y.C.E.; Etherton, T.D.
Riccheman, M.E.; Pan, Y.C.E.; Etherton, T.D.
Riccheman, M.E.; Pan, Y.C.E.; Etherton, T.D.
A; Title: Identification and NH2-terminal amino acid sequence of three insulin-like growt A; Reference number: JH0515; MUID:92109718; PMID:1722398
A; Accession: JH0516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          insulin-like growth factor-binding protein 3 - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 23-Mar-1995
                                                                                                                                                                                                                                                                                                                                                                                                         insulin-like growth factor-binding protein 3 - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 23-Mar-1995
                   A;Cross-references: EMBL:Z49959; NID:g887504; PIDN:CAA90230.1; PID:g887505
C;Keywords: T-cell receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                 Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
                                                                                                                                                                                                                                                US-09-824-647-16 (1-2095) x S57574 (1-14)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (1-14)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-824-647-16 (1-2095) x JH0516 (1-14)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-824-647-16 (1-2095) x JH0516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1163 GGGAGTGGGGCTGCT 1177
                                                                                                                                                                                                                                                                                         1222 AGCAGTGCTGGTGGT 1208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.15e+05
5.00
100.00%
100.00%
0.73%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.15e+05
5.00
100.00%
100.00%
0.72%
                                                                                                 1.15e+05
5.00
100.00%
100.00%
0.73%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 SerSerAlaGlyGly 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: protein
A;Residues: 1-14 <COL>
A;Experimental source: serum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: protein
A; Residues: 1-14 <COL>
A; Experimental source: serum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                          Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
A; Residues: 1-14 <BUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
                                                                                Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No.:
                                                                                                      Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                         RESULT 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score:
                                                                                                                           Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score:
                                                                                                                                                                                                                                                                                         ò
```

267 GGGCAGCAACTGGA 253

ð

ð

```
R; Davison, M.D.; Rixon, F.J.; Davison, A.J.
J. Gen. Virol. 73, 2709-2713, 1992
A; Title: Identification of genes encoding two capsid proteins (VP24 and VP26) of he A; Reference number: PQ0544; MUID:93019027; PMID:1328483
                                                                                                                                                                                                                                                                                                                                                                                                                                          R.KO. M.S.; Wang, X.; Horton, J.H.; Hagen, M.D.; Takahashi, N.; Maezaki, Y.; Nadeau Mamm. Genome 5, 349‡355, 1994
A;Title: Genetic mapping of 40 cDNA clones on the mouse genome by PCR.
A;Reference number: I48934; MUID:94319082; PMID:8043949
A;Recession: I49407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: human herpesvirus 1
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
                                                                                                                                                                                                                                                                                                                                                   placental calcium-binding protein - western wild mouse (fragment)
C;Species: Mus spretus (western wild mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 29-Sep-1999
C;Accession: 149407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross_references: EMBL:U05696; NID:9497016; PIDN:AAA61936.1; PID:9497017
C;Superfamily: S-100 protein; calmodulin repeat homology
C;Reywords: calcium binding; EF hand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 00000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0000
  0000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    capsid protein VP19C - human herpesvirus 1 (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative:
Mismatches:
                       Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA
A;Residues: 1-15 <RES>
                                                 Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches:
  Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (1-15)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (1-15)
                                                                                                                                                     (1-15)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-824-647-16 (1-2095) x PQ0545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-824-647-16 (1-2095) x 149407
                                                                                                                                                  US-09-824-647-16 (1-2095) x I52734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1322 GATAAGGAACCGCGG 1308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.14e+05
5.00
100.00%
100.00%
0.72%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  215 CTGCCGGCCACTCCT 229
                                                                                                                                                                                                    729 GCAGGTGGCGTTGGG 715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.14e+05
5.00
100.00%
100.00%
0.73%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AsplysGluProArg 13
                                                                                                                                                                                                                              11 AlaGlyGlyValGly 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Experimental source: strain 17
5.00
100.00%
100.00%
0.73%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Keywords: capsid protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: protein A; Residues: 1-15 <DAV>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
                          Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Accession: PQ0545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: PQ0545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: UL38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chaccession: 152734

Rirakahashi, T.; Moyer, M.P.; Cano, M.; Wang, Q.J.; Mountjoy, C.P.; Sanger, W.; Adrian, Carcinogenesis 16, 931-939, 1995

A;Title: Differences in molecular biological, biological and growth characteristics betw A;Reference number: 152734; MUID:95246257; PMID:7728976

A;Reference number: 152734; MUID:95246257; PMID:7728976

A;Reference number: 152734

A;Reference number: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene c-K1-ras protein - hamster (fragment)
C;Species: Cricetinae gen. sp. (hamster)
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 28-May-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-15 <CRO>
A; Cross-references: EMBL:X06604; NID:g48244; PIDN:CAA29823.1; PID:g48245
A; Note: the source is designated as Thermus thermophilus
C; Superfamily: Thermus aquaticus leu leader peptide
                               not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15
0
0
0
                                                                                                                                                                                    40000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                Conservative:
Mismatches:
Indels:
                                                                                                                                                                                 Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                              (1-14)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-824-647-16 (1-2095) x LFTWL (1-15)
                                                                                                                                                                                                                                                                                                                                                              US-09-824-647-16 (1-2095) x D35141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1625 GACAGGGCTGGGCCT 1639
                                                                                                                                                                                                                                                                                                                                                                                                             412 GGCATTCGAACTGAC 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.14e+05
5.00
                                                                                                                                                                               1.15e+05
5.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.14e+05
                                                                                                                                                                                                                                                                                                                                                                                                                                          100.00%
100.00%
0.72%
                                                                                                                                                                                                                           100.00%
100.00%
0.73%
     A; Accession: D35141
A; Status: preliminary; not of A; Molecule type: mRNA
A; Residues: 1-14 <SINA
C; Keywords: T-cell receptor
                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
Pred. No!:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
                                                                                                                                                            Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match:
DB:
                                                                                                                                                                                                                                                                                  Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No.:
                                                                                                                                                                                 Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
```

à

Search completed: July 7, 2003, 16:12:15 Job time: 80.5 secs

us-09-824-647-16.lim.rsp

```
nephrops no
locusta mig
ascaris suu
                                                                                                                                                      scyliorhinu
scyliorhinu
                                                                                                                                                                                                                  stomopneute
                                                                                                                                                                                   cyprinus ca
                                                                                                                                                                                                     squalus aca
                                                                                                                                                                                                                               azotobacter
                                                                                                                                                                                                                                                bothrops in
                                                                                                                                                                                                                                                             oncorhynchu
                                                                                                                                                                                                                                                                             homo sapien
                                                                                                                                                                                                                                                                                                          ridibu
                                                                                                                                                                                                                                                                                                                                        homo sapien
                 mus musculu
                                                                           carcinus ma
                                                                                           conus stria
                                                                                                                                                                                                                                                                                                                                                                     phocine dis
                              mus musculu
                                                homo sapien
                                                            herpes simp
                                                                                                                                                                                                                                                                                                                                                        rattus norv
                                                                                                                                                                                                                                                                                                                                                                                       rana tempor
                                                                                                                                                                                                                                                                                           chelyosoma
                                                                                                                                                                                                                                                                                                                          bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MYOTROPIC ACTIVITY).

- MISCELLANDOUS: AN ANALOG WITHOUT THE N-TERMINAL PCA RESIDUE WAS SYNTHESIZED AND FOUND TO EXHIBIT GREATER ACTIVITY (144%) THAN THE PARENT NEUROPEPTIDE. THE PORTION OF THE SEQUENCE OF LAR MOST CRITICAL FOR THE MYOTROPIC PROPERTIES IS LIMITED TO THE PENAPREPTIDE FRAGMENT FPRL.
- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
PIR; A23967; A23967.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Leukopyrokinin (LEM. PR).
Leukopyrokinin (LEM. PR).
Leucophaea maderae (Madeira cockroach).
Eukaryota: Metazoa: Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
Blaberoidea; Blaberidae; Leucophaea.
                                                                                                                                                                                                                                                                                                             rana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE—87052651; PubMed-2877794;
Holman G.M., Cook B.J., Nachman R.J.;
Primary structure and synthesis of a blocked myotropic
neuropeptide isolated from the cockroach, Leucophaea maderae.";
Comp. Biochem. Physiol. 85c:219-224(1986).
-i- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                     P35946
P56923
                                                                                                                                                      P42996
                                                                                                                                                                                                                                                                                                                                        P22103
                                                                                                         P24816
                                                                                                                                                                                   P23879
                                                                                                                                                                      P42997
                                                                                                                                                                                                                                                               09prz1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-86269041; PubMed=3015140;
Nachman R.J., Holman G.M., Cook B.J.;
Active fragments and analogs of the insect neuropeptide leucopyrokinin: structure-function studies.";
Biochem. Biophys. Res. Commun. 137:936-942(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PYRROLIDONE CARBOXYLIC ACID. AMIDATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JAN-1990 (Rel. 13, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                    ALIGNMENTS
                                           UPAA_HUMAN
VGLG_HSV2B
AL11_CARMA
CONO_CONST
                                                                                                                                                                                                  OXYV_SQUAC
SAP_STOVA
YBFR_AZOVI
BPP8_BOTIN
BRK_ONCMY
GAJU_HUMAN
                                                                                                      DI_NEPNO
DNF1_LOCMI
FAR9_ASCSU
OXYA_SCYCA
                                                                                                                                                                                                                                                                                                            GRP_RANRI
ODP2_BOVIN
                                                                                                                                                                                                                                                                                           GON2_CHEPR
                                                                                                                                                                                                                                                                                                                                        PNEU_HUMAN
                                                                                                                                                                                                                                                                                                                                                                     RRPL_PHODV
                                                                                                                                                                                     OXYT_CYPCA
                                                                                                                                                                      OXYF_SCYCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001484; Pyrokinin.
PROSITE; PS00539; PYROKININ; 1.
Neuropeptide; Amidation; Pyrokinin.
MOD_RES 8 AMIDATI
                                                                                                                                                                                                                                                                                                                                                        PNEU_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE, AND SYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                            မ.မ မ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=6988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IISSUE=Head
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LPK_LEUMA P13049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 1
                              υ
                                                                                                                                                                                                                                                000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Command line parameters:
-MODEL-frame+_n2p_model -DEV=xlp
-MODEL-frame+_n2p_model -DEV=xlp
-G-Cgn2_1/USPTO_spool/US09824647/runat_07072003_154758_26613/app_query.fasta_1.2247
-G-Cgn2_1/USPTO_spool/US09824647/runat_07072003_154758_26613/app_query.fasta_1.2247
-DB=SW1SSPTOC.40 -QFWI-fastan -SUFFIX-lim.rsp -MIRMATCH=0.1 -LOOPCL=0
-LISTA-6 -DCALIGN=200 -THR_SCORE-quality -THR_MIN-1 -ALIGN-45 -MODE-LOCAL
-USFRY=pto -NORM-ext -HEAFSIZE-500 -MINLEN-0 -MAXIEN-15
-USER-US09824647_eCGN_1_1.46_erunat_07072003_154758_26613 -NCPU-6 -ICPU-3
-NO_MARP -LARREQUERY -NG_SCORES-0 -WAAT -DSPBALCK=100 -LONGLOG
-DEV_TIMEOUT-120 -WARN_THREOUT-30 -THREADS-1 -XGAPOP-60 -XGAPEXT-60 -FGAPOP-6
-FGAPEXT-7 -YGAPOP-60 -YGAPEXT-60 -DELDP-6 -DELEXT-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     streptomyce
achatina fu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  conus spuri
vespa manda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              thermus the
physcomitre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     litoria xan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    oncorhynchu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                litoria gil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 litoria gil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               conus betul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         zea mays (m
morganella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         couns burbu
                                                                                                      (without alignments)
5891.045 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P13049 leucophaea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 litoria
                                                                                                                                                                                   1 cgcaggcagaccatgtggac.....ataaagtttgtcactttctt 2095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P56246 1
P83327 C
P58805 C
                                                                                         ; Search time 29.5 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P01255 8 P19149 8 P22790 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P56247
P56248
P82077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P17338
P58785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P58624
P80701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P21234
P80659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P04205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P80631
                                                                                                                                                                                                                                                                                                                                                                       1326
5.1.6
Compugen Ltd.
                                                           protein search, using frame_plus_n2p model
                                                                                                                                                                                                                                                                                                                                                                     Potal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                        112892 seqs, 41476328 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
GenCore version
Copyright (c) 1993 - 2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                THYF_PIG
XYLA_STRSQ
CEP1_ACHFU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DIDH_PSESP
LPL_THETH
PGKH_PHYPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MAST_VESMA
CDN2_LITGI
CDN3_LITGI
CDN5_LITCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CD14_LITXA
H2AX_ONCMY
RF1_CONSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CX1B_CONBE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          UC25_MAIZE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         URE2_MORMO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COW2_CONPU
                                                                                                                                                                                                                                60.0
60.0
7.0
7.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LPK LEUMA
                                                                                        July 7, 2003, 15:55:22
                                                                                                                                                                                                                               , Ygapext 6
, Ygapext 6
, Fgapext
, Delext
                                                                                                                                                      US-09-824-647-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SwissProt_40:*
                                                                                                                                                                                                                             60.0 X 60.0 Y 60.0 Y 6.0 Y 6.0 Y F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                  Minimum DB seq length: 0
Maximum DB seq length: 15
                                                                                                                                                                                                                OLIGO
Xgapop (
Ygapop (
Fgapop
Delop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   000000000000
                                                                                                                                                   Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score
                                                         OM nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Database :
                                                                                                                                                                                                                                                                                                                                       Word size:
                                                                                                                                                                                                                                                                                                          Searched:
                                                                                        Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ٠
چ
```

υ 00 U

00000

Conservative: Mismatches: Indels:

100.00% 100.00% 0.73%

Length: Matches:

9.22e+06 5.00

983 MW; F64BAlEDC5B87DD1 CRC64;

```
-i- SUBCELLUIAR LOCATION: Cytoplasmic.
                                                                                                                                   Isomerase; Pentose shunt; Xylose metabolism; Magnesium
                                                                                                  INTERPITO: IPR001998; Xylose isom.
PROSITE; PS00172; XYLOSE_ISOMERASE_1; PARTIAL.
PROSITE; PS00173; XYLOSE_ISOMERASE_2; PARTIAL.
                                                                                                                                                                                                                                                                           US-09:824-647-16 (1-2095) x XYLA_STRSQ (1-9)
                                                                                                                                                                                                                                                                                                 1380 GCAGGTTCCGCCCAC 1366
                                                                                                                                                                                                                                                                                                             3 AlaGlySerAlaHis 7
                                                      -!- SUBUNIȚ: HOMOTETRAMER.
                                                                                         PIR; A31576; A31576
                                                                                                                                                                                                                                Best Local Similarity:
                                                                                                                                                                                                                     Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
                                                                                                                                                                                   Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                    CEP1_ACHFU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SECUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOD_RES
                                                                                                                                                                                                                                          Query Match:
                                                                                                                                                                                                ..
9
                                                                                                                                                                                                                                                                                                                                                          CEP1_ACHFU
                                                                                                                                                                                                red.
                                                                                                                                                                                                           Score
                                                                                                                                                                                                                                                                                                                                                                                 ð
  Pawar H.S., Kannan K., Srinivasan M.C., Vartak H.G.; Perification and characterisation of glucose (xylose) isomerase from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces. NCBL_TaxID=1931;
                                                                                                                                                                                                                                                                                                                                                          Pleau J.-M., Dardenne M., Blouquit Y., Bach J.-F.;
"Structural study of circulating thymic factor: a peptide isolated
                                                                                                                                                                                                                                                                     Thymic factor.
Sus scrofa (P1g).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                from pig serum. II. Amino acid sequence.";
J. Biol. Chem. 252:8045-8047 (1977).
-I- MISCELLANBOUS: THE BIOLOGICAL SOURCE(S) AND PHYSIOLOGICAL ACTIVITIES OF THIS PEPTIDE HAVE NOT BEEN DETERMINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                       PYRROLIDONE CARBOXYLIC ACID.
MW; D500B87866C5B33D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90000
    949 MW; 92341771A9D5A1B6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative:
Mismatches:
Indels:
                                    Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         XYIA_STRSQ STANDARD; PRT; 9 AA. P19149; 01-NOV-1990 (Rel. 16, Created) 1-NOV-1990 (Rel. 16, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Xylose isomerase (EC 5.3.1.5) (Fragment).
                                                                                                                                                                                                                                21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1986 (Rel. 01, Last annotation update)
                                                                                                                                                                                                             9
R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
                                                                                  Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps:
                                                                                             Gaps:
                                                                                                                  US-09-824-647-16 (1-2095) x LPK_LEUMA (1-8)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptomyces sp. (strain NCL 82-5-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (1-9)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-88326335; PubMed-3415697;
                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-824-647-16 (1-2095) x THYF_PIG
                                                                                                                                                                                                                                                                                                                                                  MEDLINE-78026571; PubMed-914862;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1568 ACGTCCTTCACACCC 1554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9.22e+06
5.00
100.00%
100.00%
0.72%
                                 1.04e+07
5.00
100.00%
100.00%
0.73%
                                                                                                                                                     Thrserpherhrpro 6
                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                           1
876 N
                                                                                                                                                                                                                                                                                                                                                                                                                              A01523; YFPG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
Best Local Similarity:
                                                        Percent Similarity:
Best Local Similarity:
Query Match:
DB:
     A);
                                                                                                                                                                                                                                                                                                                NCBI_TaxID-9823;
    æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
                           Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
     SEQUENCE
                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                XYLA_STRSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               XYLA.
                                                                                                                                                                                                                                                                                                                                                                                                                              PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                g
```

```
Achatina fulica (Glant Africana).

Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora; Achatinacea; Achatinidae; Achatina.

NCBI_TaxID=6530;
                                                                                                                                                                                                                                                                                                                           AMIDATION.
82D6D5B9C7741365 CRC64;
                                                                                                                                                                                                                                                                      MOVEMENT OF ACHATINA.
                                                                                                                                                                                                                                                                                                                                                                             0000
                                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
Conservative:
Mismatches:
                                     01-AUG-1991 (Rel. 19, Last sequence update) 01-DEC-1992 (Rel. 24, Last annotation update)
11 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JS-09-824-647-16 (1-2095) x CEP1_ACHFU (1-11)
                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps:
                                                                                                                                                       STRAIN-Ferussac; TISSUE-Heart atrium;
                                                            peptide-1 (ACEP-1)
                           01-AUG-1991 (Rel. 19, Created)
                                                                                                                                                                                                                                                                                                                                                                            5.88e+04
5.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ArgProGlnGlyArg 10
                                                                                                                                                                                                                                                                                                                           11 11
AA; 1305 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100 AGGCCACAGGGCAGA 86
 STANDARD;
                                                                                                                                                                                                                                                                                                 PIR; A34662; A34662.
                                                                                                                                                                                                                                                                                                              Hormone; Amidation.
                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
                                                                 Cardio-excitatory
```

```
secretions of rainbow trout, Oncorhynchus mykiss.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-824-647-16 (1-2095) x RF1_CONSP (1-12)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                        ..
Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RF1_CONSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred.
SPITING SPICE STATE OF SPICE S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPECIES-L.chloris; TISSUE-Skin;
MEDLINE-98175802; PubMed-9516047;
Steinborner S.T., Currie G.J., Bowie J.H., Wallace J.C., Tyler M.J.;
Steinborner S.T., Currie G.J., Bowie J.H., Wallace J.C., Tyler M.J.;
New antiblotic caerin 1 peptides from the skin secretion of the Australian tree frog Litoria chloris. Comparison of the activities of the caerin 1 peptides from the genus Litoria.";
J. Pept. Res. 51:121-126(1998).
-I- FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR ANTIBIOTIC ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-97374000; PubMed-9230483;
Steinborner S.T., Waugh R.J., Bowie J.H., Wallace J.C., Tyler M.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUB-Skin mucus;
Fernandes J.M.O., Kemp G.D., Molle G., Smith V.J.;
"Antimicrobial properties of a histone H2A-like protein from skin
                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygil; Neopterygil; Teleostei; Euteleostei;
Protacanthopterygil; Salmoniformes; Salmonidae; Oncorhynchus.
NCBI_TaxID-8022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "New caerin antibacterial peptides from the skin glands of the Australian tree frog Litoria xanthomera."; J. Pept. Sci. 3:181-185(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -i- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS
-i- MASS SPECTROMETRY: MW-1096; METHOD-FAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AMIDATION.
28225503E3772728 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                      15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
                                                                                                                                                                                                   Litoria xanthomera (Orange-thighed frog), and Litoria chloris (Blue-thighed frog).
                                                                12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-824-647-16 (1-2095) x CD14_LITXA (1-12)
                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE, AND MASS SPECTROMETRY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       915 GGGGCCTGGGGCTG 929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE 12 AA; 1097 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5.8e+04
5.00
100.00%
100.00%
0.72%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Amphibian skin; Amidation.
MOD_RES 12 12
                                                                STANDARD;
                                                                                                                                                                                                                                                                                      NCBI_TaxID-79697, 86064;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Histone H2A (Fragment)
Oncorhynchus mykiss (R
                                                                                                                                                                                                                                                                                                                                                                                      SPECIES-L. xanthomera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          H2AX_ONCMY
P83327;
                                                                                                                                                                           Caeridin 1.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ramsay S.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
                                                                CD14_LITXA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         H2AX_ONCMY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 6
                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ð
```

```
TISSUE-Venom;
MEDLINE-21605839; PubMed-11738233;
Maillo M., Aguilar M.B., Lopez-Vera E., Craig A.G., Bulaj G.,
Olivera B.M., Heimer de la Cotera E.P.;
"Conorfamide, a Conus venom peptide belonging to the RFamide family of neuropeptides.";
Submitted (APR-2002) to the SWISS-PROT data bank.

-!- FUNCTION: Has antibacterial activity against Gram-positive bacteria and antibacterial activity against S.cerevisiae.
-!- SUBGNIT: The nucleosome is an octamer containing two molecules of H2A, H2B, H3, and H4; which wrap approximately 146 bp of DNA.
-!- SUBGELUCIAN LOCATION: Nuclear.
-!- MASS SPECTROMETRY: MW-13639; METHOD-MALDI.
-!- SIMILARITY: BELONGS TO THE HISTONE H2A FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -i- SUBCELLUIAR LOCATION: Secreted.
-i- TISSUE SPECIFICITY: Expressed by the venom duct.
-i- MASS SPECTROMETRY: MW=1454.8; METHOD=Electrospray.
-i- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conus spurius (Alphabet cone).
Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
NCBI_TaxID=192919;
                                                                                                                                                                                                         Chromosomal protein; Nucleosome core; Nuclear protein; DNA-binding; Antibiotic; Fungleide; Acetylation.
                                                                                                                                                                                                                                                                                                                       CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOD_RES 12 12 AMIDATION.
SEQUENCE 12 AA; 1456 MW; 2510671E49D772D3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          00000
                                                                                                                                                                                                                                                                                                                                                                                       000027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative:
                                                                                                                                                                                                                                                                                                                     3EF28D9668D87DD8
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Conorfamide-Srl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -1- FUNCTION: Causes hyperactivity in mice.
                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels:
                                                                                                                                                                                                                                                                               ACETYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-824-647-16 (1-2095) x H2AX_ONCMY (1-12)
                                                                                                                                                                        InterPro; IPR002119; Histone_H2A.
PROSITE; PS00046; HISTONE_H2A; PARTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1391 AGGGTGGGAGCTGGG 1405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Neurotoxin; Toxin; Amidation.
                                                                                                                                                                                                                                                                                                   12
1202 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.8e+04
5.00
100.00%
0.73%
                                                                                                                                                                                                                                                                                                                                                                                   5.8e+04
5.00
                                                                                                                                                                                                                                                                                                                                                                                                                           100.008
100.008
0.728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 ArgValGlyAlaGly 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Toxicon 40:401-407(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity?
                                                                                                                                                                                                                                                                                                                       12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity
                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RF1_CONSP
P58805;
                                                                                                                                                                                                                                                                           MOD_RES
NON_TER
SEQUENCE
```

ð

```
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Aliqnment Scores:
                 Alignment Scores:
                                                                                                                                                                                                                                                                             CDN3_LITGI
P56248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Caeridin 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDN5_LITCE
P82077;
                                                                                                                                                                                                                                                                                                                                                                 Caeridin 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                             Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDNS_LITCE
                                  Pred. No.:
                                                                                                                                                                                                                                                                 CDN3_LITGI
                                                                                                                                                                                                                                                RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1- TISSUE SPECIFICITY: SECRETED BY THE SKIN PAROTOID AND/OR ROSTRAL
                                                                                                                                                                                                              Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita;
Aculeata; Vespoidea; Vespidae; Vespinae; Vespa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Parotoid gland;
Waugh R.J., Stone D.J.M., Bowie J.H., Wallace J.C., Tyler M.J.;
Waugh R.J., Stone D.J.M., Bowie J.H., Wallace J.C., Tyler M.J.;
Waugh R.J., Stone Australian frogs. The structures of the caerins and
caeridins from Litoria gillen!";
J. Chem. Res. 139:937-961(1993).
-1- FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR
ANTIBIOTIC ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Litoria gilleni (Centralian tree frog).

Litoria gilleni (Centralian tree frog).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;

Pelodryadinae; Litoria.

NCBI_TaxID~39405;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AMIDATION.
06F1BBF272550CBF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14 14 AMIDATION.
14 AA; 1480 MW; C85A7ECA1D7B00DD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7.0000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative:
Mismatches:
Indels:
                                                                                                                          20-MAR-1987 (Rel. 04, Created)
20-MAR-1987 (Rel. 04, Last sequence update)
01-MOC-1992 (Rel. 23, Last annotation update)
wastoparan M (Mast cell-degranulating peptide).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15 AA.
                                                                                                 14 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- MASS SPECTROMETRY: MW=1408; METHOD=FAB. Amphibian skin; Amidation. AMIDATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (1-14)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps:
                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-824-647-16 (1-2095) x MAST_VESMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE, AND MASS SPECTROMETRY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              571 CTGGCAAAGAAGCTC 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15 AA; 1410 MW;
GGGTGGGTGCCCGTG 555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5.66e+04
5.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 LeuAlaLysLysLeu 13
             GlyTrpValProval
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity
                                                                                                                                                                                                                                                                                                                     rissue-venom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDN2_LITGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GLANDS
                                                                                                 MAST_VESMA
P04205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOD_RES
SEQUENÇE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
 269
                                                                                                                                                                                                                                                                                                  SEOUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDN2_LITGI
                                                                                MAST_VESMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred
```

ò

NAME OF THE PROPERTY OF THE PR

```
ANTIBIOTIC ACTIVITY.
-I- TISSUE SPECIFICITY: SECRETED BY THE SKIN PAROTOID AND/OR ROSTRAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Parotoid gland;
Waugh R.J., Stone D.J.M., Bowie J.H., Wallace J.C., Tyler M.J.;
Waugh R.J., Stone D.J.M., Bowie J.H., Wallace J.C., Tyler M.J.;
Waugh R.J., Stone D.J.M., Bowie J.H., Wallace J.C., Tyler M.J.;
Caeridins from Litoria gilleni.";
J. Chem. Res. 139:937-961(1993).
-i- FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Litoria caerulea (Green tree frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
Pelodryadinae; Litoria.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Litoria gilleni (Centralian tree frog).
Skaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
Pelodryadinae; Litoria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AMIDATION.
06E90A797AF70CBF CRC64;
  0000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative:
Mismatches:
Indels:
                                      Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                   15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15 AA
                                                                                                                                                                                                                                                                                                               15 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -1- MASS SPECTROMETRY: MW=1428; METHOD=FAB Amphibian skin; Amidation.

MOD_RES 15 15 AMIDATION.
  Length:
Matches:
                                                                                                                                          US-09-824-647-16 (1-2095) x CDN2_LITGI (1-15)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-824-647-16 (1-2095) x CDN3_LITGI (1-15)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE, AND MASS SPECTROMETRY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE, AND MASS SPECTROMETRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            915 GGGGGCCTGGGGCTG 929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5.57e+04
5.00
100.00%
100.00%
0.72%
                                                                                                                                                                                     915 GGGGCCTGGGGCTG 929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 GlyGlyLeuGlyLeu 15
5.57e+04
5.00
100:00%
100.00%
0.72%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15 AA; 1430 MW;
                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
Query Match:
                                                             Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=30344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=39405;
```

15 AA.

Score:

ŏ 셤

STACCCCCRATES

```
Oppermann U.C.T., Maser E.;
"Characterization of a 3 alpha-hydroxysteroid dehydrogenase/carbonyl reductase from the Gram-negative bacterium Comamonas testosteroni.";
Eur. J. Blochem. 241:744-749(1996)
IEUR. J. BLOCHEM. 241:744-749(1996)
INCLION: ALONG WITH THE 3 ALPHA-HYDROXYSTEROID DEHYDROGENASE AND 3-OXO-REDUCTASE ACTIVITIES TOWARDS A VARIETY OF CIS OR TRANS FUSED AF RING STEROIDS, IT ALSO REDUCES SEVERAL XENOBIOTIC CARBONYL COMPOUNDS; INCLIDING A METYRARONE-BASED CLASS OF INSECTICIDES, TO THE RESPECTIVE ALCOHOL METABOLITES.
-I- CATALITIC ACTIVITY: Androsterone + NAD(P)(+) = 5-alpha-androstane-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3,17-dione + NAD(P)H.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
                                                                               01-OCT-1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
3-alpha-hydroxysteroid dehydrogenase (EC 1.1.1.50) (3-alpha-HSD)
(Hydroxyprostaglandin dehydrogenase) (HSD29) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INVOLVED IN COFACTOR BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9506860D070A7790 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-824-647-16 (1-2095) x DIDH_PSESP (1-15)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SDK) FAMILI.
InterPro; IPR002198; ADH_Short.
PROSITE; PS00061; ADH_SHORT; PARTIAL.
PRT;
                                                                                                                                                                                                                                                                                                                 MEDLINE-97100200; PubMed-8944761;
                                                      (Rel. 34, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1193 GCCTCTGGGATTGGA 1179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15
1315 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5.57e+04
5.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.00%
100.00%
0.73%
                                                                                                                                                                                                            Bacteria, Proteobacteria.
NCBL_TaxID=306;
     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    in Escherichia coli.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Leu leader peptide.
Thermus thermophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00061; AL Oxidoreductase; NAD. DOMAIN 6 >
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15
15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SDR) FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OF LEUCINE.
                                                                                                                                                                                    Pseudomonas sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
                                                      01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LPL_THETH P21234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LPL_THETH
        SO THE TAKEN OCCOUNTY TO THE TAKEN OCCOUNTY 
                                                                                               J. Chem. Soc. Perkin Trans. 1:573-576(1993).
-1- FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR ANTIBIOTIC ACTIVITY.
-1- TISSUE SPECIFICITY: SECRETED BY THE SKIN PAROTOID AND/OR ROSTRAL.
                           Waugh R.J., Stone D.J.M., Bowie J.H., Wallace J.C., Tyler M.J.; "Peptides from Australian frogs. Structures of the caeridins from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conus betulinus (Beech Cone).
Usukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda; Conoldea; Conidae; Conus.
NCBI_TaxID-89764;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chen J.-S., Fan C.-X., Hu K.-P., Wei K.-H., Zhong M.-N.; "Studies on conotoxins of Conus betulinus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROBABLE.
3749B4F08E311337 CRC64;
                                                                                                                                                                                                                                                                                                                 9FF1A646BD550CAE. CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                0000
                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P58624;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15 AA.
                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
                                                                                                                                                                                                                                  -1- MASS SPECTROMETRY: MW-1355; METHOD-FAB Amphibian skin; Amidation.
MOD_RES 15 15 AMIDATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (1-15)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-824-647-16 (1-2095) x CDN5_LITCE (1-15)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROBABLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROBABLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Venom;
MEDLINE-20058566; PubMed-10591037;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-824-647-16 (1-2095) x CXIB_CONBE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE, AND MASS SPECTROMETRY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.57e+04
5.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              673 TGCTGTGAGCTGCCC 687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   915 GGGGCCTGGGGCTG 929
                                                                                                                                                                                                                                                                                                                 SEQUENCE 15 AA; 1357 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 GlyGlyLeuGlyLeu 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1650 MW;
                                                                                                                                                                                                                                                                                                                                                                                             5.57e+04
                                                                                                                                                                                                                                                                                                                                                                                                                   5.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.72%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
  TISSUE-Parotoid gland;
                                                                                 Litoria caerulea."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Æ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conotoxin BeTXIb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15
                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CX1B_CONBE
                                                                                                                                                                                                            GLANDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..
Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 13
DIDH_PSESP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 12
CX1B_CONBE
```

Conservative: Mismatches: Indels:

Length: Matches:

```
This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                            STRAIN-HB8 / ATCC. 27634;
MEDLINE-88121725; PubMed=3323845;
Croft J.E., Love D.R., Bergquist P.L.;
"Expression of leucine genes from an extremely thermophilic bacterium
                                                                                                                                                                                                                                                                              Gen. Genet. 210:490-497(1987).
FUNCTION: THIS PROTEIN IS INVOLVED IN CONTROL OF THE BIOSYNTHESIS
                                                                                                                Bacteria; Thermus/Deinococcus group; Deinococci; Thermales; Thermaceae; Thermus.
                              01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
15 AA
PRT;
```

Score:

ö

```
MaizeDB; 123957;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID-582;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        URE2_MORMO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hydrolase.
                UC25_MAIZE
                                                                                                                     (Fragment)
                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ٠.
چ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          URE2_MORMO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score:
                                and for commercial
                                                                 (See http://www.isb-sib.ch/announce/
Swiss Institute of Bioinformatics and the EMBL outstation
              the Buropean Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modificated and this statement is not removed. Usage by and for commercentities requires a license agreement (see http://www.isb-sib.ch/annout or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kasten B., Buck F., Nuske J., Reski R., Retokinin affects nuclear and plastome-encoded energy-converting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        plastid enzymes.

1 CATALYIC ACTIVITY: ATP + 3-phospho-D-glycerate = ADP + 3-phospho-D-glyceraty: Calvin cycle.

1 SUBUNIT: MONOMER (BY SIMILARITY).

1 SIMILARITY: BELONGS TO THE PHOSPHOGLYCERATE KINASE FAMILY.

1 THEAPPO: IPROGLYGE PGK.

PROSITE: PSOB111; PGLYCERATE KINASE; PARTIAL.

TRANSferase; Kinase; Multigene family; Calvin cycle; Chloroplast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Phosphoglycerate Klunase, chloroplast (BC 2.7.2.3) (Fragment).
Physcomitrella patens (Moss).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryopsida; Funaridae; Funariales; Funariaceae; Physcomitrella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1531 MW; 56A5ECC1F677EEC6 CRC64;
                                                                                                                                                     Lide; Leucine biosynthesis.
15 AA; 1666 MW; C2F107A386D7620B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       000027
                                                                                                                                                                                                                           0000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-824-647-16 (1-2095) x PGKH_PHYPA (1-15)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps:
                                                                                                                                                                                                                                                                                                             Gaps:
                                                                                                                                                                                                                                                                                                                                              US-09-824-647-16 (1-2095) x LPL_THETH (1-15)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Protonema;
MEDLINE-97275459; PubMed-9129336;
                                                                                                                                                                                                                                                                                                                                                                                1625 GACAGGCCTGGGCCT 1639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             168 ACTGAGCAGGCATCT 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.57e+04
5.00
100.00%
100.00%
0.72%
                                                                                                                       EMBL; X06604; CAA29823.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                  ThrGluGlnAlaSer 7
                                                                                                                                                                                                                                         5.00
100.00%
100.00%
0.72%
                                                                                                                                                                                                                         5.57e+04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                         S00901; LFTWL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15 AA;
                                                                                                                                                                                                                                                           Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity:
                                                                                                                                                         Leader peptide;
SEQUENCE 15 A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
     the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
                                                                                                                                                                                                           Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  РСКН_РНҮРА
Р80659;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                  10
     between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match:
                                                                                                                                                                                                                                                                                             Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 15
PGKH_PHYPA
ID PGKH_P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..
Q
```

ŏ

```
Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
Pernollet J.-C., Zivy M., de Vienne D.,
"The maize two dimensional gel protein database: towards an integrated
genome analysis program.":
                                                                                                                       Zea mays (Maize).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACC clade;
Pandcoldeae; Andropogoneae; Zea.
NCBI_TaxID=4577;
                                                                                                                                                                                                                                                                                                                                                 Theor. Appl. Genet. 93:997-1005(1996).
-i- MISCELLANBOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN PROTEIN IS: 4.9, ITS MW IS: 31.6 kDa.
Maize-2DPAGE: P80631; COLEOPTILE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=90264298; PubMed=2345135; MEDLINE=90264298; PubMed=2345135; Lynch M.J., Mobley H.L.T.; Micholson E.B., Jones B.D., Lynch M.J., Mobley H.L.T.; Morganella morganii urease: purification, characterization, and isolation of gene sequences. 7.

J. Bacteriol 172:3073-3080(1990).

-I - CAPALYTIC ACTIVITY: Urea + H(2)0 - CO(2) + 2 NH(3).

-I - SIMILARITY: TO OTHER UREASES BETA SUBUNITS.

PPR; B35389; B35389.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Morganella morganii (Proteus morganii).
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Morganella.
                                   01-OCT-1996 (Rel. 34, Created)
1-OCT-1996 (Rel. 34, Last sequence update)
15-UL-1999 (Rel. 38, Last annotation update)
Unknown protein from 2D-page of etiolated coleoptile (Spot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-AUG-1990 (Rel. 15, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Urease beta subunit (EC 3.5.1.5) (15 kDa subunit) (Urea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15 15 15 2D98944F2F20C7EB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       NON_TER 1 1
NON_TER 15 15
SEQUENCE 15 AA: 1580 MW; 83C54CFOCE1614D0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Š
15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-824-647-16 (1-2095) x UC25_MAIZE (1-15)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps:
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-AUG-1990 (Rel. 15, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1861 GGAGGCCTGAGCAGA 1847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.57e+04
5.00
100.00%
100.00%
0.73%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amidohydrolase) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GlyGlyLeuSerArg 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
STANDARD;
                                                                                                                                                                                                                                                                TISSUE-Coleoptile;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
```

Alignment Scores

RESULT 16

à

Score:

36.

@4000

Conservative: Mismatches: Indels:

Gaps:

Length: Matches:

8 AA.

PRT;

```
Submitted (DEC-1997) to the SWISS-PROT data bank.
-!- CAUTION: We are unable to find this protein in the translation of the genome of strain H37Rv.
                                                                                                                                                                                                                                                                                                                                                                   Mycobacterium intracellulare.
Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                            919 MW; 8D3DC40B19CDC2D2 CRC64;
                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                   US-09-824-647-16 (1-2095) x NS3_MYCTU (1-8)
                                                                                                                                                                                                                                                                                                                                            30S ribosomal protein S7 (Fragment)
                                                                                                                                                                                                                                                                                                       01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequ
01-FEB-1994 (Rel. 28, Last anno
                                                                                                1.04e+07
4.00
                                                                                                                    100.00%
100.00%
0.58%
                                                                                                                                                                                                          815 GTGGTAGCGTTC 804
                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                        1 ValvalAlaPhe 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   850
                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                       Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INIT_MET 0
NON_TER 8
SEQUENCE 8 AA;
                                                            8 AA;
                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=1767;
                                                                                     Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
                                                                                                                                                                                                                                                                                RS7_MYCIT
P33564;
                                                NON_TER
SEQUENCE
                                      NON_TER
                                                                                                                                                Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match:
                                                                                                 Pred. No.:
                                                                                                                                                                                                                                                                                                                                                          RPSG.
                                                                                                                                                                                                                                                         RESULT 20
                                                                                                                                                                                                                                                                     RS7_MYCIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score:
     300FF8
                                                                                                                                                                                                                                                                                             Jacobsen R.B., Jimenez E.C., De la Cruz R.G.C., Gray W.R., Cruz L.J.,
                                                                                                                                                                                                                                                                                                                                                                            "A novel D-leucine-containing Conus peptide: diverse conformational dynamics in the contryphan family.";
J. Pept. Res. 54:93-99(199).
I- SUBCELLUIAR LOCATION: Secreted.
I- TISSUE SPECIFFICITY: Expressed by the venom duct.
I- TISSUE SPECIFFICITY: MW-888.4; METHOD-LSIMS.
I- MASS SPECIFONETRY: MW-888.4; METHOD-LSIMS.
TOATH. SELONGS TO THE CONTRYPHAN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacterium
                                                                                                                                                                                                                                                       Conus purpurascens (Purple cone).
Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Neogastropoda; Conoidea; Conus.
  .
.
.
.
.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 D-LEUCINE.
890 MW; 75A367672732CEB8 CRC64;
 Length:
Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative:
Mismatches:
Indels:
                                    Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
16-CCT-2010 (Rel. 40, Last annotation update)
30 kDa non-secretory protein 3 (Fragment).
                                                                                                                                                                                                       15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                  8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
                                                                                                                                                                                                                                                                                                                   SYNTHESIS, AND MASS SPECTROMETRY.
                                                                                    (1-15)
                                                            Gaps:
                                                                                                                                                                                                                                                                                                                              STRAIN-Clipperton Island; TISSUE-Venom; MEDLINE-99388839; PubMed-10461743;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-824-647-16 (1-2095) x COW2_CONPU (1-8)
                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                  US-09-824-647-16 (1-2095) x URE2_MORMO
                                                                                                         1827 ACCCCACTCGGAGGG 1841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.04e+07
4.00
100.00%
100.00%
0.58%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-H37Rv;
Prasad H.K., Annapurna P.S.;
 .57e+04
                                                                                                                      ThrProLeuGlyGly 11
                     100.00%
100.00%
0.72%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 945 GGCTGTGTGCTG 956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GlyCysValLeu 4
                      Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE 8 AA;
                                                                                                                                                                                                                                             Leu-contryphan-P.
                                                                                                                                                                                                                                                                                          NCBI_TaxID-41690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                   Olivera B.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alignment Scores:
                                                                                                                                                                                  CONPU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NS3_MYCTU
P81152;
                                                                                                                                                                                                                                                                                                                   SEQUENCE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEOUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match:
                                                                                                                                                                    COW2_CONPU
ID COW2_C
 ..
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..
                                                                                                                                                         RESULT 18
             Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score:
 Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred.
                                                                                                          à
                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                its
                                                                                                                                                                                                                                                                                                                                                                 and for commercial
                                                                                                                                                                                                                                                                                                                                                                                            (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer.
                                                                                 Mycobacterium intracellulare.";
Nucleic Acids Res. 21:1039-1039(1993).
--- FUNCTION: PROFIEIN S7 BINDS SPECIFICALLY TO PART OF THE 3' END OF
16S RIBOSOMAL RNA (BY SIMILARITY).
--- SIMILARITY: BELONGS TO THE S7P FAMILY OF RIBOSOMAL PROTEINS.
MEDLINE-93197130; Pubmed-8451173;
Nair J., Rouse D.A., Morris S.L.;
"Nucleotide sequence analysis of the ribosomal S12 gene of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MW; 63276DC768732417 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; S35538; S35535.
InterPro; IPR000235; Ribosomal_S7.
PROSITE; PS00052; RIBOSOMAL_S7; PARTIAL.
Fibosomal protein; FRNa-binding.

BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-824-647-16 (1-2095) x RS7_MYCIT (1-8)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; L08171; AAA25376.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 · 1.04e+07
4.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.00%
100.00%
0.58%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1407 GGCCCAGCTCCC 1396
```

UF06_MOUSE P38644;

```
Liljeqvist J.-A., Svennerholm B., Bergstrom T.;
Submitted (APR-1999) to the SWISS-PROT data bank
-!- MISCELLANDOUS: HENER ARE SEEVEN EXTERNAL GLYCOPROTEINS IN HSV1 AND
-:- GH, GB, GC, GG, GD, GI, AND GE.
-!- MISCELLANEOUS: GLYCOPROTEIN G IS MUCH LARGER IN HSV-2 THAN IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "plasma protein map: an update by microsequencing.";
Electrophoresis 13:707-714(1992).
-!- MISCELLANDOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
PROTEIN IS: 7, ITS MIS: 12 kDa.
SWISS-2DPAGE; P:30096; HUMAN.
                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                    01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
16-CT-2001 (Rel. 40, Last annotation update)
Unknown protein from 2D-page of plasma (Spot 36) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-93092937; PubMed-1459097;
Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquall C.,
Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
Hochstrasser D.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glycoprotein G (Fragment).
Herpes simplex virus (type 2 / strain B4327UR).
Viruses; abbNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Simplexvirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86677B59D1A72042 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F -> P.
/FIId-VAR_000004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 AA.
                                                                                                                                                                                     8
A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-824-647-16 (1-2095) x UPAA_HUMAN (1-8)
Gaps:
                                 US-09-824-647-16 (1-2095) x UF06_MOUSE (1-8)
                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.04e+07
4.00
100.00%
100.00%
0.58%
                                                                      1036 ceregreeecc 1025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            909 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       936 TTTTACCCAGGC 947
                                                                                                                                                                                 UPAA_HUMAN , STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 PheTyrProGly 8
                                                                                         4 ProGlyGlyAla 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID-103921;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 AA;
                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VGLG_HSV2B
P81780;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VGLG_HSV2B
                                                                                                                                                               UPAA_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-9500907; PubMed-7523108; Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.; Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.; Separation and sequencing of familiar and novel murine proteins using preparative two-dimensional gel electrophoresis. "; Electrophoresis 15:735-745(1994).
-!- MISCELLANDOUS: ON THE 2D-CEL THE DETERMINED PI'OF THIS UNKNOWN NOW_TER 15:2, ITS MW IS: 50 kba.
                                                                                                                                                                                                                                                                                                                                   MEDLINE-95009907; PubMed-7523108;
Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
"Separation and sequencing of familiar and novel murine proteins using preparative two-dimensional gel electrophoresis.";
Electrophoresis 15:35-745(1994).
-I. MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
PROTEIN IS: 5.2, ITS MW IS: 50 kDa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_raxID=10090;
                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-0CT-1994 (Rel. 30, Created)
01-0CT-1994 (Rel. 30, Last sequence update)
01-FEB-1995 (Rel. 31, Last annotation update)
Unknown protein from 2D-page of fibroblasts (P50) (Fragment).
Mus musculus (Mouse).
                                                                                                                          01-0CT-1994 (Rel. 30, Created)
01-0CT-1994 (Rel. 30, Last sequence update)
01-FEB-1995 (Rel. 31, Last annotation update)
Unknown protein from 2D-page of fibroblasts (P50) (Fragment).
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 AA; 817 MW; A35DD878676B05B1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              817 MW; A35DD878676B05B1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-824-647-16 (1-2095) x UF06_MOUSE (1-8)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.04e+07
4.00
100.00%
100.00%
0.58%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.04e+07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.00%
100.00%
0.58%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 112 CCCGGAGGAGCC 123
                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 ProGlyGlyAla 7
GlyProAlaPro 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FISSUE-Fibroblast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score:
Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                 TISSUE-Fibroblast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 AA;
                                                                                                                                                                                                                                                           NCBI_TaxID-10090;
```

Alignment Scores:

Pred.

SEQUENCE

SEQUENCE

UF06_MOUSE

RESULT 22

P38644;

Alignment Scores:

Pred. No.:

Query Match;

SEQUENCE

SEQUENCE

Pred. No.:

AL11_CARMA

RESULT 25

g

ð

```
Lunaiyota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Crustacea; Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea; Nephropoidea; Nephropidae; Nephrops.
MEDLINE-88058932; PubMed-3680228;
Cruz L.J., de Santos V., Zafaralla G.C., Ramilo C.A., Zeikus R.D.,
Gray W.R., Olivera B.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Favrel P., Kegel G., Sedlmeier D., Keller R., van Wormhoudt A.; "Structure and biological activity of crustacean gastrointestinal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              peptides identified with antibodies to gastrin/cholecystokinin.";
                                                       "Invertebrate vasopressin/oxytocin homologs. Characterization of peptides from Conus geographus and Conus straitus venoms."; J. Biol. Chem. 262:15821-15824(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY. PIR; A48398; A48398.
                                                                                                                                              Biochimie 73:1233-1239(1991).
-1- FUNCTION: MAY CONTROL DIGESTION PROCESSES IN CRUSTACEANS
                                                                                                                                                                                                                                                                                                                                                                                                                    9 AMIDATION.
1031 MW; 17EB176EB4540050 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 AA; 1038 MW; 60EC79CAB6D8787B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
01-MAR-1992 (Rel. 21, Last annotation update)
03-MAR-1992 (Rel. 21, Last annotation update)
03-MAR-1992 (Rel. 21, Last annotation update)
Nephrops norvegicus (Norway lobster)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels:
                                                                                                                                                                                                                                                                                                                                             Pfam; PF00220; hormone4; 1.
PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-824-647-16 (1-2095) x CONO_CONST (1-9)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                          nterPro; IPR000981; Neurhyp_horm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE~Stomach;
MEDLINE-92082847; PubMed-1747388;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9.22e+06
4.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9.22e+06
4.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.00%
100.00%
0.58%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.00%
100.00%
0.58%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       307 TGCCCACGGGGC 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 CysProArgGly 9
                                                                                                                                                                                                                                                                                                                                                                                     Hormone; Amidation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                          9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      D1_NEPNO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hormone
                                                                                                                                                                                                                                                                                                                                                                                                                          MOD_RES
                                                                                                                                      REVIEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        D1_NEPNO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Carcinus maenas (Common shore crab) (Green crab).
Bukaryota, Metazoa, Arthropoda, Mandibulata; Pancrustacea; Crustacea;
Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata;
Brachyura; Eubrachyura; Portunoidea; Portunidae; Carcinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IISSUE=Cerebral ganglion, and Thoracic ganglion;
MEDLINE=98121193; PubMed=9461295;
Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conus striatus (Striated cone).
Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
NCBI_TaxID=6493;
                   683 MW; 7847686772C865B8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 AA; 927 MW; 832D79CDCB46D861 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches:
Conservative:
Mismatches:
                                                                           Length:
Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                 30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                    Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1988 (Rel. 09, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 AA.
                                                                                                                                                        Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels:
                                                                                                                                                                                                           US-09-824-647-16 (1-2095) x VGLG_HSV2B (1-8)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-824-647-16 (1-2095) x AL11_CARMA (1-9)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AMIDATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9.22e+06
4.00
100.00%
100.00%
0.58%
                                                                           1.04e+07
4.00
100.00%
100.00%
                                                                                                                                                                                                                                                  1834 AGTGGGGTCCCG 1823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1545 GCTACGGGCCAG 1534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       · STANDARD;
                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 SerGlyValPro 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arg-conopressin S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity:
Query Match:
 8 AA;
                                                                                                                                    Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Carcinustatin 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=6759;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
                                                                                                                Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
                                                           Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CONO_CONST
P05487;
                                                                                                                                                                                                                                                                                                                                                                 AL11_CARMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
 NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                    Query Match:
                                                                                                                                                                                                                                                                                                                                                                               P81814;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOD RES
```

Pred. No.:

Score:

CONO_CONST

RESULT 26

ò

```
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 AA;
                                                                                                                                                 Percent Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 31
OXYF_SCYCA
ID OXYF_SCYCA
                                                                                                             Alignment Scores:
                                                                                                                                                                                                                                                                                                                  OXYA_SCYCA
P42996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                  Asvatocin.
                                                  FAMILY
                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match:
                                                                                                                          ..
Q
                                                                                                                                                                                                                                                                                                        OXYA_SCYCA
                                                                                                                                                                                                                                                                                         RESULT 30
                                                                                                                          Pred.
TISSUB-Suboesophageal ganglion, and Thoracic ganglion;
MEDLINE-88077077; PubMed-3689410;
Proux J.P., Miller C.A., Li J.P., Carney R.L., Girardie A.,
Delaage M., Schooley D.A.;
Identification of an arginine vasopressin-like diuretic hormone from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ascaris suum (Pig roundworm) (Ascaris lumbricoides).
Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;
Ascarididae; Ascaris.
                                                                                                                                                                                                   Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caelifera;
Acridomorpha; Acridoidea; Acrididae; Oedipodinae; Locusta.
                                                                                                                                                                                                                                                                                                                                                                                  1- SUBUNIT: F2 IS AN ANTIPARALLEL DISULFIDE LINKED DIMER OF F1.
1- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INTERCHAIN (WITH C-6') (IN F2). INTERCHAIN (WITH C-1') (IN F2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AMIDATION.
56EB176EB451A057 CRC64;
                                                                                                                                                                                                                                                                                                                                                           Biochem. Biophys. Res. Commun. 149:180-186(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
                                                                                                                                      01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
10-DEC-1998 (Rel. 37, Last annotation update)
Locupressin (Diuretic neuropeptide F1/F2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 A
                                                                                                              9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (1-9)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps:
             US-09-824-647-16 (1-2095) x D1_NEPNO (1-9)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neuropeptide; Amidation.
                                                                                                                                                                                           locust)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                         nterPro; IPR000981; Neurhyp_horm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-824-647-16 (1-2095) x DNF1_LOCMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-95380362; PubMed-7651904;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FMRFamide-like neuropeptide AF9
                                                                                                                                                                                           Locusta migratoria (Migratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cowden C., Stretton A.O.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9.22e+06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.00%
100.00%
0.58%
                                      1955 TCAGAAGGGGGT 1966
                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00220; hormone4; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGCCCACGGGC 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                   SerGluGlyGly 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          916
                                                                                                                                                                                                                                                                                                                                                                                                           PIR; A29477; A2947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=6253;
                                                                                                                                                                                                                                            NCBI_TaxID=7004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
                                                                                                              DNF1_LOCMI P16339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FAR9_ASCSU
P43172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FAR9_ASCSU
                                                                                        RESULT 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                              셤
```

```
"Eight novel FMRPamide-like neuropeptides isolated from the nematode Ascaris suum ";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Scyliorhinus canicula (Spotted dogfish) (Spotted catshark).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;
Scyliorhinidae; Scyliorhinus.
NCBI_TaxID=7830;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Pituitary;
MEDLINE-95062247; PubMed=7972045;
MEDLINE-95062247; PubMed=7972045;
MEDLINE-95062247; PubMed=7972045;
"Special evolution of neurohypophysial hormones in cartilaginous fishes: asvatocin and phasvatocin, two oxytocin-like peptides fishes: asvatocin and phasvatocin, two oxytocin-like peptides fishes: asvatocin and phasvatocin, two oxytocin-like peptides proc. Natl. Acad. Sci. U.S.A. 91:11266-11270(1994).
-1- FUNCTION: DISPLAKS OXYTOCIC ACTIVITY ON RAT UTENUS.
-1- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
                                                                  THE FARP (FMRFAMIDE RELATED PEPTIDE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          040000
                                                                                                                               AMIDATION.
524F073774176877 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AMIDATION.
17EDD76EB444404B CRC64;
                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00220; hormone4; 1.
PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-824-647-16 (1-2095) x OXYA_SCYCA (1-9)
                                                                                                                                                                                                                                                                                                                             Gaps:
                                                                                                                                                                                                                                                                                                                                                                  US-09-824-647-16 (1-2095) x FAR9_ASCSU (1-9)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Interpro; IPR000981; Neurhyp_horm.
Interpro; IPR001230; Prenyl_site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9.22e+06
4.00
100.00%
100.00%
0.58%
                                                                                                                                                                                                               9.22e+06
4.00
100.00%
100.00%
0.58%
                                            Peptides 16:491-500(1995).
                                                                                                                                                   9 AA; 1012 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           982 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    683 TGCCCAGTGGGA 694
                                                                                                                                                                                                                                                                                                                                                                                                              283 CCACGGCCTCTG 272
                                                                                                         Neuropeptide; Amidation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 CysProValGly
                                                                                                                                                                                                                                                                                                                                                                                                                                       Hormone; Amidation.
```

Endocrinol. 70:152-157(1988).

```
-1. SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY. PIR; B61364; B61364. B61365. S06375; S06375.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-824-647-16 (1-2095) x OXYV_SQUAC (1-9)
           1. FUNCTION: ANTIDIURETIC HORMONE
                                                              InterPro;
                                                                                                                                                                             :.
9
                                                                                                                                                                                                                Best Local
                                                                                                                                                                                                                                                                                                                                              RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score:
                                                                                                                                                                                                                                                                                                                                                                                             අ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPECIES-C.carpio; TISSUE-Pituitary;
Acher R., Chauvet J., Chauvet M.-T., Crepy D.;
"Characterization of neurohypophyseal hormones, from a fresh water bony
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Petromyzon marinus (Sea lamprey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the carp (Cyprinus carpio). Comparison with hormones from sea
bony fishs.";
                                                          Scyliorhinus canicula (Spotted dogfish) (Spotted catshark).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;
Scyliorhinidae; Scyllorhinus.
                                                                                                                                                                      Chauvet J., Roulle Y., Chauveau C., Chauvet M.-T., Acher R.,
"Special evolution of neurohypophysial hormones in cartilaginous
fishes: asvatocin and phasvatocin, two oxytoch-like peptides
isolated from the spotted dogfish (Scyliorhiuus caniculus).";
Proc. Natl. Acad. Sci. U.S.A. 91:11266-11270(1994).
-! FOWATION: DISPLAYS OXYTOCIC ACTIVITY ON RAT UTERUS.
-! SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY:
InterPro: IPRO00981; Neurhyp_horm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-88225976; PubMed-3371648; Lane T.E., Sower S.A., Kawauchi H.; Lane T.E., Sower S.A., Kawauchi H.; Lane T.E., Sower S.A. Languen the pitnitary gland of the lamprey (Petromyzon marinus): isolation and amino acid sequence.";
                                                                                                                                                                                                                                                                                                                                                        17EDD76EB44449DB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
         01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Comp. Biochem. Physiol. 14:245-254(1965)
                                                                                                                                                                                                                                                                                        Pfam; PF00220; hormone4; I. PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-824-647-16 (1-2095) x OXYF_SCYCA (1-9)
                                                                                                                                                                                                                                                                                                                                             AMIDATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .marinus; TISSUE-Pituitary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                 TISSUE-Pitultary;
MEDLINE-95062247; PubMed-7972045;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cyprinus carpio (Common carp),
                                                                                                                                                                                                                                                                                                                                                                                             .22e+06
.00
                                                                                                                                                                                                                                                                                                                                                                                                                   100.00%
100.00%
0.58%
                                                                                                                                                                                                                                                                                                                                                       1016 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              683 TGCCCAGTGGGA 694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 CysProValGly 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cyprinidae; Cyprinus.
NCBI_TaxID=7962, 7757;
                                                                                                                                                                                                                                                                                                                  Hormone; Amidation.
                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                          9 AA;
                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 32
OXYT_CYPCA
ID OXYT_CYPCA
AC P23879;
                                                  Phasvatocin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPECIES-P.
                                                                                                                                                                                                                                                                                                                                             MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                               Мо.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       water
                                                                                                                                                                                                                                                                                                                                                                                                            Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      õ
```

```
MEDLINE-73031727; PubMed-5083097; Acher R., Chauvet J., Chauvet M.-T.; "Phylogeny of the neurohypophysial hormones. Two new active peptides lsolated from a cartilaginous fish, Squalus acanthias.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE.
MEDLINE-72128038; PubMed-4622083;
Acher R., Chauvet J., Chauvet M.-T., Fontaine M.;
"Identification of 2 new neurohypophyseal hormones, valitocin (Val8-"Identification of 2 new neurohypophyseal hormon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Squalus acanthias (Spiny dogfish).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
Elasmobranchii; Squalea; Squaloidei; Squalidae; Squalus.
NCBI_TaxID=7797;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           oxytocin) and aspartocin (Asn4-oxytocin) in a selachian fish, spiny dog-fish (Squalus acanthias).";
C. R. Acad. Sci., D, Sci. Nat. 274:313-316(1972).
-1- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY. InterPro; IPR000981; Neurhyp.horm.
                                                     State.
                                                                                                                                                                                         9 AMIDATION.
1053 MW; 17EB176EB456D04B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9. AMIDATION. MW; 17EDD76EB456D04B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                           Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
11-NOV-1995 (Rel. 32, Last annotation update)
Valitocin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
                                                                                                                                                                                                                                                                                                                                                      Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
                                Pfam; PF00220; hormone4; 1.
PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-824-647-16 (1-2095) x OXYT_CYPCA (1-9)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
IPR000981; Neurhyp_horm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               isolated from a cartilaginous fil
Eur. J. Biochem. 29:12-19(1972).
                                                                                                                                                                                                                                                                                                                                                 9.22e+06
4.00
100.00%
100.00%
0.58%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9.22e+06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                307 TGCCCACGGGC 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00220; hormone4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 CysProArgGly 9
                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hormone; Amidation.
DISULFID 1
                                                                                                                   Hormone; Amidation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity:
                                                                                                                                                                                                                              9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similari
                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
                                                                                                                                                                                                                                                                                                                 Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OXYV_SQUAC
P43000;
                                                                                                                                                DISULFID
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOD RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match:
```

```
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity
                                                           PIR; B41983;
Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
                                                                                                                              Aliqument Scores
                                                                                                                                                                                                                                                                                                                                            BPP8_BOTIN
P30426;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BRK_ONCMY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        m
                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match:
                                                                                          NON_TER
                                                                                                                                                                                              Query Match:
                                                                                                                                              Pred. No.:
                                                                                                                                                                                                                                                                                                                                 BPP8_BOTIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ..
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BRK_ONCMY
ID BRK_O
                                                                                                                                                                                                                                                                                                                  RESULT 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 37
                                                                                                                                                           Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                        Stomopneutes variolaris (Sea urchin).
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Diadematacea; Phymosomatoida; Stomechinidae;
                                                                                                                                                                                                                                                                                                        disulfide linkage-containing sperm-activating peptide by tandem mass
                                                                                                                                                                                                                                                                                                                   spectrometry.";
FEBS Lett. 294:179-182(1991).
-!- FUNCTION: CAUSE STIMULATION OF SPERM RESPIRATION AND MOTILITY
THROUGH INTRACELLULAR ALLNIZATION, TRANSIENT ELEVATIONS OF
CAMP, CGMP AND CLACIUM LEYELS IN SPERM CELLS, AND TRANSIENT
ACTIVATION AND SUBSEQUENT INACTIVATION OF THE MEMBRANE FORM OF
                                                                                                                                                                                                                                                    TISSUE-Egg jelly;
MEDLINE-92097763; PubMed=1756858;
Yoshimo K.-I., Tavor T., Shimonishi Y., Suzuki N.;
"Determination of the amino acid sequence of an intramolecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Grossman M.J., Hinton S.M., Minak-Bernero V., Slaughter
                                                                                                                                                                                                                                                                                                                                                                                                                          3 8
9 AA; 1010 MW; C469B3387B076EB9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Stiefel E.I.; "Unification of the ferritin family of proteins."; Proc. Natl. Acad. Sci. U.S.A. 89:2419-2423(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              040000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein in BFR 3'region (Fragment).
Azotobacter vinelandii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                    01-WAR-1992 (Rel. 21, Created)
01-WAR-1992 (Rel. 21, Last sequence update)
01-WAR-1992 (Rel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 AA.
                                                                            9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-824-647-16 (1-2095) x SAP_STOVA (1-9)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-92196129; PubMed-1549605;
                                                                                                                                              Sperm-activating peptide (SAP)
                                                                                                                                                                                                                                       SEQUENCE, AND DISULFIDE BOND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9.22e+06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4.00
100.00%
100.00%
0.58%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                154 TGTCCAGAAGGG 143
683 TGCCCAGTGGGA 694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CysProGluGly 6
                                                                            STANDARD;
                       6
                                                                                                                                                                                                                                                                                                                                                                                                 GUANYLATE CYCLASE.
S19329; S19329.
             6 CysProValGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity:
                                                                                                                                                                                                             NCBI_TaxID-7663;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=354;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
                                                                                                                                                                                                 Stomopneustes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Azotobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YBFR_AZOVI P25825;
                                                                           SAP_STOVA P24047;
                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local
                                                                                                                                                                                                                                                                                                                                                                                                               PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 35
                                                  RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ð
```

```
modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cintra A.C.O., Vieira C.A., Giglio J.R.;

Cintra A.C.O., Vieira C.A., Giglio J.R.;

"Primary structure and biological activity of bradykinin potentiating heptides from Bothrops insularis snake venom.";

J. Protein Chem. 9:21-227 (1990).

-1- FUNCTION: THIS PEPTIDE BOTH INHIBITS THE ACTIVITY OF THE ANGOTERNIA-CONVERTING FURNEME AND ENHANCES THE ACTION OF BRADXKININ BY INHIBITING THE KINASES THAT INACTIVATE IT.

IT ACTS AS AN INDIRECT HYPOTENSIVE AGENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Queimada jararaca).
Lepidosauria; Squamata; Chordata; Craniata; Vertebrata; Euteleostomi;
Viperidae; Crotalinae; Bothrops.
1111-TaxID-8723;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
Bradykinin-potentiating peptide 55,1 (Angiotensin-converting
enzyme inhibitor)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PYRROLIDONE CARBOXYLIC ACID. 2FF835545761F6D8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0000
                                                                                                                                                                                        DF98B5A1B417776D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
Conservative:
                                                                                                                                                                                                                                                                                            Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 AA.
                                                                                                                                                                                                                                                       Length:
Matches:
institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JS-09-824-647-16 (1-2095) x BPP8_BOTIN (1-10)
                                                                                                                                                                                                                                                                                                                                                                                                       US-09-824-647-16 (1-2095) x YBFR_AZOVI (1-9)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Venom;
MEDLINE=90351557; PubMed=2386615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-APR-1993 (Rel. 25, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.45e+05
4.00
                                                                                                                                                                                                                                                       9.22e+06
4.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 AA; 1173 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.00%
100.00%
0.58%
                                                                                                                                                                                                                                                                                            100.00%
100.00%
0.58%
                                                                                                                                                                                        AA; 947 MW;
                                                                                                      EMBL; M83692; AAA22122.1;
PIR; B41983; B41983.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypotensive agent; Venom.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGGCAGCACCCC 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                812 CCACGGACCTCC 823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 ProArgThrSer 7
                                                                                                                                                 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; H37196; H37196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity:
                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
```

10 AA.

PRT;

```
-!- TISSUE SPECIFICITY: GNRH NEDRONS LIE WITHIN BLOOD SINUSES CLOSE TO THE GONODCTS AND GONADS IN BOTH JUVENILES AND ADULTS, IMPLYING THAT THE NERROPPETIDE IS RELEASED INTO THE BLOODSTREAM.
-!- MASS SPECTROMETRY: MW-117.52; METHOD-MALDI.
                                                                                                                                                                                                                                                                                                           MEDLINE-96413669; PubMed-8816823;
Powell J.F.F., Reska-Skinner S.M., Prakash M.O., Fischer W.H.,
Powell J.F.F., Reska-Skinner S.M., Prakash M.O., Fischer W.H.,
F., Reska-Skinner S.M., Mackie G.O., Sherwood N.M.;
"Two new forms of gonadotropin-releasing hormone in a protochordate
                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phiebobranchia; Corellidae; Chelyosoma.
NCBL_TaxID=71177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rana ridibunda (Laughing frog) (Marsh frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
NCBI_TaxID=8406;
                                                                                                                                                                                                                                                                                                                                                                            and the evolutionary implications.";
Proc. Natl. Acad. Sci. U.S.A. 93:10461-10464(1996).
-1- FUNICION: STRUILATES THE SECRETION OF BOTH LUTEINIZING AND
FOLLICLE-STIMULATING HORMONES.
                                                                                                                         01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Gonadoliberin II (Gonadotropin-releasing hormone II) (GnRH-II)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PYRROLIDONE CARBOXYLIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AMIDATION (BY SIMILARITY).
284B38D1EEB735A3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 AA.
                                                                                            10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBUNIT: HOMODIMER; DISULFIDE-LINKED. SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INTERCHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-824-647-16 (1-2095) x GON2_CHEPR (1-10)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Brain;
MEDLINE-91315477; PubMed-1859413;
Conlon J.M., O'Harte F., Vaudry H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.45e+05
4.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1135 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.00%
100.00%
0.58%
1416 CTGGCAGCAGGC 1405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR002012; GnRH. PROSITE; PS00473; GNRH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                465 CATGCCCCAGGC 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 HisAlaProGly 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                              STANDARD;
                 1 LeuAlaAlaGly
                                                                                                                                                                                               (Luliberin: II).
Chelyosoma productum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hormone; Amidation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neuromedin C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
                                                                                              GON2 CHEPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GRP_RANRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YOD_RES
                                                                                                             P80678;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No.:
                                                                                GON2_CHEPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GRP_RANRI
                                                               RESULT 39
                                                                                               ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID-9606;
                           16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
Lisyl-bradykinin-like.
Lysyl-bradykinin-like.
Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Protacanthopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
NCBI_TaxiD-8022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MISSING (IN 2ND COMPONENT).
/FTId=VAR_005255.
CFEECGAB02C3387D CRC64;
                                                                                                                                                                                                                                                                                                                                                                              10 AA; 1193 MW; 33C59075A3786777 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                               40000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-JUL-1986 (Rel. 01, Last sequence update) 01-FEB-1991 (Rel. 17, Last annotation update) 62stric julce peptide. Homo saplens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Heathcote J.G., Washington R.J.;
"Peptides of normal human gastric juice.";
Int. J. Protein Res. 2:117-126(1970).
PIR, A01628; GXHUI.
PIR, 137220; -...
I MINSING (IN 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-824-647-16 (1-2095) x GAJU_HUMAN (1-10)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-824-647-16 (1-2095) x BRK_ONCMY (1-10)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-75150968; PubMed-5538385;
                                                                                                                                                                                              MEDLINE-94039817; PubMed-8224232;
                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JUL-1986 (Rel. 01, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                5.45e+05
4.00
100.00%
100.00%
0.58%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1004 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5.45e+05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.00
100.00%
100.00%
0.58%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1372 CGCCCACCGGC 1361
                                                                                                                                                                                                                                                                                                                                                               Bradykinin; Vasodilator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 ArgProProGly 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAJU_HUMAN
P01358;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                              SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
```

Query Match:

.. Q

GAJU_HUMAN

RESULT 38

ð 셤

```
Alignment Scores:
Pred. No.:
                                                                                                                a
                                                                                                                                                                ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           용
                                                                                                                                                                                                                                                                                             01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
115-JUN-2002 (Rel. 41, Last annotation update)
Dihydrollpoamide acetyltransferase component of pyruvate dehydrogenase complex (EC 2.3.1.12) (E2) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                "Primary structures of the bombesin-like neuropeptides in frog brain show that bombesin is not the amphibian gastrin-releasing peptide."; Biochem. Biochem. Biochem. 178:526-530(1991).
-: SUBCELLULAR LOCATION: Secreted.
-: SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBUNIT: FORMS A 24-POLYPEPTIDE STRUCTURAL CORE WITH OCTAHEDRAL
                                                                                                                                                                                                                                                                                                                                                                  Bos taurus (Bovine).
Sukaryota Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glycolysis; Transferase; Acyltransferase; Repeat; Mitochondrion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BELONGS TO THE 2-OXOACID DEHYDROGENASE FAMILY CONTAINS 2 LIPOYL-BINDING DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       889BECD1ADD33AB1 CRC64;
                                                                                                       AMIDATION. F81FBAE862CDC371 CRC64;
                                                                                                                                             0.000
                                                                                                                                            Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: Mitochondrial matrix.
                                                                                                                                                                                                                                                                                          10 AA.
                                                                                                                                                                                   Indels:
                                                                                                                                                                                           Gaps:
                                                                                                                                                                                                              US-09-824-647-16 (1-2095) x GRP_RANRI (1-10)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LIPOYL.
                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR003016; Lipoyl.
PROSITE; PS00189; LIPOYL; PARTIAL.
                                                      PIR; PQ0177; PQ0177.
InterPro; IPR000874; Bombesin.
Pfam; PF02044; Bombesin; 1.
PROSITE; PS00257; BOMBESIN; 1.
Bombesin family; Amidation.
                                                                                                                                            5.45e+05
4.00
100.00%
100.00%
0.58%
                                                                                                                SEQUENCE 10 AA; 1094 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1066 MW;
                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                              Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   I - SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY:
                                                                                                                                   Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SYMMETRY
                                                                                                                                                                                                                                                                                         ODP2_BOVIN
P11180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BINDING
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NON TER
                                                                                                      MOD RES
                                                                                                                                                                                 Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lipoy]
                                                                                                                                              ٠:
چ
                                                                                                                                                                                                                                                                               ODP2_BOVIN
                                                                                                                                                                                                                                                                       RESULT 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <u>:</u>
                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                  ð
```

```
TISSUE-Lung;
MEDLINE-91110910; PubMed-2274681;
Batta V.K., Mathur M., Mir S.A., Kapoor R., Kumar M.A.;
Batta V.K., Mathur M., Mir S.A., Kapoor R., Kumar M.A.;
Pneumadin: a new lung peptide which triggers antidiuresis.";
Regul. Pept. 30:77-87(1990).
-!- FUNCTION: AWTIDIURETIC PEPTIDE THAT TRIGGERS THE RELEASE OF ADH.
PIR; B33143; B33143.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Batra V.K., Mathur M., Mir S.A., Kapoor R., Kumar M.A.;
"Ineumadin: a new lung peptide which triggers antidiuresis.";
Regul. Pept. 30;77-87(1990).
-i- FUNCTION: THIS ANTIDIURETIC PEPTIDE TRIGGERS THE RELEASE OF ADH.
                                                                                                                                                                                                                                                                                                                                Homo sapiens (Humah).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                         . Sé.,
0000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOD_RES 10 10 AMIDATION.
SEQUENCE 10 AA; 956 MW; 6403780AA723276B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
Conservative:
Mismatches:
                                Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                            01-AUG-1991 (Rel. 19, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-AUG-1991 (Rel. 19, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 AA.
                                                                                                                                                                                                                                             10 AA
                  Matches:
 Length:
                                                                Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels:
                                                                                                               US-09-824-647-16 (1-2095) x ODP2_BOVIN (1-10)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-824-647-16 (1-2095) x PNEU_HUMAN (1-10)
                                                                               Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps:
                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-91110910; PubMed-2274681;
                                                                                                                                                                                                                                                                             01-AUG-1991 (Rel. 19, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-AUG-1991 (Rel: 19, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.45e+05
4.00
100.00%
100.00%
0.58%
5.45e+05
               4.00
100.00%
100.00%
0.58%
                                                                                                                                            GAGAAGGCCACT 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      234 GATGCAGGAGTG 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE, AND SYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 AspAlaGlyVal 10
                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pneumadin (PNM).
Rattus norvegicus (Rat).
                                                                                                                                                             4 Asplysalathr 7
                              Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                          Pneumadin (PNM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
                                                                                                                                                                                                                                       PNEU_HUMAN
P22103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Amidation.
MOD_RES
                                                                                                                                              620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PNEU_RAT P21996;
                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match:
                                                                                                                                                                                                                             PNEU_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 43
                                                                                                                                                                                                              RESULT 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PNEU_RAT
```

ð g

```
AshGlnIleLeu 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . .
                                                                  FEMK_RANTE
                                                                                                                                   remporin K,
                                                                                                                                                                                                                                                                                                                                                                                     FAMILY
                                                                                                                                                                                                                    SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                              MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred.
                                                                               à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration observeen the Swiss Institute of Bioinformatics and the EMEND utstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Д
                                                                                                                                                                                                                                                                                                                              01-JUN-1994 (Rel. 29, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
RNA polymerase beta subunit (EC 2.7.7.48) (Large structural protein)
(L protein) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION IN MRNA SYNTHESIS, CAPPING, METHYLATION AND POLY(A) SYNTHESIS OF WEAL SYNTHESIS. RNA EDITING OF THE GENE TRANSCRIPT, APROTEIN KINASE ACTIVITY.

-I- CATALYTIC ACTIVITY: N nucleoside triphosphate - N diphosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=Ulster/88;
BEDLINE-29268877;
Curran M.D., O'Loan D., Kennedy S., Rima B.K.;
"Molecular characterization of phocine distemper virus: gene order and sequence of the gene encoding the attachment (H) protein.";
J. Gen. Virol. 73:1189-1194(1992).
-I- FUNCTION: PROBABLE COMPONENT OF THE ACTIVE POLYMERASE. IT MAY
                                                                                                                                                                                                                                                                                                                                                                                               Phocine distemper virus (PDV).
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Paramyxovirinae; Morbillivirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                {RNA}(N).
-1- SIMILARITY: WITH L PROTEIN OF OTHER PARAMYXOVIRUSES.
                          AMIDATION.
641D00DAA723276B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE 10 AA; 1105 MW; 9C2B7FD452D5A2D5 CRC64;
                                                                                             40000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
                                                                            Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                      10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [ndels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; D10371; BAA01208.1; -.
Transferase; RNA-directed RNA polymerase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-824-647-16 (1-2095) x RRPL_PHODV (1-10)
                                                                                                                                                                           US-09-824-647-16 (1-2095) x PNEU_RAT (1-10)
                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                     RRPL_PHODV STANDARD; F P35946; 01-JUN-1994 (Rel. 29, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.45e+05
4.00
100.00%
100.00%
0.58%
                                                                             5.45e+05
4.00
100.00%
100.00%
0.58%
                            10
1048 MW;
                                                                                                                                                                                                      234 GATGCAGGAGTG 223
                                                                                                                                                                                                                  7 AspAlaGlyVal 10
PIR; A33143; A33143.
Amidation.
                          10
10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                        Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                        ICBI_TaxID=11240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
                                                                                                          Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
                                                                  Alignment Scores:
                                       SEQUENCE
                            MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NON TER
                                                                                                                                   Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :.
9
                                                                                  :.
9
                                                                                                                                                                                                                                                                         RRPL_PHODV
                                                                                                                                                                                                                                                           RESULT 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score:
                                                                                             Score:
                                                                                                                                                                                                                                                                                      SFS
```

1877 AACCAAATTCTC 1888

ò

```
-i- SUBCELLULAR LOCATION: Secreted.
-i- SIMILARITY: BELONGS TO THE BREVININ/ESCULENTIN/GAEGURIN/RUGOSIN
                                                                                                                                                                                                                                                                                          "Temporins, antimicrobial peptides from the European red frog Rana temporaria.";
                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana
                                                                                                                                                                                                                                                                                                                                                Eur. J. Biochem. 242:788-792(1996).
                                                                                                                                                                                                                                                                    Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,
                                    di.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Amphibian skin; Antibiotic; Amidation; Multigene family. MOD RES 10 10 AMIDATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AMIDATION.
390549B337272457 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches:
Conservative:
Mismatches:
Indels:
                    P56923;
30-MR-2000 (Rel. 39, Created)
16-CCT-2001 (Rel. 40, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
  10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-824-647-16 (1-2095) x TEMK_RANTE (1-10)
                                                                                                                Rana temporaria (European common frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7, 2003, 16:08:30
  PRT;
                                                                                                                                                                                                                                   TISSUE-Skin;
MEDLINE-97175050; PubMed-9022710;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE 10 AA; 1123 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4.00
100.00%
100.00%
0.58%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5.45e+05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           702 CTGCTGCCCAAT 713
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Search completed: July
Job time: 33.5 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
                                                                                                                                                                         CBI_TaxID-8407;
                                                                                                                                                                                                                                                                                                                                                                                           BACTERIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
```

```
060014 homo sapten
091938 homo sapten
015997 homo sapten
065901 leavenworth
054226 saccharopol
013695 homo sapten
013695 homo sapten
090c37 homo sapten
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           zea mays (m
lupinus lut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bovine herp
bovine herp
                                                                                                                                                                                                                                                                                                                                                                         hepatitis g
hepatitis g
mus musculu
bombina var
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9elu2 hepatitis b
Q9elu1 hepatitis b
Q9elu0 hepatitis b
Q9elt9 hepatitis b
Q9elt8 hepatitis b
Q52840 rhizoblum l
                                                                                                                                                                                                                                                                                                                 glycine max
                                                                                                                                                                                                                                                                                                                                               mns mnscnjo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hepatitis
hepatitis
hepatitis
hepatitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hepatitis
hepatitis
hepatitis
hepatitis
                                                                                                                           rattus sp.
bradypodion
                                                                                                                                                                                                                                                                                    calumma nas
                                                                                                                                                                                         calumma boe
                                                                                                                                                                                                                      calumma fur
                                                             bos taurus
bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hepatitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hepatitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , Nikiforov V.G.;
Tn5041 in environmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q93x21
Q93wf2
Q69232
Q69232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09elu5
09elu4
.09elu3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2002 (TrEMBLrel, 21, Last sequence update)
01-JUN-2002 (TrEMBLrel, 21, Last annotation update)
Porin-like protein (Fragment).
Pseudomonas fluorescens.
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                    09tru6 b
09t2p3 r
08shp0 b
08shh2 c
08sh13 c
08sh10 c
                                                                                                                                                                                                                                                                                                           098905
070580
090346
090347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9e1v3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9e1v0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9e1u6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09e1v4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09e1v2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         091xp1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases. EMBL, AJ422128; CAD19527.1; -. EMBL; AJ422129; CAD19528.1; -. EMBL; AJ422130; CAD19529.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 AA; 1206 MW; 23C47E7401F5A417 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-NC16-2, TC29-5, AND TC97;
TRANSPOSON-TN5041A1, TN5041B1, AND TN5041B1;
Kholodii G.Y., Gorlenko Z.M., Mindlin S.Z.,
"Distribution of distinct microvariants of bacteria.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2002 (TrEMBLrel. 21, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9E1T9
Q9E1T8
Q52840
008979
P83056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q69232
Q91XP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9E1U1
Q9E1U0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9B249
Q13695
Q9UC37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              093X21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           093WF2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               069232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9E1V4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pseudomonas.
NCBI_TaxID=294;
                                                             00000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 1
QBRJF1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q8RJF1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q8RJF1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A PAC OCC OCT BE SELL 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -WODEL-frame+_n2p.model -DEV=xlp
-QP-QDA2_1/X02PQ_2000_1/X030924647/runat_07072003_154759_26619/app_query.fasta_1.2247
-QP-QDA2_1/X02PQ_2000_1/X030924647/runat_07072003_154759_26619/app_query.fasta_1.2247
-LOSPEXT=0 -UNITS-bits -START=1 -END=-1 -MATRIX=0.119 -TRANS=human40.cdi
-LIST=45 -DGXALIGN=200 -THR_SCOREM=QUA11ty -THR_MIN=1 -IAIGN=45 -MODE=LCCAL
-USTRT-pto -NORM=ext -HEAPSIZE=500 -MINICBN=0 -MAXIEN=15
-USER-US09824647_CGGN_1 1_231_erunat_07072003_154759_26619 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEC_SCORES=0 -WART -DSPENCK=100 -LONGIGG
-FGAPOP=60 -YGAPOP=60 -YGAPEXT=60 -DELGEN=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q8rjfl pseudomonas
                                                                                                                                                                                                                      (without alignments)
6466.947 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                               1 cgcaggcagaccatgtggac.....ataaagtttgtcactttctt 2095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Description
                                                                                                                                                                                         ; Search time 133.5 Seconds
   GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

    protein search, using frame_plus_n2p model

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fotal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                671580 seqs, 206047115 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60.0
60.0
7.0
7.0
                                                                                                                                                                                  7, 2003, 16:07:27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q8RJF1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , Ygapext 6
, Ygapext 6
, Fgapext
, Delext
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      _unclassified:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sp_invertebrate:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sp_vertebrate:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sp_rvirus:*
sp_bacteriap:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sp_organelle:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sp_bacteria:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sp_archeap:*
                                                                                                                                                                                                                                                                                                              US-09-824-647-16
694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sp_rodent:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sp_archea:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sp_mammal:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sp_plant:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sp_virus:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sp_fung1:*
sp_human:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.0 , 16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sp_phage:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPTREMBL 21:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sp_mhc:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Minimum DB seq length: 0
Maximum DB seq length: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Command line parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xgapop
Ygapop
Fgapop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6.0
                                                                                                                                                                                                                                                                                                                                                                                                                                          OLIGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Delop
                                                                                                                                                                                      July
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                              Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                             Scoring table:
                                                                                                                           nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Word size:
                                                                                                                                                                                                                                                                                                                                                                            Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Database
                                                                                                                                                                                      Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Š
```

```
J. Virol. 71:5080-5087(1997).
EMBL; Y11802; CAA72496.1; -.
                                                                                                                                                  Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alignment Scores:
                                                                                                  SEQUENCE
                                                  NON_TER
                                                                              NON_TER
                                                                                                                                                                                                                                                                      Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P82923
P82923;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P83056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P83056
                                                                                                                                                                                                     Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P82923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Howell A.M., Cool D., Hewitt J., Ydenberg B., Smith M.J., Honda B.M.;

*Organization and Unusual Expression of Histone Genes in the Sea Star Pisaster ochraceus.*;

J. MOI. Evol. 25:29-36(1987).

BEMBL: X05619; CAA29106.1;

NON_TER 11 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-NURI: TISSUE-MURINE RETROVIRUS INDUCED TUMOR;
STRAIN-NURI: TISSUE-MURINE RETROVIRUS INDUCED TUMOR;
STRAIN-NURI: DAMAG-9188573;
AMtoft H.W., Sorensen A.B., Bareil C., Schmidt J.; Luz A.,
Pedersen F.S.;
"Stability of AMLI (core) site enhancer mutations in T-lymphomas induced by attenuațed SL3-3 murine leukemia virus mutants.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pisaster ochraceus (Sea star).
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Asterozoa; Asteroidea; Forcipulatacea; Forcipulatida; Asteriidae; Pisaster.NCBI_TaxID=7612;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE 11 AA; 1128 MW; 5173974A3865BDD3 CRC64;
                                                     0000
                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Sea StAR histone H2B gene 5'region (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 AA.
                                                                                                                                                                                                                           US-09-824-647-16 (1-2095) x Q8RJF1 (1-10)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-824-647-16 (1-2095) x Q26092 (1-11)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               454 CCCAGGAGCCATCGACCA 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.18e+04
6.00
100.00%
                                             2.21e+04
6.00
100.008
100.008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUL-1997 (TrEMBLrel. 04, 01-JUL-1997 (TrEMBLrel. 04, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                  3 ProArgSerHisArgPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AML1 protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
                                                                                                Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-SPERM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
                              Alignment Scores:
                                                                                                                                                  Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        008979;
                                                                                                                                                                                                                                                                                                                                                                                                                                             026092;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               008979
                                                                                                                                                                                                                                                                                                                                                                                                                    026092
                                                  Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 3
                                                                                                                                                                                                                                                                                                                                                                       RESULT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        008979
                                                                                                                                                                                                                                                                                                                                                                                                                                             õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCOCO OS NEW REST OF THE REST
                                                                                                                                                                                                                                                                         ò
```

```
01-0CT-2001 (TrEMBLrel. 18, Created)
01-0CT-2001 (TrEMBLrel. 18, Last sequence update)
01-0CT-2001 (TrEMBLrel. 18, Last annotation update)
Bradykinin-like peptide ([Ala3,Thr6]bradykinin).
Bombina variegata (Tellow-bellied toad).
Bukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bos taurus (Bovine).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE.
TISSUE-LIVER;
Koc E.C., Burkhart W., Blackburn K., Moseley A., Spremulli L.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2001 (TrEMBLrel. 16, Created)
1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-UNN-2001 (TrEMBLrel. 17, Last annotation update)
Mitochondrial 28S ribosomal protein S2 (MRP-S2) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
                                                        00000
 981 MW; 293E01E865A776D8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
                                                    Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-824-647-16 (1-2095) x P83056 (1-9)
                                                                                                                                                                                   US-09-824-647-16 (1-2095) x 008979 (1-9)
                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              979 CCCGCGGGGTTTACG 993
                                                                                                                                                                                                                     665 CCATCAGGGCACCGG 651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.58e+07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5.00
100.00%
100.00%
0.72%
                                                        4.58e+07
                                                                         5.00 .
100.00%
100.00%
0.73%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 ProSerGlyHisArg 8
                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                        Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity:
cal Similarity:
9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=8348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9913;
```

```
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBL_TaxID=10118;
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Cytochrome P-450 27/25-HYDROXYLASE-52 kDa isoform (Fragment).
Rattus sp.
                                                                                                                   SEQUENCE.
MEDIINE-91355184: PubMed-1883820;
Addya S., Zheng Y.M., Shayiq R.M., Fan J.Y., Avadhani N.G.;
"Characterization of a female-specific hepatic mitochondrial
cytochrome:P-450 whose steady-state level is modulated by
testosteroñe.";
                                                                                                                                                                                                                                10 AA; 1092 MW; 316CEFB4072DDDC7 CRC64;
                                                                                                                                                                                            Biochemistry 30:8323-8330(1991).
                                                                                                                                                                                                                                                                                                                     Best Local Similarity: `
Query Match:
                                                                                                                                                                                                                                                                                                       Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mitochondrion.
                                                   Mitochondrion
                                                                                                                                                                                                                                                                  Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bradypodion.
                                                                                                                                                                                                              NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q8SHP0
                                                                                                                                                                                                                                                                                Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
                                                                                                                                                                                                                                                                                               Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q8SHP0
            "Small subunit of the mammalian mitochondrial ribosome. Identification of the full complement ribosomal proteins present.";
Submitted (DEC-2000) to the SWISS-PROT data bank.
-1 - SUBCELGULAR LOCATION MITOCHONDRIAL.
-1 - SIMILARITY: BELOWGS TO THE S2P FAMILY OF RIBOSOMAL PROTEINS.
InterPro; IPR001865; Ribosomal_S2.
                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
GAP-3, GTPasse-activating protein (Fragment).
Bos taurus (Bovine).
Bovines; Metacos; Chordata; Cranlata; Vertebrata; Euteleostomi; Bovinae; Bovinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The purification of a Rapl GTPase-activating protein from bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-92112868; PubMed-1309786;
Nice E.C., Fabri L., Hammacher A., Holden J., Simpson R.J.,
                                                                                                                                                                        10 AA; 1246 MW; 6A7A6679C04B476B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59370A51A72321A7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                            Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                 ·10 AA.
                                                                                PEGNI; PF00118; RIDOSOMAL_S2; PARTIAL.
PRINTS; PR00395; RIBOSOMAL_S2; PARTIAL.
PROSTIFE; PS00962; RIBOSOMAL_S2_1; PARTIAL.
RIDOSOMAL PROTOFILITY MITCHONDIALOR.
                                                                                                                                                                                                                                                                                                       US-09-824-647-16 (1-2095) x P82923 (1-10)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-824-647-16 (1-2095) x Q9TRU6 (1-10)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         brain cytosol.";
J. Biol. Chem. 267:1546-1553(1992).
NON TER 1
                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.21e+05
5.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                   358 ATCTTTGGAAGCAGG 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             820 CTCCTCACTAAGCTG 834
                                                                                                                                                                                                             2.21e+05
5.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 AA; 1149 MW;
                                                                                                                                                                                                                                                                                                                                                6 IlePheGlySerArg 10
                                                                                                                                                                                                                                   100.00%
100.00%
0.73%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                   Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MCBI_TaxID-9913;
                                                                                                                                                                                                                                      Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Surgess A.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Aliqnment Scores:
                                                                                                                                                                                                 Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NON_TER
SEQUENCE
                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. BICL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9T2P3
Q9T2P3;
                                                                                                                                                            NON_TER
                                                                                                                                                                                                                                                               Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                               Q9TRU6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..
No.
                                                                                                                                                                                                                 ..
0
                                                                                                                                                                                                                                                                                                                                                                                      RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0912P3
ID 099
AC 099
DT 01
                                                                                                                                                                                                                                                                                                                                                                                                      O9TRU6
           ð
                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                 ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
```

Length: Matches:

2.21e+05

```
Townsend T.M., Larson A.L.; "Molecular Phylogenetics and Mitochondrial Genomic Evolution in the Chamaeleonidae (Reptilia, Squamata)."; submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AF448727; AAL90463.1;
                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Iguania; Acrodonta; Chamaeleonidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5E218E2733641767 CRC64;
00000
                                                                                                                                                                                                                                                                                       l, Last sequence update)
l, Last annotation update)
                               Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                           10 AA
                                                                                                                                                                                                                                                                                                     Cytochrome c oxidase subunit I (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps:
                                                                                                                                                                                                                                                        QBSHP0;
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last seq
01-JUN-2002 (TrEMBLrel. 21, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (1-10)
                                                                                                              (1-10)
                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-824-647-16 (1-2095) x Q8SHP0
                                                                                                              US-09-824-647-16 (1-2095) x Q9T2P3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.21e+05
5.00
100.00%
100.00%
0.72%
                                                                                                                                            890 GCTATACCTGCTGCC 904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NON_TER 10 10
SEQUENCE 10 AA; 1303 MW;
                                                                                                                                                                                                                                                                                                                                                   Bradypodion adolfifriderici.
Mitochondrion.
              5.00
100.008
1.00.008
0.728
                                                                                                                                                              1 AlaileProAlaAla 5
                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=179885;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A
```

```
879 CTGCCCAGATGGCTA 893
                              ٣
                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                         3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NON TER
                                                                                                                                                                                                                                                                                              NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q8SHK1;
                                                                                    08SHLO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08SHK1
                                                                         OBSHLO
                                                     RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S
                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Townsend T.M., Larson A.L.; "Molecular Phylogenetics and Mitochondrial Genomic Evolution in the Chamaeleonidae (Reptilia, Squamata)."; Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases. EMBL, AF448736; AAL90490.1;
                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Iguania; Acrodonta; Chamaeleonidae; Calumma
NCBL_TaxID=179899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mitochondrion.
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Iguania; Acrodonta; Chamaeleonidae; Calumma
NCBI_TaxID=179902;
                                                                                                                                                                                   the
                                                                                                                                                                       Townsend T.M., Larson A.L.;
"Molecular Phylogenetics and Mitochondrial Genomic Evolution in Chamaeleonidae (Replilia, Squamata).";
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF448733; AAL90481.1;
Mitochondrion.

NOV-FRR
                                                                                                                                                                                                                                                    CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5E218E2733641767 CRC64;
                                                                                                                                                                                                                                                                                    00000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90000
                                        Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                    5E218E2733641767
                     10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                10 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2002 (TIEMBLRE). 21, Last sequence of JUN-2002 (TIEMBLRE). 21, Last annotation Cytochrome c oxidase subunit I (Fragment).
                                                                          Cytochrome c oxidase subunit I (Fragment).
                                                                                                                                                                                                                                                                                                                                         Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-824-647-16 (1-2095) x Q8SHL3 (1-10)
                                                                                                                                                                                                                                                                                                                                                              (1-10)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                     PRT;
                                                                                                                                                                                                                                                                                                                                                             US-09-824-647-16 (1-2095) x Q8SHM2
                                                                                                                                                                                                                                                                                                                                                                                CTGCCCAGATGGCTA 893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.21e+05
5.00
100.00%
100.00%
0.72%
                                                                                                                                                                                                                                         10
1303 MW;
                                                                                                                                                                                                                                                                                 2.21e+05
5.00
100.00%
100.00%
0.72%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NON_TER 10 10
SEQUENCE 10 AA; 1303 MW;
                                        01-JUN-2002 (TrEMBLrel. 21, 01-JUN-2002 (TrEMBLrel. 21, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                Calumma boettgeri.
                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                  SEQUENCE 10 AA;
                                                                                                                                                                                                                                                                                                                   Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Calumma furcifer.
                                                                                                                                                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tochondrion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity
                                                                                                         Mitochondrion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                        Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                   879
                                                                                                                                                                                                                                                                                                                                                                                                                                                           OBSHL3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q8SHL3
                     Q8SHM2
                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 10
RESULT 9
Q8SHM2
                                                                                                                                                                                                                                                                                                                                                                                                                                      Q8SHL3
                                                                                                                                                                                                                                                                                                                                                                                                                                                           οy
```

```
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Iguania; Acrodonta; Chamaeleonidae; Calumma.
NCBI_FaxID=179905;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Townsend T.M., Larson A.L.;
"Molecular Phylogenetics and Mitochondrial Genomic Evolution in the Chamaeleonidae (Reptilia, Squamata).";
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF448740; AAL90502.1;
                                                                                                                                                                                                                                                                                                                                       Townsend T.M., Jarson A.L.;
"Molecular Phylogehetics and Mitochondrial Genomic Evolution in the Chamaeleonidae (Reptilla, Squamata).";
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF448737; AAL90493.1;
                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Iguania; Acrodonta; Chamaeleonidae; Calumma.
NCBL_TaxID=179903;
                                                                                 41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5E218E2733641767 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5E218E2733641767 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10
5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   00000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TrEMBLrel. 21, Created)
(TrEMBLrel. 21, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                       10 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cytochrome c oxidase subunit I (Fragment).
                                                                                                                                                                             Cytochrome c oxidase subunit I (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-824-647-16 (1-2095) x Q8SHLO (1-10)
                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 AA; 1303 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.21e+05
5.00
100.00%
100.00%
0.72%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             879 CIGCCCAGAIGGCIA 893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10
1303 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2.21e+05
5.00
100.00%
                                                                                                                         01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
LeuProArgTrpLeu 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                         PRELIMINARY;
                                                                                                                                                                                                                    Calumma gastrotaenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 AA;
                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Calumma nasuta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mitochondrion.
                                                                                                                                                                                                                                       Mitochondrion
                                                                                                                                                                                                                                                                                                                                                                                                                                           Mitochondrion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2002
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2002
```

```
Viruses; SSRNA positive-strand viruses, no DNA stage; Flaviviridae; GBV-C/HGV group.
NCBI_TaxID=45255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
GBV-C/HGV group.
NCBL_TaxID=45255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wong J., Chan S.H., Ren E.C.;
Wong J., Chan S.H., Ren E.C.;
"High isolates from Singapore: Evidence for novel Asian variants.";
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF078058; AAC32365.1;
                                                                                                                                                                                                                                                                                                                                                                                              Wong S.B.J., Chan S.H., Ren E.C.;
"Diversity of GB virus C/hepatitis G virus isolates in Singapore: predominance of group 2a and the Asian group 3 variant.";
J. Med. Virol. 58:146-153(1999).
EMBL; AF078055, AAC3262.1;
NON_TER
                                                                                              :47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64FE2E672DC5A774 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  623E3E272DC5A774 CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             00000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                         Created) () Last sequence update) Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative:
Mismatches:
Indels:
          Conservative:
Mismatches:
                                                                                                                                                                                               10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
Matches:
                                       Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (1-10)
                                                                                 US-09-824-647-16 (1-2095) x 070580 (1-10)
                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                    STRAIN-SG3322;
MEDLINE-99266893; PubMed-10335862;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-824-647-16 (1-2095) x 090346
                                                                                                            1466 GCTACACCTGCAACG 1480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10
1071 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.21e+05
5.00
100.00%
100.00%
0.73%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         341 CGCCCGTCTGCACTG 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 AA; 1101 MW;
                                                                                                                                                                                                                         01-NOV-1998 (TrEMBLrel. 08, 01-NOV-1998 (TrEMBLrel. 08, 01-DEC-2001 (TrEMBLrel. 19, Polyprotein (Fragment). Hepatitis G virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1998 (TrEMBLrel. 08, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                           6 AlaThrProAlaThr 10
          100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 ArgProSerAlaLeu 7
                                       0.728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1998 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polyprotein (Fragment)
Hepatitis G virus.
                                                                                                                                                                                                                                                                                                                                                        SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
       Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-SG3332;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Aliqnment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       090347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           090347
                                                                                                                                                                                               090346
                                                                                                                                                                                                                 090346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 16
                                                                                                                                                                    RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 090347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
Sowden J., Smith H., Morrison K., Edwards Y.;
Sowden J., Smith H., Morrison K., Edwards Y.;
Sequence comparisons and functional studies of the proximal promoter of the carbonic anhydrase 3 (CA3) gene.";
Gene 214:157-165(1999).
EMBL; AJ006474; CAA07057.1; -.
MGD; MGI:1351477; Cars.
                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MN-2002 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
S3 peptide (Fragment)
Glycine max (Soybean).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudlcotyledons; core eudlcots; Rosidae;
eurosids I; Fabales; Fabaceae; Papillionoideae; Phaseoleae; Glycine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 AA; .1105 MW; 56F7FE71ADC37B13 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10
                                                                                                                                                                                                                                                                                                                                                                                                                            975 MW; 3C733271A879D1B7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , Last sequence update)
 000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . 10 AA
                                                                                                                                                                      10 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
                           Gaps:
                                                      US-09-824-647-16 (1-2095) x Q8SHK1 (1-10)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-824-647-16 (1-2095) x Q9S905 (1-10)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last ann
Carbonic anhydrase III (Fragment).
                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                       MEDLINE-9223221; PubMed-1368037;
                                                                                                                                                                                                                                                                                                                                                                       Hirano H., Kagawa H., Okubo K.;
Phytochemistry 31:731-735(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1824 GGGACCCCACTCGGA 1838
                                                                                  879 CTGCCCAGATGGCTA 893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.21e+05
5.00
100.008
100.008
0.728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.21e+05
Best Local Similarity: 100.00%
Query Match: 0.72%
                                                                                                            3 LeuProArgTrpLeu 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MGL:88270; Car3.
TER 10 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAR3 OR CARS OR CA3
                                                                                                                                                                                                                                                                                                                                                                                                                            10 AA;
                                                                                                                                                                                                                                                                                                                                                                       Hirano H., Kagawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                               NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     070580
                                                                                                                                                                    098905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No.:
                                                                                                                                        RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         070580
                                                                                                                                                         06860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                            g
```

```
Alignment Scores:
                                                                          Alignment Scores:
NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                             Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                065901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           065901
                                                                                                                                                                                                                                                                                                                                                                                         015997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..
ON
                                                                                                 ..
Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RARA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 20
                                                                                                                                                                                                                                                                                                                                                     RESULT 19
                                                                                                                                                                                                                                                                                                                                                                       015997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             065901
                                                                                               Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RXX OCC OCS NEET TO THE REAL PROPERTY OF THE REAL P
                                                                                                                                                                                                                                                                                                                                                                                                              Auf der Maur A., Belser T., Wang T., Gunes C., Lichtlen P.,
Georgiev O., Schaffner W.;
"Characterization of the mouse gene for the heavy metal-responsive
transcription factor MTF-1.";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ251881; CAB71327.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
Heavy metal-responsive transcription factor (Fragment).
  000020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CF001CE4DDD86772 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0000
                                                                                                                                                                                                                                                                                                                               01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MTG8 related protein (Fragment)
                                      Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 AA
                                                                                                                                                                                                                                                                                             11 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
  Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TrEMBLrel. 15, Created)
(TrEMBLrel. 15, Last sequ
(TrEMBLrel. 15, Last anno
                                                                                                                                   (1-10)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (1-11)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=99009318; PubMed=9790752;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-824-647-16 (1-2095) x 060614
                                                                                                                                     US-09-824-647-16 (1-2095) x 090347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         920 CCTGGGGCTGCTGCC 934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.19e+05
5.00
100.00%
100.00%
0.72%
                                                                                                                                                                         341 CGCCCGTCTGCACTG 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA; 1047 MW;
  2,21e+05
                                  100.00%
100.00%
0.73%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F ProGlyAlaAlaAla 9
                                                                                                                                                                                              ArgProSerAlaLeu 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                          PRELIMINARY;
                    00.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-BRAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-0CT-2000
01-0CT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09NY38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09NY38
  No.:
                                                                                                                                                                                                                                                                                             060614
                                                                                                                                                                                                                                                                                                                                                                                                              MTGR1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 18
                                                                                                                                                                                                                                                      RESULT 17
                                                                                                                                                                                                                                                                      Score:
  Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
```

```
SEQUENCE FROM N.A.
MEDLINE-93222087; bubmed-7682097;
Dong S., Geng J.P., Tong J.H., W., Cai J.R., Sun G.L., Chen S.R.,
Mang Z.Y., Larsen C.J., Barger R., et al;
Breakpoint clusters of the PML gene in acute promyelocytic leukemia:
primary structure of the reciprocal products of the PML-RARA gene in a patient with t(15:17).";
Genes Chromosomes Cancer 6:133-139(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Leavenworthia crassa.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Leavenworthia.
NCBI_TaxID-70805;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
               11
1099 MW; A8653693773772C6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 AA; 1277 MW; 33C70E22CDDDC417 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0000
                                                                                       150000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                   Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                  11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ş
                                                                                                                                                                                 Gaps:
                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-824-647-16 (1-2095) x Q15997 (1-11)
                                                                                                                                                                                                                 US-09-824-647-16 (1-2095) x Q9NY38 (1-11)
                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Phosphoglucose isomerase (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1461 CGGCCAGCAGTGCTG 1447
                                                                                                                                                                                                                                                     2.19e+05
5.00
100.00%
100.00%
0.73%
                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1996 (TrEMBLE). 01,
01-NOV-1996 (TrEMBLE). 01,
01-DEC-2001 (TrEMBLE). 19,
                                                                                   2.19e+05
5.00
100.00%
100.00%
0.73%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 ArgAlaAlaValLeu 9
                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            RARA protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
1
11
11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity:
                                                                                                                         Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity
```

```
Salah Bey K., Doumith M., Michel J.M., Haydock S., Cortes J.,
Leadiay P.F., Raynal M.C.;
"Targetted gene inactivation for the elucidation of deoxysugar
blosynthesis in the erythromycin producer saccharopolyspora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          erythraea.";
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
EMBL: Y14332; CAA74712.1; ...
SEQUENCE FROM N.A.
STRAIN-CV. CR8919/CR15, AND CV. CR8919/CD6;
Liu F., Charlesworth D., Kreitman M.;
Submitted (WAR-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF054493; AAC19033.1; -.
EMBL; AF054492; AAC19032.1; -.
                                                                                                                                                                                                                                                                                                                                                Saccharopolyspora erythraea (Streptomyces erythraeus).
Bacteria; Firmicutes; Actinobacteriae; Actinomycetales; Actinomycetales; Pseudonocardineae; Saccharopolyspora.
NCBI_TaxID=1836;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE 12 AA; 1282 MW; D4BA3E57E277337D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                         5026B3A4BDD87337 CRC64;
                                                                                                                                                                                                                                                                                                               01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
                                                                                                                         0000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                           Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12 AA
                                                                                                                                                                                                                                                                                 Ź
                                                                                                                       Length:
Matches:
                                                                                                                                                                           Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-824-647-16 (1-2095) x O54226 (1-12)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                              US-09-824-647-16 (1-2095) x 065901 (1-11)
                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                   Polyketide synthase (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1881 TGGTTAGGGGGAGGT 1867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TrEMBLrel. 17, C
(TrEMBLrel. 17, I
(TrEMBLrel. 17, I
                                                                                                                                                                                                                   1766 CTCAAAGGGGCGTCC 1752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.17e+05
5.00
100.00%
100.00%
0.73%
                                                                      1 1
11 11
11 AA; 1208 MW;
                                                                                                                       2.19e+05
5.00
100.00%
100.00%
0.73%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-1998 (TrEMBLrel. 06,
                                                                                                                                                                                                                              4 LeuLysGlyAlaSer 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                            Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-NRRL2338;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      O9BZ49;
01-JUN-2001 (
01-JUN-2001 (
01-JUN-2001 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
                                                                                                               Alignment Scores:
                                                               Isomerase.
                                                                                  NON_TER
SEQUENCE
                                                                       NON_TER
                                                                                                                                                                 Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09BZ49
                                                                                                                                                                                                                                                                                 054226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..
S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 22
                                                                                                                                                                                                                                                            RESULT 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score:
                                                                                                                                                                                                                                                                        054226
                                                                                                                          Pred.
                                                                                                                                                                                                                                                                                 44446
                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                        g
```

```
Mihovilovic M., Mai Y., Herbstreith M., Rubboll F., Tarroni P., Clementi F., Roses A.D.; "Splicing of an anti-sense Alu sequence generates a coding sequence variant for the alpha-3 subunit of a neuronal acetylcholine,
Glycophorin C (Fragment).

Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                          "The association of the glycophorin C exon 3 deletion with ovalocytosis and malaria susceptibility in the Wosera, Papua New
                                                                                                                         Patel S.S., Mehlotra R.K., Kastens W., Mgone C.S., Kazura Jaw., Zimmerman P.A.;
                                                                                                                                                                                                          Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF342984; AAK01459.1; -
NON_TER 1 1 1 1 1 NON_TER 1 2 12 343; 1361 MW; 2A07044DB8377378 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1282 MW; 8B0B423A6FC1B2D5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               00002
                                                                                                                                                                                                                                                                                                                                            0000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Blochem. Blophys. Res. Commun. 197:137-144(1993)
EMBL; L18973; AAA86792.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12 AA
                                                                                                                                                                                                                                                                                                                                                                                                                  Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-824-647-16 (1-2095) x Q13695 (1-12)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-824-647-16 (1-2095) x Q9BZ49 (1-12)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Acetylcholine receptor (Fragment). Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=THYMUS;
MEDLINE-94071933; PubMed-8250918;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1904 CAGAATGGGGTCCAG 1890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.17e+05
5.00
                                                                                                                                                                                                                                                             12 12
12 AA; 1361 MW;
                                                                                                                                                                                                                                                                                                                                          2.17e+05
5.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.00%
.100.00%
0.73%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity;
                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
                                                                                                                                                                                                                                                                                                                               Aliqnment Scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           receptor."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   013695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         013695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ::
Q
                                                                                                                                                                                                                                                                                                                                                  Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 23
013695
```

```
Eukaryota; Viridiplantae.
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Fabales; Fabaceae; Papliionoideae; Genisteae; Lupinus.
NCBI_TaxID=3873;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bublot M., Lomonte P., Lequarre A.-S., Albrecht J.-C., Nicholas J., Fleckenstein B., Pastoret P.-P., Thiry E.; Genetic relationships between bovine herpesvirus 4 and the "Genetic relationships between bovine herpesvirus 4 and the virology 190:654-665(1992).

EMBL, M90772; AAA46019.1; -...

NON_TER 12 12 12.

SEQUENCE 12 AA: 1338 MW; 4B800FF17BCDDDD7 CRC64;
                                                                                   鷮.
                                                                                                                                                                                                                                       DECLEMENT ELVAR ALT.

STRAIN-CY. Grabowska B., Kisiel A., Dlugaszewska B. Nimmagadda G.;

"ENDOBOUR from Lupihus luteus.";

Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AF352375; AAK51422.1;

EMBL; AF352372; AAK51419.1;

SEQUENCE 12 AA; 1403 MW; 283958AE7CB326C3 CRC64;
                                                                                       Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RNA stage; Herpesviridae;
                                                                                                                                                                                                                                                                                                                                                                            0000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Herpesvirus saimiri gene 7 homologue (Fragment).
Viruses; dSDNA viruses, no RNA stage; Herpesviridae Gammaherpesvirinae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             00027
                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches:
Indels:
                                                                12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-824-647-16 (1-2095) x Q93WF2 (1-12)
                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=V.TEST;
MEDLINE-92391082; PubMed=1325698;
                                                                                                                                                     Lupinus luteus (Yellow lupine)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1601 TTATCATGCCAGAAG 1587
                                                                                     01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001: (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                        2.17e+05
5.00
100.00%
100.00%
0.73%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2.17e+05
5.00
100.00%
100.00%
0.72%
               S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LeuSerTrpGlnLys 7
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID-10385;
                                                                                                                             Early nodulin.
                                                                                                                                                                                                                                                                                                                                                            Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
                                                                            093WF2;
                                                                                                                                          ENOD40B
                                                               Q93WF2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                069232
                                     RESULT 26
Q93WF2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
                                                                                                                                                                                                                                                                                                                                                                                      Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   069232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score:
```

· (5)...

```
"Additional organizational features of the murine gamma-glutamyl hydrolase gene. Two remotely situated exons within the complement C3 gene locus encode an alternate 5' end and proximal ORF under the control of a bidirectional promoter.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ha-Lee Y.M., Lee J., Pyun H., Kim Y., Sohn J., Cho Y.J., Kim Y.; Sequence variation of Hepatitis B virus promoter regions in Pesistently infected patients."; Arch. virol. 146:279-292(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.NCBI_TaxID=10407;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE 13 AA; 1434 MW; 99C40D3FFD0FDEBE CRC64;
                                                                                                                                                                                                                           7EBA4BEA194E2734 CRC64
                                                                                                                                                                                                                                                                                                              000027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                               Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13 AA
                                                                                                                                                                                                                                                                                                           Length: Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (1-13)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-824-647-16 (1-2095) x Q9EIV4 (1-13)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=2F-1;
MEDLINE=21213459; PubMed=11315638;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arch. Virol. 146:279-292(2001).
EMBL; AF276519; AGC3986.1; -.
InterPro; IPR000295; TransactX.
Pfam; PF00739; X; 1.
                                                                                     control of a bidirectional pror
Gene 268:183-194(2001).
EMBL: AR367375; AAK58013.1; -.
Hydrolase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JS-09-824-647-16 (1-2095) x Q91XP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13
1544 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    447 CTCCTGGGGGTGCTG 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.15e+05
5.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16,
19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.15e+05
                                                                                                                                                                                                                                                                                                                                     5.00
100.00%
100.00%
0.72%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.00%
100.00%
0.72%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09EIV3;
01-MAR-2001 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
X protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X protein (Fragment).
                                                                                                                                                                                                 13
.13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
                                                                                                                                                                                                                                                                                   Alignment Scores:
                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9E1V4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9E1V3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09E1V4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9E1V3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09E1V4
  RATE RATE SO STATE SO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8855588
8655588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-129/SVU; TISSUE-SPLEEN;
MEDLINE-98434456; PubMed-9756990;
ESAKI T., ROY K., TAO R., Gallvan J., Sirotnak F.M.;
"Cloning of mouse gamma-glutamyl hydrolase in the form of two cDNA variants with different 5' ends and encoding alternate leader peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bublot M., Lomonte P., Lequarre A.-S., Albrecht J.-C., Nicholas J., Pleckenstein B., Pastoret P.-P., Thiry B.;
"Genetic relationships between bovine herpesvirus 4 and the gammaherpesviruss Epstein-Barr virus and herpesvirus saimiri.";
Wirology 190:654-665(1992).
WHEL; M90772; ARA46019.1;
NON.TER 12 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                               Boyine herpesvirus 4.
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
                                                                                                                                                                                                                                                                                                                                                               01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (Fremmer)
01-DEC-2001 (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE 12 AA; 1338 MW; 4B800FF17BCDDDD7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Gamma-glutamyl hydrolase variant II (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13 AA.
                                                                                                                                                                                                                                                                                   12 AA.
  Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-129/SVU; TISSUE-SPLEEN;
MEDLINE-21261955; Pubmed-11368914;
Masumoto N., Esaki T., Sirotnak F.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last anno
                                                    US-09-824-647-16 (1-2095) x Q69232 (1-12)
                                                                                                                                                                                                                                                                                                                                  (TrEMBLrel. 01, Created)
(TrEMBLrel. 01, Last seq
(TrEMBLrel. 19, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-824-647-16 (1-2095) x Q69232 (1-12)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-92391082; PubMed-1325698;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1158 CGTGAGTTGGCAGCA 1144
                                                                                                         899 GCTGCCGTCTACAGT 913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.17e+05
5.00
100.00%
100.00%
                                                                                                                                         6 AlaAlaValTyrSer 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 ArgGluLeuAlaAla 7
                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sene 219:37-44(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gammaherpesvirinae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10385;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-V. TEST;
                                                                                                                                                                                                                                                                                                                                  01-NOV-1996 (
01-NOV-1996 (
01-DEC-2001 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seduences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match:
DB:
                                                                                                                                                                                                                                                                             069232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         091XP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 29
                                                                                                                                                                                                                      RESULT 28
                                                                                                                                                                 윰
                                                                                                                                                                                                                                                                                THE SECOND SECON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
```

13 AA

PRT;

PRELIMINARY;

```
US-09-824-647-16 (1-2095) x Q9E1U9 (1-13)
                                                                                                                                                                                                                                                                                                                                                    Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9E1U9
                                                                                                                                                                                                                                                                                                        Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 34
09E1U9
                                                                                                                                                                                                                                                                                                                   Score:
                                                                                                                                                                                                                                                                                                                                                                                                                à
                                                       STRAIN-2F-2;
MEDLINE-21213459; PubMed=11315638;
MEDLINE-21213459; PubMed=11315638;
MEDLINE-21213459; PubMed=11315638;

"Sequence variation of Hepatitis B virus promoter regions in persistently infected patients.";
Arch. Virol. 146:279-292(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ha-Lee Y.M., Lee J., Pyun H., Kim Y., Sohn J., Cho Y.J., Kim Y.; "Sequence variation of Hepatitis B virus promoter regions in persistently infected patients.", Arch. Virol. 146:279-292(2001). EMBL; AR276521; AR29888.1; - InterPro; IPR000236; TransactX.
Hepatitis B virus.
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
NCBL_raxID=10407;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE 13 AA; 1434 MW; 99C40D3FFD0FDEBE CRC64;
                                                                                                                                                                               SEQUENCE 13 AA; 1434 MW; 99C40D3FFD0FDEBE CRC64;
                                                                                                                                                                                                                   0000
                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                     13 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels:
                                                                                                                                                                                                                                                                                                      US-09-824-647-16 (1-2095) x Q9E1V3 (1-13)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-824-647-16 (1-2095) x Q9E1V2 (1-13)
                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-21213459; PubMed-11315638;
                                                                                                                     Arch. Virol. 146:279-292(2001).
EMBL; AF2/6520; AAG29987.1; -.
InterPro; IPR000236; TransactX.
Pfam; PF00739; X; 1.
NON_TER
                                                                                                                                                                                                                                                                                                                           1487 CTCGATCCTGCGAGA 1501
                                                                                                                                                                                                                 2.15e+05
5.00
100.00%
100.00%
0.72%
                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.15e+05
5.00
100.00%
100.00%
0.72%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13
                                                                                                                                                                                                                                                                                                                                                                                                                                                              X protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hepatitis B virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                           Percent Similarity:
Best Local Similarity:
                         NCBI_TaxID=10407;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alignment Scores:
                                                                                                                                                                                                        Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-2F-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6
                                                                                                                                                                                                                                                                 Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                               09E1V2;
                                                                                                                                                                                                                                                                                                                                                                                                  09E1V2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 33
Q9E1V0
                                                                                                                                                                                                                                                                                                                                                                            RESULT 32
Q9E1V2
                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                     a
```

```
STRAIN=2F-6;
MEDINE=21213459; PubMed=11315638;
MEDINE=21213459; PubMed=11315638;
Ha-Lee Y.M., Lee J., Pyun H., Kim Y., Sohn J., Cho Y.J., Kim Y.;
"Sequence variation of Hepatitis B virus promoter regions in persistently infected patients.";
Arch. Virol. 146:279-292(2001).
                                                                                                                                                                                                          STRAIN-2F-5;
MEDLINE-21213459; PubMed-11315638;
MEDLINE-21213459; PubMed-11315638;
MEDLINE-21213459; PubMed-11315638;

Sacuence T. M., Lee J., Pyun H., Kim Y., Sohn J., Cho Y.J., Kim Y., Sequence variation of Hepatitis B virus promoter regions in persistently infected patients.";

Persistently infected patients.";

Arch. Virol. 146:279-292(2001).
                                                                                                                Hepatitis B virus.
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
NCBI_TaxID=10407;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus
NCBI_TaxID=10407;
                                                                                                                                                                                                                                                                                                                                                                                                   NON_TER 13 AA; 1434 MW; 99C40D3FFD0FDEBE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE 13 AA; 1434 MW; 99C40D3FFD0FDEBE CRC64;
                  Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09E1U9;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  000023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-824-647-16 (1-2095) x Q9EIVO (1-13)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                             Arch. Virol. 146:279-292(2001).
EMBL; AF2/6523; AAG29990.1; -
Interpro; IPR000236; TransactX.
Pfam; PF00739; X; 1.
NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF276524; AAG29991.1; -...
InterPro; IPR000236; TransactX.
Pfam; PF00739; X; 1. 13
NON-TER. 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1487 CTCGATCCTGCGAGA 1501
09E1V0;
01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2.15e+05
5.00
100.00%
100.00%
0.72%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.15e+05
5.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 LeuAspProAlaArg 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.008
100.008
0.728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            X protein (Fragment).
                                                                            X protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hepatitis B virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
```

3

0000

us-09-824-647-16.lim.rspt

```
Ha-Lee Y.M., Lee J., Pyun H., Kim Y., Sohn J., Cho Y.J., Kim Y.; "Sequence variation of Hepatitis B virus promoter regions in persistently infected patients."; Arch. Virol. 146:279-222(2001).

EMBL; AF276529; AAG29996.1;
                                                                                                                                                                                                                                                                                                                                                                              Ha-Lee Y.M., Lee J., Pyun H., Kim Y., Sohn J., Cho Y.J., Kim Y.; Sequence variatation of Hepatitis B virus promoter regions in persistently infected partients "; Arch. Virol. 146:279-292(2001).
BARDL, AFZ76528, AAG29995.1; -. InterPro; IPR000236; Transactx.
Pfam; PF00739; X; I.
                                                                                                                                                                                                                                                                                  Hepatitis B virus.
Viruses; Retroid Viruses; Hepadnaviridae; Orthohepadnavirus.
NCBI_TaxID=10407;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
NCBI_TaxID=10407;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE 13 AA; 1434 MW; 99C40D3FFD0FDEBE CRC64;
                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
        Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                      13 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13 AA
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last anno
                                                                            US-09-824-647-16 (1-2095) x Q9E1U6 (1-13)
                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-824-647-16 (1-2095) x Q9EIU5 (1-13)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                         PRT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=21213459; PubMed=11315638;
                                                                                                                                                                                                                                                                                                                                                      STRAIN=4F-7;
MEDLINE=21213459; PubMed=11315638;
                                                                                                     1487 CTCGATCCTGCGAGA 1501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.15e+05
5.00
100.00%
100.00%
0.72%
                                                                                                                                                                                                                             01-MAR-2001 (TrEMBLrel. 16, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TrEMBLrel. 16, (TrEMBLrel. 19,
                                                                                                                                                                                                               01-MAR-2001 (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 LeuAspProAlaArg 13
           100.00%
100.00%
                                      0.72%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                       PRELIMINARY;
5.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein (Fragment).
                                                                                                                                                                                                                                                          X protein (Fragment).
  Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hepatitis B virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=4F-6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09E1U4
09E1U4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match:
                                                                                                                                                                                                    Q9E1U5;
                                                                                                                                                                                      Q9E1U5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 38
                                                                                                                                                           RESULT 37
                                                                                                                                                                           Q9E1U5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09E1U4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred.
                                                                                                                                                                                                                             STRAIN-4F-9;
MDEL/INE-21213459; PubMed-11315638;
Ha-Lee Y.M., Lee J., Pyun H., Kim Y., Sohn J., Cho Y.J., Kim Y.;
Ha-Lee Y.M., Lee J., Pyun H., Kim Y., Sohn J., Cho Y.J., Kim Y.;
Sequence variation of Hepatitis B virus promoter regions in persistently infected patients.";
Arch. Virol 16-279-292(2001).
EMBL: AR27657; AAG29941:---
InterPro; IRR000236; TransactX.
                                                                                                                                                                                                                                                                                  Sohn J., Cho Y.J., Kim Y.;
                                                                                                                                                                                                                                                              MEDIARS—21213459; PubMed=11315638;
Ha-Lee Y.M., Lee J., Pyun H., Kim Y., Sohn J., Cho Y.J., Kim "Sequence variation of Hepatitis B virus promoter regions in persistently infected patients.";
Arch. Virol. 146:279-292(2001).
EMBL; AF276525; AAG29992.1; -.
InterPro; IPR000236; TransactX.
Pfam, PF00739; X; 1.
NON_TER 13 13
SEQUENCE 13 AA; 1434 MW; 99C40D3FFD0FDEBE CRC64;
                                                                                                                                                                                Hepatitis B virus.
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
NCBL_TaxID=10407;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hepatitis B virus.
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
NCBI_TaxID=10407;
                                                                                                                                                                                                                                                                                                                                                                                      13 AA; '1434 MW; 99C40D3FFD0FDEBE CRC64;
                                                                                                            01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE 13 AA; 1434 MW; 99C40D3FFD0FDEBE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
Conservative:
Mismatches:
                                                                                         13 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (1-13)
                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-824-647-16 (1-2095) x Q9E1U8
        1487 CTCGATCCTGCGAGA 1501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1487 CTCGATCCTGCGAGA 1501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TrEMBLrel. 16, C
(TrEMBLrel. 16, I
(TrEMBLrel. 19, I
                                                                                                                                                                                                                                                                                                                                                                                                                                  2.15e+05
5.00
                      9 LeuAspProAlaArg 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.15e+05
                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.008
100.008
0.728
                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00739; X; 1.
                                                                                                                                                          protein (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2001 (
01-MAR-2001 (
01-DEC-2001 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
                                                                                                                                                                                                                                                     STRAIN-2F-7
                                                                                                     Q9E1U8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09E1U6;
                                                                                      Q9E1U8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09E1U6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 36
Q9E1U6
                                                           RESULT 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                Score:
                                                                                         ò
```

Query Match:

Pred. No.:

8 2 E 8

Score:

Q9E1U3;

09E1U3

RESULT 39

å 용 **39E1U3**

```
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-4F-3;
MEDLINE-21213459; PubMed-11315638;
                                                                                                                                                                                                                                                                                                            1487 CTCGATCCTGCGAGA 1501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1487 CTCGATCCTGCGAGA 1501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2.15e+05
5.00
100.00%
100.00%
0.72%
                                                                                                                                                                                   2.15e+05
5.00
100.00%
100.00%
0.72%
                                                                                                                                                                                                                                                                                                                                                                                                              Q9E101;
01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                           9 LeudspProblaArg 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 LeuAspProAlaArg 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                              13
                                                                                                              Pfam; PF00739; X; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X protein (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00739; X; 1
                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hepatitis B virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                              13
                                                                                                                                                                      Alignment Scores:;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              O9E1U0;
01-MAR-2001 (
01-MAR-2001 (
01-DEC-2001 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alignment Scores:
                                                                                                                              NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9E1U0
                                                                                                                                                                                                                                                                                                                                                                                                 09E1U1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..
Q
                                                                                                                                                                                    Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 42
Q9E1U0
                                                                                                                                                                                                                                                                                                                                                                      RESULT 41
                                                                                                                                                                                                                                                                                                                                                                                     09E1U1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred.
    Ha-Lee Y.M., Lee J., Pyun H., Kim Y., Sohn J., Cho Y.J., Kim Y.; "Sequence variation of Hepatitis B virus promoter regions in persistently infected patients."; Persistently infected patients."; EMBL, Virol. 146:279-295(2001).

EMBL, AP276530; AAC29997.1; -.. InterPro; IPR000236; TransactX.
                                                                                                                                                                                                                                                                                                                                                                                                    Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
NCBI_TaxID=10407;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VIruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus NCBI_TaxID=10407;
                              NON_TER 13 13 SEQUENCE 13 AA; 1434 MW; 99C40D3FFD0FDEBE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE 13 AA; 1434 MW; 99C40D3FFD0FDEBE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0000213
                                                                                       0000
                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                   Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                     13 AA.
                                                                                                                                                          Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-824-647-16 (1-2095) x Q9EIU3 (1-13)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                      US-09-824-647-16 (1-2095) x Q9E1U4 (1-13)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-21213459; PubMed-11315638;
InterPro; IPR000236; TransactX. Pfam; PF00739; X; 1.
                                                                                                                                                                                                               1487 CTCGATCCTGCGAGA 1501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1487 CTCGATCCTGCGAGA 1501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.15e+05
5.00
100.00%
100.00%
0.72%
                                                                                                                                                                                                                                                                                                                           01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                    2.15e+05
5.00
100.00%
100.00%
0.72%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 LeuAspProAlaArg 13
                                                                                                                                                                                                                                          9 LeuAspProAlaArg 13
                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                      X protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00739; X; 1
                                                                                                                                                                                                                                                                                                                                                                                                  depatitis B virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
                                                                                                              Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hepatitis B virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
                                                                       Alignment Scores:
```

NON TER

Query Match:

Pred. No.:

Q9E1U2

RESULT 40
09ELU2
00ELU3
AC 09ELU
DT 01-MA
DT 01-MA
DT 01-DE X pro
GN X pro
GN Hepat
OC VITUS
OX NCBIRP SEQUE

```
STRAIN-4F-4;

MEDLINE-21133459; PubMed-11315638;

Ha-Lee Y.M., Lee J., Pyun H., Kim Y., Sohn J., Cho Y.J., Kim Y.;

"Sequence variation of Hepatitis B virus promoter regions in persistently infected patients.";

Arch. Virol. 146.279-99.2(2001).

EMBL; AF276531; AG299981.;

InterPro. IPR000236; TransactX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ha-Lee Y.M., Lee J., Pyun H., Kim Y., Sohn J., Cho Y.J., Kim Y., "Sequence variation of Hepatitis B virus promoter regions in persistently infected patients.";
Arch. Virol. 146.279-292 (2001).
EMBL; AF276532; AG299999.1; -...
InterPro; IPR000236; TransactX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
NCBL_raxID-10407;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE 13 AA; 1434 MW; 99C40D3FFD0FDEBE CRC64;
                                                                                                                                                                                                                                                             SEQUENCE 13 AA; 1434 MW; 99C40D3FFD0FDEBE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TrEMBLrel. 16, Created)
(TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-824-647-16 (1-2095) x Q9E1U2 (1-13).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-824-647-16 (1-2095) x Q9EIU1 (1-13)
```

us-09-824-647-16.lim.rspt

```
Query Match:
                                                                            Q9E1T8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   052840;
                                                     09E1TB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           052840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No.:
       RESULT 44
Q9E1T8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     052840
                                                                              DE PACE DE PAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ha-Lee Y.M., Lee J., Pyun H., Kim Y., Sohn J., Cho Y.J., Kim Y., Sequence variation of Hepatitis B virus promoter regions in persistently infected patients.";

Arch. Virol. 146:279-292(2001).
                                                                                                                                                            STRAIN-4F-2;
MEDLINE-21213459; PubMed-11315638;
Ha-Lee Y.M., Lee J., Pyun H., Kim Y., Sohn J., Cho Y.J., Kim "Sequence variation of Hepatitis B virus promoter regions in
                                            Hepatitis B virus.
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
NCBI_TaxID=10407;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hepatitis B virus.
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
NCBL_TaxID=10407;
                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE 13 AA; 1434 MW; 99C40D3FFD0FDEBE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE 13 AA; 1434 MW; 99C40D3FFD0FDEBE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last anno
X protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-824-647-16 (1-2095) x Q9E1U0 (1-13)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-824-647-16 (1-2095) x Q9E1T9 (1-13)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-21213459; PubMed=11315638;
                                                                                                                                                                                                                                                          persistently infected patients.";
Arch. Vitool. 16:179-292(2001).
EMBL; AR77653; AA300000.1;
InterPro; IPR000236; Transactx.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF276534; AAG30001.1; -. InterPro; IPR000236; TransactX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.15e+05
5.00
100.00%
100.00%
0.72%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.15e+05
5.00
100.00%
100.00%
0.72%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                               13
protein (Fragment)
                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00739; X; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00739; X; 1.
                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-4F-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                               NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09E1T9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9E1T9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..
Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09E1T9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sred.
셤
```

```
Ha-Lee Y.M., Lee J., Pyun H., Kim Y., Sohn J., Cho Y.J., Kim Y., Separater and the partitis B virus promoter regions in persistently infected patients.";
Arch. Virol. 146:279-292(2001).
BMBL, ARZ16535, AAG30002.1;
InterPro; IPR35, AAG30002.1;
Pfam: PF00739; X:\l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2001 (TrEMBLrel. 01, Last sequence update)
Homology with C-terminus of other Rhizobium nodB genes.
Rhizobium loti (Mesorhizobium loti).
Bacteria: Proteobacteria: alpha subdivision; Rhizobiaceae group; Phyllobacteriaceae; Mesorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE-97002748; PubMed-8850088;
Scott D.B., Young C.A., Collins-Emerson J.M., Terzaghi B.A.,
Rockman E.S., Lewis P.E., Pankhurst C.E.;
"Novel and complex chromosomal arrangement of Rhizobium loti
nodulation genes.";
                                                                                                                                            Hepatitis B virus.
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
NCBL_TaxID=10407;
                                                                                                                                                                                                                                                                                                                                                                                                                                         NON_TER 13 13 SEQUENCE 13 AA; 1434 MW; 99C40D3FFDOFDEBE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90C26EC32C8F34C5 CRC64;
                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mol. Plant Microbe Interact. 9:187-197(1996).
EMBL; L06241; AAB47352.1; -
SEQUENCE 14 AA; 1600 MW; 90C26EC32C8F34C5
  13 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-824-647-16 (1-2095) x Q9E1T8 (1-13)
  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                   STRAIN=4F-10;
MEDLINE-21213459; Pubmed-11315638;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1487 CTCGATCCTGCGAGA 1501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.15e+05
5.00
100.00%
100.00%
                                       01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 LeuAspProAlaArg 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.14e+05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.728
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                     01-MAR-2001 (TrEMBLrel.
                                                                                                    X protein (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match:
```

US-09-824-647-16 (1-2095) x Q52840 (1-14)

1487 CTCGATCCTGCGAGA 1501

ö g

9 LeuAspProAlaArg 13

Tue Jul 8 07:45:11 2003

501 CTGCTGTCCGCACGG 515

\$ B

5 LeuLeuSerAlaArg 9

Search completed: July 7, 2003, 16:19:29 Job time: 137.5 secs